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**GENE PRODUCTS DIFFERENTIALLY EXPRESSED IN CANCEROUS COLON
CELLS AND THEIR METHODS OF USE**

CROSS-REFERENCE TO RELATED APPLICATIONS

- [0001]** This application claims the benefit of prior U.S. Provisional Application Serial No. 60/270,855, filed February 21, 2001, which application is incorporated herein by reference.

SEQUENCE LISTING

- [0002]** A Sequence Listing is provided as part of this specification on duplicate compact discs, which compact discs named "Copy 1" and "Copy 2", each of which compact discs contain the following file: "SEQLIST.TXT", created February 21, 2002, 800 kilobytes, which are incorporated herein by reference in their entirety.

FIELD OF THE INVENTION

- [0003]** The present invention relates to polynucleotides of human origin and the encoded gene products that are differentially expressed in colon cancer cells.

BACKGROUND OF THE INVENTION

- [0004]** Cancer, like many diseases, is not the result of a single, well-defined cause, but rather can be viewed as several diseases, each caused by different aberrations in informational pathways, that ultimately result in apparently similar pathologic phenotypes. Identification of polynucleotides that correspond to genes that are differentially expressed in cancerous, pre-cancerous, or low metastatic potential cells relative to normal cells of the same tissue type, provides the basis for diagnostic tools, facilitates drug discovery by providing for targets for candidate agents, and further serves to identify therapeutic targets for cancer therapies that are more tailored for the type of cancer to be treated.

[0005] Identification of differentially expressed gene products also furthers the understanding of the progression and nature of complex diseases such as cancer, and is key to identifying the genetic factors that are responsible for the phenotypes associated with development of, for example, the metastatic phenotype. Identification of gene products that are differentially expressed at various stages, and in various types of cancers, can both provide for early diagnostic tests, and further serve as therapeutic targets and the basis for screening assays to identify chemotherapeutic agents that modulate the activity (*e.g.*, expression, biological activity, and the like) of the gene product of the differentially expressed gene.

[0006] Early disease diagnosis, especially in diseases such as cancer, is of central importance to halting disease progression, and reducing morbidity. Analysis of a patient's tumor to identify the gene products that are differentially expressed, and administration of therapeutic agent(s) designed to modulate the activity of those differentially expressed gene products, provides the basis for more specific, rational cancer therapy, which therapy may result in diminished adverse side effects relative to conventional therapies. Furthermore, confirmation that a tumor poses less risk to the patient (*e.g.*, that the tumor is benign) can avoid unnecessary therapies. In short, identification of genes and the encoded gene products that are differentially expressed in cancerous cells can provide the basis of therapeutics, diagnostics, prognostics, therametrics, and the like.

[0007] In exemplary aspects, the invention described herein provides colon cancer diagnostics, prognostics, therametrics, and therapeutics based upon polynucleotides and/or their encoded gene products.

SUMMARY OF THE INVENTION

[0008] The present invention provides methods and compositions useful in detection of cancerous cells, identification of agents that modulate the phenotype of cancerous cells, and identification of therapeutic targets for chemotherapy of cancerous cells. Cancerous colon cells are of particular interest in each of these aspects of the invention. More

specifically, the invention provides polynucleotides, as well as polypeptides encoded thereby, that are differentially expressed in colon cancer cells. These polynucleotides and polypeptides are thus useful in a variety of diagnostic, therapeutic, and drug discovery methods. In some embodiments, a polynucleotide that is differentially expressed in colon cancer cells can be used in diagnostic assays to detect colon cancer cells. In other embodiments, a polynucleotide that is differentially expressed in colon cancer cells, and/or a polypeptide encoded thereby, is itself a target for therapeutic intervention.

[0009] Accordingly, in one aspect the invention provides a method for detecting a cancerous colon cell comprising contacting a sample obtained from a test colon cell with a probe for detection of a gene product of a gene differentially expressed in colon cancer, wherein the gene comprises a sequence selected from the group consisting of SEQ ID NOS: 1-1303, and where contacting is for a time sufficient for binding of the probe to the gene product; and comparing a level of binding of the probe to the sample with a level of probe binding to a control sample obtained from a control colon cell, wherein the control colon cell is of known cancerous state. An increased level of binding of the probe in the test colon cell sample relative to the level of binding in a control sample is indicative of the cancerous state of the test colon cell. In specific embodiments, the probe is a polynucleotide probe and the gene product is nucleic acid. In other specific embodiments, the gene product is a polypeptide. In further embodiments, the gene product or the probe is immobilized on an array.

[0010] In another aspect, the invention provides a method for assessing the cancerous phenotype (*e.g.*, metastasis, aberrant cellular proliferation, and the like) of a colon cell comprising detecting expression of a gene product in a test colon cell sample, wherein the gene comprises a sequence selected from the group consisting of SEQ ID NOS: 1-1303; and comparing a level of expression of the gene product in the test colon cell sample with a level of expression of the gene in a control cell sample. Comparison of the level of expression of the gene in the test cell sample relative to the level of expression in the control cell sample is indicative of the cancerous phenotype of the test cell sample. In specific embodiments, detection of expression of the gene is by detecting a level of an

RNA transcript in the test cell sample. In other specific embodiments detection of expression of the gene is by detecting a level of a polypeptide in a test sample.

[0011] In another aspect, the invention provides a method for suppressing or inhibiting a cancerous phenotype of a cancerous cell, the method comprising introducing into a mammalian cell an antisense polynucleotide for inhibition of expression of a gene comprising a sequence selected from the group consisting of SEQ ID NOS: 1-1303. Inhibition of expression of the gene inhibits development of a cancerous phenotype in the cell. In specific embodiments, the cancerous phenotype is metastasis, aberrant cellular proliferation relative to a normal cell, or loss of contact inhibition of cell growth.

[0012] In another aspect, the invention provides a method for assessing the tumor burden of a subject, the method comprising detecting a level of a differentially expressed gene product in a test sample from a subject suspected of or having a tumor, the differentially expressed gene product comprising a sequence selected from the group consisting of SEQ ID NOS: 1-1303. Detection of the level of the gene product in the test sample is indicative of the tumor burden in the subject.

[0013] In another aspect, the invention provides a method for identifying a gene product as a target for a cancer therapeutic, the method comprising contacting a cancerous cell expressing a candidate gene product with an anti-cancer agent, wherein the candidate gene product corresponds to a sequence selected from the group consisting of SEQ ID NOS: 1-1303; and analyzing the effect of the anti-cancer agent upon a biological activity of the candidate gene product and upon a cancerous phenotype of the cancerous cell. Modulation of the biological activity of the candidate gene product and modulation of the cancerous phenotype of the cancerous cell indicates the candidate gene product is a target for a cancer therapeutic. In specific embodiments, the cancerous cell is a cancerous colon cell. In other specific embodiments, the inhibitor is an antisense oligonucleotide. In further embodiments, the cancerous phenotype is aberrant cellular proliferation relative to a normal cell, or colony formation due to loss of contact inhibition of cell growth.

[0014] In another aspect, the invention provides a method for identifying agents that decrease biological activity of a gene product differentially expressed in a cancerous cell,

[0016] These and other objects, advantages, and features of the invention will become apparent to those persons skilled in the art upon reading the details of the invention as more fully described below.

DETAILED DESCRIPTION OF THE INVENTION

[0017] Before the present invention is described, it is to be understood that this invention is not limited to particular embodiments described, as such may, of course, vary. It is also to be understood that the terminology used herein is for the purpose of describing particular embodiments only, and is not intended to be limiting.

[0018] Unless defined otherwise, all technical and scientific terms used herein have the same meaning as commonly understood by one of ordinary skill in the art to which this invention belongs. Although any methods and materials similar or equivalent to those described herein can be used in the practice or testing of the present invention, the preferred methods and materials are now described. All publications and patent applications mentioned herein are incorporated herein by reference to disclose and describe the methods and/or materials in connection with which the publications are cited.

[0019] It must be noted that as used herein and in the appended claims, the singular forms "a", "and", and "the" include plural referents unless the context clearly dictates otherwise. Thus, for example, reference to "a polynucleotide" includes a plurality of such polynucleotides and reference to "the colon cancer cell" includes reference to one or more cells and equivalents thereof known to those skilled in the art, and so forth.

[0020] The publications and applications discussed herein are provided solely for their disclosure prior to the filing date of the present application. Nothing herein is to be construed as an admission that the present invention is not entitled to antedate such publication by virtue of prior invention. Further, the dates of publication provided may be different from the actual publication dates which may need to be independently confirmed.

Definitions

[0021] The terms "polynucleotide" and "nucleic acid", used interchangeably herein, refer to a polymeric forms of nucleotides of any length, either ribonucleotides or deoxynucleotides. Thus, these terms include, but are not limited to, single-, double-, or multi-stranded DNA or RNA, genomic DNA, cDNA, DNA-RNA hybrids, or a polymer comprising purine and pyrimidine bases or other natural, chemically or biochemically modified, non-natural, or derivatized nucleotide bases. These terms further include, but are not limited to, mRNA or cDNA that comprise intronic sequences (see, *e.g.*, Niwa et al. (1999) *Cell* 99(7):691-702). The backbone of the polynucleotide can comprise sugars and phosphate groups (as may typically be found in RNA or DNA), or modified or substituted sugar or phosphate groups. Alternatively, the backbone of the polynucleotide can comprise a polymer of synthetic subunits such as phosphoramidites and thus can be an oligodeoxynucleoside phosphoramidate or a mixed phosphoramidate-phosphodiester oligomer. Peyrottes *et al.* (1996) *Nucl. Acids Res.* 24:1841-1848; Chaturvedi *et al.* (1996) *Nucl. Acids Res.* 24:2318-2323. A polynucleotide may comprise modified nucleotides, such as methylated nucleotides and nucleotide analogs, uracyl, other sugars, and linking groups such as fluororibose and thioate, and nucleotide branches. The

sequence of nucleotides may be interrupted by non-nucleotide components. A polynucleotide may be further modified after polymerization, such as by conjugation with a labeling component. Other types of modifications included in this definition are caps, substitution of one or more of the naturally occurring nucleotides with an analog, and introduction of means for attaching the polynucleotide to proteins, metal ions, labeling components, other polynucleotides, or a solid support.

[0022] The terms "polypeptide" and "protein", used interchangeably herein, refer to a polymeric form of amino acids of any length, which can include coded and non-coded amino acids, chemically or biochemically modified or derivatized amino acids, and polypeptides having modified peptide backbones. The term includes fusion proteins, including, but not limited to, fusion proteins with a heterologous amino acid sequence, fusions with heterologous and homologous leader sequences, with or without N-terminal methionine residues; immunologically tagged proteins; and the like.

[0023] "Heterologous" means that the materials are derived from different sources (*e.g.*, from different genes, different species, etc.).

[0024] As used herein, the terms "a gene that is differentially expressed in a colon cancer cell," and "a polynucleotide that is differentially expressed in a colon cancer cell" are used interchangeably herein, and generally refer to a polynucleotide that represents or corresponds to a gene that is differentially expressed in a cancerous colon cell when compared with a cell of the same cell type that is not cancerous, *e.g.*, mRNA is found at levels at least about 25%, at least about 50% to about 75%, at least about 90%, at least about 1.5-fold, at least about 2-fold, at least about 5-fold, at least about 10-fold, or at least about 50-fold or more, different (*e.g.*, higher or lower). The comparison can be made in tissue, for example, if one is using in situ hybridization or another assay method that allows some degree of discrimination among cell types in the tissue. The comparison may also or alternatively be made between cells removed from their tissue source.

[0025] "Differentially expressed polynucleotide" as used herein refers to a nucleic acid molecule (RNA or DNA) comprising a sequence that represents a differentially expressed gene, *e.g.*, the differentially expressed polynucleotide comprises a sequence (*e.g.*, an open

reading frame encoding a gene product; a non-coding sequence) that uniquely identifies a differentially expressed gene so that detection of the differentially expressed polynucleotide in a sample is correlated with the presence of a differentially expressed gene in a sample. "Differentially expressed polynucleotides" is also meant to encompass fragments of the disclosed polynucleotides, *e.g.*, fragments retaining biological activity, as well as nucleic acids homologous, substantially similar, or substantially identical (*e.g.*, having about 90% sequence identity) to the disclosed polynucleotides.

[0026] "Corresponds to" or "represents" when used in the context of, for example, a polynucleotide or sequence that "corresponds to" or "represents" a gene means that a sequence of the polynucleotide is present in the gene or in the nucleic acid gene product (*e.g.*, mRNA). The polynucleotide may be wholly present within an exon of a genomic sequence of the gene, or different portions of the sequence of the polynucleotide may be present in different exons (*e.g.*, such that the contiguous polynucleotide sequence is present in an mRNA, either pre- or post-splicing, that is an expression product of the gene). In some embodiments, the polynucleotide may represent or correspond to a gene that is modified in a cancerous cell relative to a normal cell. For example, the gene in the cancerous cell may be modified by insertion of an endogenous retrovirus, a transposable element, or other naturally occurring or non-naturally occurring nucleic acid. In such cases, the polynucleotide may include sequences of both the native gene (*e.g.*, the gene without the heterologous sequence) and the inserted, non-native sequence.

[0027] "Diagnosis" as used herein generally includes determination of a subject's susceptibility to a disease or disorder, determination as to whether a subject is presently affected by a disease or disorder, prognosis of a subject affected by a disease or disorder (*e.g.*, identification of pre-metastatic or metastatic cancerous states, stages of cancer, or responsiveness of cancer to therapy), and use of therapeutics (*e.g.*, monitoring a subject's condition to provide information as to the effect or efficacy of therapy).

[0028] As used herein, the term "a polypeptide associated with colon cancer" refers to a polypeptide encoded by a polynucleotide that is differentially expressed in a colon cancer cell.

- [0029] The term “biological sample” encompasses a variety of sample types obtained from an organism and can be used in a diagnostic or monitoring assay. The term encompasses blood and other liquid samples of biological origin, solid tissue samples, such as a biopsy specimen or tissue cultures or cells derived therefrom and the progeny thereof. The term encompasses samples that have been manipulated in any way after their procurement, such as by treatment with reagents, solubilization, or enrichment for certain components. The term encompasses a clinical sample, and also includes cells in cell culture, cell supernatants, cell lysates, serum, plasma, biological fluids, and tissue samples.
- [0030] The terms "treatment", "treating", "treat" and the like are used herein to generally refer to obtaining a desired pharmacologic and/or physiologic effect. The effect may be prophylactic in terms of completely or partially preventing a disease or symptom thereof and/or may be therapeutic in terms of a partial or complete stabilization or cure for a disease and/or adverse effect attributable to the disease. "Treatment" as used herein covers any treatment of a disease in a mammal, particularly a human, and includes: (a) preventing the disease or symptom from occurring in a subject which may be predisposed to the disease or symptom but has not yet been diagnosed as having it; (b) inhibiting the disease symptom, i.e., arresting its development; or (c) relieving the disease symptom, i.e., causing regression of the disease or symptom.
- [0031] The terms “individual,” “subject,” “host,” and “patient,” used interchangeably herein and refer to any mammalian subject for whom diagnosis, treatment, or therapy is desired, particularly humans. Other subjects may include cattle, dogs, cats, guinea pigs, rabbits, rats, mice, horses, and the like.
- [0032] As used herein the term "isolated" refers to a polynucleotide, a polypeptide, an antibody, or a host cell that is in an environment different from that in which the polynucleotide, the polypeptide, the antibody, or the host cell naturally occurs. A polynucleotide, a polypeptide, an antibody, or a host cell which is isolated is generally substantially purified. As used herein, the term "substantially purified" refers to a compound (*e.g.*, either a polynucleotide or a polypeptide or an antibody) that is removed

from its natural environment and is at least 60% free, preferably 75% free, and most preferably 90% free from other components with which it is naturally associated. Thus, for example, a composition containing A is "substantially free of" B when at least 85% by weight of the total A+B in the composition is A. Preferably, A comprises at least about 90% by weight of the total of A+B in the composition, more preferably at least about 95% or even 99% by weight.

[0033] A "host cell", as used herein, refers to a microorganism or a eukaryotic cell or cell line cultured as a unicellular entity which can be, or has been, used as a recipient for a recombinant vector or other transfer polynucleotides, and include the progeny of the original cell which has been transfected. It is understood that the progeny of a single cell may not necessarily be completely identical in morphology or in genomic or total DNA complement as the original parent, due to natural, accidental, or deliberate mutation.

[0034] The terms "cancer", "neoplasm", "tumor", and "carcinoma", are used interchangeably herein to refer to cells which exhibit relatively autonomous growth, so that they exhibit an aberrant growth phenotype characterized by a significant loss of control of cell proliferation. In general, cells of interest for detection or treatment in the present application include precancerous (*e.g.*, benign), malignant, pre-metastatic, metastatic, and non-metastatic cells. Detection of cancerous cell is of particular interest.

[0035] The term "normal" as used in the context of "normal cell," is meant to refer to a cell of an untransformed phenotype or exhibiting a morphology of a non-transformed cell of the tissue type being examined.

[0036] "Cancerous phenotype" generally refers to any of a variety of biological phenomena that are characteristic of a cancerous cell, which phenomena can vary with the type of cancer. The cancerous phenotype is generally identified by abnormalities in, for example, cell growth or proliferation (*e.g.*, uncontrolled growth or proliferation), regulation of the cell cycle, cell mobility, or cell-cell interaction.

[0037] "Therapeutic target" generally refers to a gene or gene product that, upon modulation of its activity (*e.g.*, by modulation of expression, biological activity, and the like), can provide for modulation of the cancerous phenotype.

[0038] As used throughout, "modulation" is meant to refer to an increase or a decrease in the indicated phenomenon (*e.g.*, modulation of a biological activity refers to an increase in a biological activity or a decrease in a biological activity).

POLYNUCLEOTIDE COMPOSITIONS

[0039] The present invention provides isolated polynucleotides that represent genes that are differentially expressed in colon cancer cells. The polynucleotides, as well as polypeptides encoded thereby, find use in a variety of therapeutic and diagnostic methods.

[0040] The scope of the invention with respect to polynucleotide compositions useful in the methods described herein includes, but is not necessarily limited to, polynucleotides having a sequence set forth in any one of the polynucleotide sequences provided herein; polynucleotides obtained from the biological materials described herein or other biological sources (particularly human sources) by hybridization under stringent conditions (particularly conditions of high stringency); genes corresponding to the provided polynucleotides; cDNAs corresponding to the provided polynucleotides; variants of the provided polynucleotides and their corresponding genes, particularly those variants that retain a biological activity of the encoded gene product (*e.g.*, a biological activity ascribed to a gene product corresponding to the provided polynucleotides as a result of the assignment of the gene product to a protein family(ies) and/or identification of a functional domain present in the gene product). Other nucleic acid compositions contemplated by and within the scope of the present invention will be readily apparent to one of ordinary skill in the art when provided with the disclosure here. "Polynucleotide" and "nucleic acid" as used herein with reference to nucleic acids of the composition is not intended to be limiting as to the length or structure of the nucleic acid unless specifically indicated.

[0041] The invention features polynucleotides that represent genes that are expressed in human tissue, specifically human colon tissue, particularly polynucleotides that are differentially expressed in colon cancer cells. Nucleic acid compositions described

herein of particular interest comprise a sequence set forth in any one of the polynucleotide sequences provided herein or an identifying sequence thereof. An "identifying sequence" is a contiguous sequence of residues at least about 10 nt to about 20 nt in length, usually at least about 50 nt to about 100 nt in length, that uniquely identifies a polynucleotide sequence, its complements and degenerate variants thereof, *e.g.*, exhibits less than 90%, usually less than about 80% to about 85% sequence identity to any contiguous nucleotide sequence of more than about 20 nt. Thus, the subject nucleic acid compositions include full-length cDNAs or mRNAs that encompass an identifying sequence of contiguous nucleotides from any one of the polynucleotide sequences provided herein.

[0042] The polynucleotides useful in the methods described herein also include polynucleotides having sequence similarity or sequence identity. Nucleic acids having sequence similarity are detected by hybridization under low stringency conditions, for example, at 50°C and 10XSSC (0.9 M saline/0.09 M sodium citrate) and remain bound when subjected to washing at 55°C in 1XSSC. Sequence identity can be determined by hybridization under high stringency conditions, for example, at 50°C or higher and 0.1XSSC (9 mM saline/0.9 mM sodium citrate). Hybridization methods and conditions are well known in the art, see, *e.g.*, USPN 5,707,829. Nucleic acids that are substantially identical to the provided polynucleotide sequences, *e.g.* allelic variants, genetically altered versions of the gene, *etc.*, bind to the provided polynucleotide sequences under stringent hybridization conditions. By using probes, particularly labeled probes of DNA sequences, one can isolate homologous or related genes. The source of homologous genes can be any species, *e.g.* primate species, particularly human; rodents, such as rats and mice; canines, felines, bovines, ovines, equines, yeast, nematodes, *etc.*

[0043] In one embodiment, hybridization is performed using at least 15 contiguous nucleotides (nt) of at least one of the polynucleotide sequences provided herein. That is, when at least 15 contiguous nt of one of the disclosed polynucleotide sequences is used as a probe, the probe will preferentially hybridize with a nucleic acid comprising the complementary sequence, allowing the identification and retrieval of the nucleic acids

that uniquely hybridize to the selected probe. Probes from more than one polynucleotide sequences provided herein can hybridize with the same nucleic acid if the cDNA from which they were derived corresponds to one mRNA. Probes of more than 15 nt can be used, e.g., probes of a size within the range of about 18 nt, 25 nt, 50 nt, 75 nt or 100 nt, but in general about 15 nt represents sufficient sequence for unique identification.

[0044] Polynucleotides contemplated for use in the invention also include naturally occurring variants of the nucleotide sequences (*e.g.*, degenerate variants (*e.g.*, sequences that encode the same polypeptides but, due to the degenerate nature of the genetic code, different in nucleotide sequence), allelic variants, *etc.*). Variants of the polynucleotides contemplated by the invention are identified by hybridization of putative variants with nucleotide sequences disclosed herein, preferably by hybridization under stringent conditions. For example, by using appropriate wash conditions, variants of the polynucleotides described herein can be identified where the allelic variant exhibits at most about 25-30% base pair (bp) mismatches relative to the selected polynucleotide probe. In general, allelic variants contain 15-25% bp mismatches, and can contain as little as even 5-15%, or 2-5%, or 1-2% bp mismatches, as well as a single bp mismatch.

[0045] The invention also encompasses homologs corresponding to any one of the polynucleotide sequences provided herein, where the source of homologous genes can be any mammalian species, *e.g.*, primate species, particularly human; rodents, such as rats; canines, felines, bovines, ovines, equines, yeast, nematodes, *etc.* Between mammalian species, *e.g.*, human and mouse, homologs generally have substantial sequence similarity, *e.g.*, at least 75% sequence identity, usually at least 90%, more usually at least 95% between nucleotide sequences. Sequence similarity is calculated based on a reference sequence, which may be a subset of a larger sequence, such as a conserved motif, coding region, flanking region, *etc.* A reference sequence will usually be at least about 18 contiguous nt long, more usually at least about 30 nt long, and may extend to the complete sequence that is being compared. Algorithms for sequence analysis are known in the art, such as gapped BLAST, described in Altschul, et al. *Nucleic Acids Res.* (1997) 25:3389-3402, or TeraBLAST available from TimeLogic Corp. (Crystal Bay, Nevada).

[0046] In general, variants of the polynucleotides described herein have a sequence identity greater than at least about 65%, preferably at least about 75%, more preferably at least about 85%, and can be greater than at least about 90%, 95%, 96%, 97%, 98%, 99% or more as determined by the Smith-Waterman homology search algorithm as implemented in MPSRCH program (Oxford Molecular). For the purposes of this invention, a preferred method of calculating percent identity is the Smith-Waterman algorithm. Global DNA sequence identity must be greater than 65% as determined by the Smith-Waterman homology search algorithm as implemented in MPSRCH program (Oxford Molecular) using an affine gap search with the following search parameters: gap open penalty, 12; and gap extension penalty, 1.

[0047] The subject nucleic acids can be cDNAs or genomic DNAs, as well as fragments thereof, particularly fragments that encode a biologically active gene product and/or are useful in the methods disclosed herein (*e.g.*, in diagnosis, as a unique identifier of a differentially expressed gene of interest, *etc.*). The term "cDNA" as used herein is intended to include all nucleic acids that share the arrangement of sequence elements found in native mature mRNA species, where sequence elements are exons and 3' and 5' non-coding regions. Normally mRNA species have contiguous exons, with the intervening introns, when present, being removed by nuclear RNA splicing, to create a continuous open reading frame encoding a polypeptide. mRNA species can also exist with both exons and introns, where the introns may be removed by alternative splicing. Furthermore it should be noted that different species of mRNAs encoded by the same genomic sequence can exist at varying levels in a cell, and detection of these various levels of mRNA species can be indicative of differential expression of the encoded gene product in the cell.

[0048] A genomic sequence of interest comprises the nucleic acid present between the initiation codon and the stop codon, as defined in the listed sequences, including all of the introns that are normally present in a native chromosome. It can further include the 3' and 5' untranslated regions found in the mature mRNA. It can further include specific transcriptional and translational regulatory sequences, such as promoters, enhancers, *etc.*,

including about 1 kb, but possibly more, of flanking genomic DNA at either the 5' and 3' end of the transcribed region. The genomic DNA can be isolated as a fragment of 100 kbp or smaller; and substantially free of flanking chromosomal sequence. The genomic DNA flanking the coding region, either 3' and 5', or internal regulatory sequences as sometimes found in introns, contains sequences required for proper tissue, stage-specific, or disease-state specific expression.

[0049] The nucleic acid compositions of the subject invention can encode all or a part of the naturally-occurring polypeptides. Double or single stranded fragments can be obtained from the DNA sequence by chemically synthesizing oligonucleotides in accordance with conventional methods, by restriction enzyme digestion, by PCR amplification, *etc.* Isolated polynucleotides and polynucleotide fragments contemplated by the invention comprise at least about 10, about 15, about 20, about 35, about 50, about 75, about 100, about 150 to about 200, about 250 to about 300, or about 350 contiguous nt selected from the polynucleotide provided herein. For the most part, fragments will be of at least 15 nt, usually at least 18 nt or 25 nt, and up to at least about 50 contiguous nt in length or more. In a preferred embodiment, the polynucleotide molecules comprise a contiguous sequence of at least 12 nt selected from any one of the polynucleotide sequences provided herein.

[0050] Probes specific to the polynucleotides described herein can be generated using the polynucleotide sequences disclosed herein. The probes are preferably at least about a 12 nt, 15 nt, 16 nt, 18 nt, 20 nt, 22 nt, 24 nt, or 25 nt fragment of a corresponding contiguous sequence any one of the polynucleotide sequences provided herein, and can be less than 10kb, 5kb, 4kb, 3kb, 2 kb, 1 kb, 0.5 kb, 0.1 kb, or 0.05 kb in length. The probes can be synthesized chemically or can be generated from longer polynucleotides using restriction enzymes. The probes can be labeled, for example, with a radioactive, biotinylated, or fluorescent tag. Preferably, probes are designed based upon an identifying sequence of any one of the polynucleotide sequences provided herein. More preferably, probes are designed based on a contiguous sequence of one of the subject polynucleotides that remain unmasked following application of a masking program for masking low

complexity (*e.g.*, XBLAST, RepeatMasker, etc.) to the sequence., *i.e.*, one would select an unmasked region, as indicated by the polynucleotides outside the poly-n stretches of the masked sequence produced by the masking program.

[0051] The polynucleotides of interest in the subject invention are isolated and obtained in substantial purity, generally as other than an intact chromosome. Usually, the polynucleotides, either as DNA or RNA, will be obtained substantially free of other naturally-occurring nucleic acid sequences, generally being at least about 50%, usually at least about 90% pure and are typically “recombinant”, *e.g.*, flanked by one or more nucleotides with which it is not normally associated on a naturally occurring chromosome.

[0052] The polynucleotides described herein can be provided as a linear molecule or within a circular molecule, and can be provided within autonomously replicating molecules (vectors) or within molecules without replication sequences. Expression of the polynucleotides can be regulated by their own or by other regulatory sequences known in the art. The polynucleotides can be introduced into suitable host cells using a variety of techniques available in the art, such as transferrin polycation-mediated DNA transfer, transfection with naked or encapsulated nucleic acids, liposome-mediated DNA transfer, intracellular transportation of DNA-coated latex beads, protoplast fusion, viral infection, electroporation, gene gun, calcium phosphate-mediated transfection, and the like.

[0053] The nucleic acid compositions described herein can be used to, for example, produce polypeptides, as probes for the detection of mRNA in biological samples (*e.g.*, extracts of human cells) or cDNA produced from such samples, to generate additional copies of the polynucleotides, to generate ribozymes or antisense oligonucleotides, and as single stranded DNA probes or as triple-strand forming oligonucleotides. The probes described herein can be used to, for example, determine the presence or absence of any one of the polynucleotide provided herein or variants thereof in a sample. These and other uses are described in more detail below.

POLYPEPTIDES AND VARIANTS THEREOF

[0054] The present invention further provides polypeptides encoded by polynucleotides that represent genes that are differentially expressed in colon cancer cells. Such polypeptides are referred to herein as "polypeptides associated with colon cancer." The polypeptides can be used to generate antibodies specific for a polypeptide associated with colon cancer, which antibodies are in turn useful in diagnostic methods, prognostics methods, therametric methods, and the like as discussed in more detail herein. Polypeptides are also useful as targets for therapeutic intervention, as discussed in more detail herein.

[0055] The polypeptides contemplated by the invention include those encoded by the disclosed polynucleotides and the genes to which these polynucleotides correspond, as well as nucleic acids that, by virtue of the degeneracy of the genetic code, are not identical in sequence to the disclosed polynucleotides. Thus, the invention includes within its scope a polypeptide encoded by a polynucleotide having the sequence of any one of the polynucleotide sequences provided herein, or a variant thereof.

[0056] In general, the term "polypeptide" as used herein refers to both the full length polypeptide encoded by the recited polynucleotide, the polypeptide encoded by the gene represented by the recited polynucleotide, as well as portions or fragments thereof. "Polypeptides" also includes variants of the naturally occurring proteins, where such variants are homologous or substantially similar to the naturally occurring protein, and can be of an origin of the same or different species as the naturally occurring protein (*e.g.*, human, murine, or some other species that naturally expresses the recited polypeptide, usually a mammalian species). In general, variant polypeptides have a sequence that has at least about 80%, usually at least about 90%, and more usually at least about 98% sequence identity with a differentially expressed polypeptide described herein, as measured by TeraBLAST using the parameters described above. The variant polypeptides can be naturally or non-naturally glycosylated, *i.e.*, the polypeptide has a glycosylation pattern that differs from the glycosylation pattern found in the corresponding naturally occurring protein.

- [0057] The invention also encompasses homologs of the disclosed polypeptides (or fragments thereof) where the homologs are isolated from other species, *i.e.* other animal or plant species, where such homologs, usually mammalian species, *e.g.* rodents, such as mice, rats; domestic animals, *e.g.*, horse, cow, dog, cat; and humans. By “homolog” is meant a polypeptide having at least about 35%, usually at least about 40% and more usually at least about 60% amino acid sequence identity to a particular differentially expressed protein as identified above, where sequence identity is determined using the TeraBLAST algorithm, with the parameters described *supra*.
- [0058] In general, the polypeptides of interest in the subject invention are provided in a non-naturally occurring environment, *e.g.* are separated from their naturally occurring environment. In certain embodiments, the subject protein is present in a composition that is enriched for the protein as compared to a control. As such, purified polypeptide is provided, where by purified is meant that the protein is present in a composition that is substantially free of non-differentially expressed polypeptides, where by substantially free is meant that less than 90%, usually less than 60% and more usually less than 50% of the composition is made up of non-differentially expressed polypeptides.
- [0059] Also within the scope of the invention are variants; variants of polypeptides include mutants, fragments, and fusions. Mutants can include amino acid substitutions, additions or deletions. The amino acid substitutions can be conservative amino acid substitutions or substitutions to eliminate non-essential amino acids, such as to alter a glycosylation site, a phosphorylation site or an acetylation site, or to minimize misfolding by substitution or deletion of one or more cysteine residues that are not necessary for function. Conservative amino acid substitutions are those that preserve the general charge, hydrophobicity/ hydrophilicity, and/or steric bulk of the amino acid substituted.
- [0060] Variants can be designed so as to retain or have enhanced biological activity of a particular region of the protein (*e.g.*, a functional domain and/or, where the polypeptide is a member of a protein family, a region associated with a consensus sequence). Selection of amino acid alterations for production of variants can be based upon the accessibility (interior vs. exterior) of the amino acid (*see, e.g., Go et al, Int. J. Peptide Protein Res.*

(1980) 15:211), the thermostability of the variant polypeptide (*see, e.g., Querol et al., Prot. Eng.* (1996) 9:265), desired glycosylation sites (*see, e.g., Olsen and Thomsen, J. Gen. Microbiol.* (1991) 137:579), desired disulfide bridges (*see, e.g., Clarke et al., Biochemistry* (1993) 32:4322; and Wakarchuk *et al., Protein Eng.* (1994) 7:1379), desired metal binding sites (*see, e.g., Toma et al., Biochemistry* (1991) 30:97, and Haezebrouck *et al., Protein Eng.* (1993) 6:643), and desired substitutions with in proline loops (*see, e.g., Masul et al., Appl. Env. Microbiol.* (1994) 60:3579). Cysteine-depleted muteins can be produced as disclosed in USPN 4,959,314.

- [0061] Variants also include fragments of the polypeptides disclosed herein, particularly biologically active fragments and/or fragments corresponding to functional domains. Fragments of interest will typically be at least about 10 aa to at least about 15 aa in length, usually at least about 50 aa in length, and can be as long as 300 aa in length or longer, but will usually not exceed about 1000 aa in length, where the fragment will have a stretch of amino acids that is identical to a polypeptide encoded by a polynucleotide having a sequence of any one of the polynucleotide sequences provided herein, or a homolog thereof. The protein variants described herein are encoded by polynucleotides that are within the scope of the invention. The genetic code can be used to select the appropriate codons to construct the corresponding variants.

ANTIBODIES AND OTHER POLYPEPTIDE OR POLYNUCLEOTIDE BINDING MOLECULES

- [0062] The present invention further provides antibodies, which may be isolated antibodies, that are specific for a polypeptide encoded by a polynucleotide described herein and/or a polypeptide of a gene that corresponds to a polynucleotide described herein. Antibodies can be provided in a composition comprising the antibody and a buffer and/or a pharmaceutically acceptable excipient. Antibodies specific for a polypeptide associated with colon cancer are useful in a variety of diagnostic and therapeutic methods, as discussed in detail herein.
- [0063] Gene products, including polypeptides, mRNA (particularly mRNAs having distinct secondary and/or tertiary structures), cDNA, or complete gene, can be prepared

and used for raising antibodies for experimental, diagnostic, and therapeutic purposes. For polynucleotides to which a corresponding gene has not been assigned, this provides an additional method of identifying the corresponding gene. The polynucleotide or related cDNA is expressed as described above, and antibodies are prepared. These antibodies are specific to an epitope on the polypeptide encoded by the polynucleotide, and can precipitate or bind to the corresponding native protein in a cell or tissue preparation or in a cell-free extract of an in vitro expression system.

[0064] Methods for production of antibodies that specifically bind a selected antigen are well known in the art. Immunogens for raising antibodies can be prepared by mixing an antigen (*e.g.*, polypeptide) with an adjuvant, and/or by making fusion proteins with larger immunogenic proteins. Antigens (*e.g.*, polypeptides) can also be covalently linked to other larger immunogenic proteins, such as keyhole limpet hemocyanin. Immunogens are typically administered intradermally, subcutaneously, or intramuscularly to experimental animals such as rabbits, sheep, and mice, to generate antibodies. Monoclonal antibodies can be generated by isolating spleen cells and fusing myeloma cells to form hybridomas. Alternatively, a polynucleotide encoding an antigen of interest is administered directly, such as by intramuscular injection, and expressed in vivo. The expressed protein antigen generates a variety of protein-specific immune responses, including production of antibodies, comparable to administration of the protein.

[0065] Preparations of polyclonal and monoclonal antibodies specific for an antigen (*e.g.*, polypeptide) are made using standard methods known in the art. For example, the antibodies can be produced so as to specifically bind to epitopes present in the polypeptides encoded by polynucleotides disclosed in the Sequence Listing. Typically, at least 6, 8, 10, or 12 contiguous amino acids are required to form an epitope. Epitopes that involve non-contiguous amino acids may require a longer polypeptide, *e.g.*, at least 15, 25, or 50 amino acids. Antibodies that specifically bind to human polypeptides encoded by the provided polypeptides should provide a detection signal at least 5-, 10-, or 20-fold higher than a detection signal provided with other proteins when used in Western blots or other immunochemical assays. In one embodiment, antibodies that specifically

bind polypeptides contemplated by the invention do not bind to other proteins in immunochemical assays at detectable levels and can immunoprecipitate the specific polypeptide from solution.

[0066] The invention also contemplates naturally occurring antibodies. For example, serum antibodies to a polypeptide of interest in a human population can be purified by methods well known in the art, e.g., by passing antiserum over a column to which the corresponding selected polypeptide or fusion protein is bound. The bound antibodies can then be eluted from the column, for example using a buffer with a high salt concentration.

[0067] The invention also contemplates genetically engineered antibodies (*e.g.*, chimeric antibodies, humanized antibodies, human antibodies produced by a transgenic animal (*e.g.*, a transgenic mouse such as the XenomousTM), antibody derivatives (*e.g.*, single chain antibodies, antibody fragments (*e.g.*, Fab, etc.)), according to methods well known in the art.

[0068] The invention also contemplates other molecules that can specifically bind a polynucleotide or polypeptide of the invention. Examples of such molecules include, but are not necessarily limited to, single-chain binding proteins (*e.g.*, mono- and multi-valent single chain antigen binding proteins (*see, e.g.*, U.S. Patent Nos. 4,704,692; 4,946,778; 4,946,778; 6,027,725; 6,121,424)), oligonucleotide-based synthetic antibodies (*e.g.*, oligobodies (*see, e.g.*, Radrizzani *et al.*, *Medicina* (B Aires) (1999) 59:753-8; Radrizzani *et al.*, *Medicina* (B Aires) (2000) 60(Suppl 2):55-60)), aptamers (*see, e.g.*, Gening *et al.*, *Biotechniques* (2001) 3:828, 830, 832, 834; Cox and Ellington, *Bioorg. Med. Chem.* (2001) 9:2525-31), and the like.

COMPUTER-RELATED EMBODIMENTS

[0069] In general, a library of polynucleotides is a collection of sequence information, which information is provided in either biochemical form (*e.g.*, as a collection of polynucleotide molecules), or in electronic form (*e.g.*, as a collection of polynucleotide sequences stored in a computer-readable form, as in a computer system and/or as part of a computer program). The sequence information of the polynucleotides can be used in a

variety of ways, *e.g.*, as a resource for gene discovery, as a representation of sequences expressed in a selected cell type (*e.g.*, cell type markers), and/or as markers of a given disease or disease state. For example, in the instant case, the sequences of polynucleotides and polypeptides corresponding to genes differentially expressed in cancer, particular in colon cancer, as well as the nucleic acid and amino acid sequences of the genes themselves, can be provided in electronic form in a computer database.

[0070] In general, a disease marker is a representation of a gene product that is present in all cells affected by disease either at an increased or decreased level relative to a normal cell (*e.g.*, a cell of the same or similar type that is not substantially affected by disease). For example, a polynucleotide sequence in a library can be a polynucleotide that represents an mRNA, polypeptide, or other gene product encoded by the polynucleotide, that is either overexpressed or underexpressed in a cancerous colon cell affected by cancer relative to a normal (*i.e.*, substantially disease-free) colon cell.

[0071] The nucleotide sequence information of the library can be embodied in any suitable form, *e.g.*, electronic or biochemical forms. For example, a library of sequence information embodied in electronic form comprises an accessible computer data file (or, in biochemical form, a collection of nucleic acid molecules) that contains the representative nucleotide sequences of genes that are differentially expressed (*e.g.*, overexpressed or underexpressed) as between, for example, i) a cancerous cell and a normal cell; ii) a cancerous cell and a dysplastic cell; iii) a cancerous cell and a cell affected by a disease or condition other than cancer; iv) a metastatic cancerous cell and a normal cell and/or non-metastatic cancerous cell; v) a malignant cancerous cell and a non-malignant cancerous cell (or a normal cell) and/or vi) a dysplastic cell relative to a normal cell. Other combinations and comparisons of cells affected by various diseases or stages of disease will be readily apparent to the ordinarily skilled artisan. Biochemical embodiments of the library include a collection of nucleic acids that have the sequences of the genes in the library, where the nucleic acids can correspond to the entire gene in the library or to a fragment thereof, as described in greater detail below.

[0072] The polynucleotide libraries of the subject invention generally comprise sequence

information of a plurality of polynucleotide sequences, where at least one of the polynucleotides has a sequence of any of sequence described herein. By plurality is meant at least 2, usually at least 3 and can include up to all of the sequences described herein. The length and number of polynucleotides in the library will vary with the nature of the library, *e.g.*, if the library is an oligonucleotide array, a cDNA array, a computer database of the sequence information, etc.

[0073] Where the library is an electronic library, the nucleic acid sequence information can be present in a variety of media. "Media" refers to a manufacture, other than an isolated nucleic acid molecule, that contains the sequence information of the present invention. Such a manufacture provides the genome sequence or a subset thereof in a form that can be examined by means not directly applicable to the sequence as it exists in a nucleic acid. For example, the nucleotide sequence of the present invention, *e.g.* the nucleic acid sequences of any of the polynucleotides of the sequences described herein, can be recorded on computer readable media, *e.g.* any medium that can be read and accessed directly by a computer. Such media include, but are not limited to: magnetic storage media, such as a floppy disc, a hard disc storage medium, and a magnetic tape; optical storage media such as CD-ROM; electrical storage media such as RAM and ROM; and hybrids of these categories such as magnetic/optical storage media.

[0074] One of skill in the art can readily appreciate how any of the presently known computer readable mediums can be used to create a manufacture comprising a recording of the present sequence information. "Recorded" refers to a process for storing information on computer readable medium, using any such methods as known in the art. Any convenient data storage structure can be chosen, based on the means used to access the stored information. A variety of data processor programs and formats can be used for storage, *e.g.* word processing text file, database format, *etc.* In addition to the sequence information, electronic versions of libraries comprising one or more sequence described herein can be provided in conjunction or connection with other computer-readable information and/or other types of computer-readable files (*e.g.*, searchable files, executable files, *etc.*, including, but not limited to, for example, search program software,

etc.).

[0075] By providing the nucleotide sequence in computer readable form, the information can be accessed for a variety of purposes. Computer software to access sequence information is publicly available. For example, the gapped BLAST (Altschul *et al.*, *Nucleic Acids Res.* (1997) 25:3389-3402) and BLAZE (Brutlag *et al.*, *Comp. Chem.* (1993) 17:203) search algorithms on a Sybase system, or the TeraBLAST (TimeLogic, Crystal Bay, Nevada) program optionally running on a specialized computer platform available from TimeLogic, can be used to identify open reading frames (ORFs) within the genome that contain homology to ORFs from other organisms.

[0076] As used herein, "a computer-based system" refers to the hardware means, software means, and data storage means used to analyze the nucleotide sequence information of the present invention. The minimum hardware of the computer-based systems of the present invention comprises a central processing unit (CPU), input means, output means, and data storage means. A skilled artisan can readily appreciate that any one of the currently available computer-based system are suitable for use in the present invention. The data storage means can comprise any manufacture comprising a recording of the present sequence information as described above, or a memory access means that can access such a manufacture.

[0077] "Search means" refers to one or more programs implemented on the computer-based system, to compare a target sequence or target structural motif, or expression levels of a polynucleotide in a sample, with the stored sequence information. Search means can be used to identify fragments or regions of the genome that match a particular target sequence or target motif. A variety of known algorithms are publicly known and commercially available, *e.g.* MacPattern (EMBL), TeraBLAST (TimeLogic), BLASTN and BLASTX (NCBI). A "target sequence" can be any polynucleotide or amino acid sequence of six or more contiguous nucleotides or two or more amino acids, preferably from about 10 to 100 amino acids or from about 30 to 300 nt. A variety of comparing means can be used to accomplish comparison of sequence information from a sample (*e.g.*, to analyze target sequences, target motifs, or relative expression levels) with

the data storage means. A skilled artisan can readily recognize that any one of the publicly available homology search programs can be used as the search means for the computer based systems of the present invention to accomplish comparison of target sequences and motifs. Computer programs to analyze expression levels in a sample and in controls are also known in the art.

[0078] A "target structural motif," or "target motif," refers to any rationally selected sequence or combination of sequences in which the sequence(s) are chosen based on a three-dimensional configuration that is formed upon the folding of the target motif, or on consensus sequences of regulatory or active sites. There are a variety of target motifs known in the art. Protein target motifs include, but are not limited to, enzyme active sites and signal sequences. Nucleic acid target motifs include, but are not limited to, hairpin structures, promoter sequences and other expression elements such as binding sites for transcription factors.

[0079] A variety of structural formats for the input and output means can be used to input and output the information in the computer-based systems of the present invention. One format for an output means ranks the relative expression levels of different polynucleotides. Such presentation provides a skilled artisan with a ranking of relative expression levels to determine a gene expression profile. A gene expression profile can be generated from, for example, a cDNA library prepared from mRNA isolated from a test cell suspected of being cancerous or pre-cancerous, comparing the sequences or partial sequences of the clones against the sequences in an electronic database, where the sequences of the electronic database represent genes differentially expressed in a cancerous cell, *e.g.*, a cancerous colon cell. The number of clones having a sequence that has substantial similarity to a sequence that represents a gene differentially expressed in a cancerous cell is then determined, and the number of clones corresponding to each of such genes is determined. An increased number of clones that correspond to differentially expressed gene is present in the cDNA library of the test cell (relative to, for example, the number of clones expected in a cDNA of a normal cell) indicates that the test cell is cancerous.

[0080] As discussed above, the “library” as used herein also encompasses biochemical libraries of the polynucleotides of the sequences described herein, *e.g.*, collections of nucleic acids representing the provided polynucleotides. The biochemical libraries can take a variety of forms, *e.g.*, a solution of cDNAs, a pattern of probe nucleic acids stably associated with a surface of a solid support (*i.e.*, an array) and the like. Of particular interest are nucleic acid arrays in which one or more of the genes described herein is represented by a sequence on the array. By array is meant an article of manufacture that has at least a substrate with at least two distinct nucleic acid targets on one of its surfaces, where the number of distinct nucleic acids can be considerably higher, typically being at least 10 nt, usually at least 20 nt and often at least 25 nt. A variety of different array formats have been developed and are known to those of skill in the art. The arrays of the subject invention find use in a variety of applications, including gene expression analysis, drug screening, mutation analysis and the like, as disclosed in the above-listed exemplary patent documents.

[0081] In addition to the above nucleic acid libraries, analogous libraries of polypeptides are also provided, where the polypeptides of the library will represent at least a portion of the polypeptides encoded by a gene corresponding to a sequence described herein.

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DIAGNOSTIC AND OTHER METHODS INVOLVING DETECTION OF DIFFERENTIALLY EXPRESSED GENES

[0082] The present invention provides methods of using the polynucleotides described herein in, for example, diagnosis of cancer and classification of cancer cells according to expression profiles. In specific non-limiting embodiments, the methods are useful for detecting colon cancer cells, facilitating diagnosis of cancer and the severity of a cancer (*e.g.*, tumor grade, tumor burden, and the like) in a subject, facilitating a determination of the prognosis of a subject, and assessing the responsiveness of the subject to therapy (*e.g.*, by providing a measure of therapeutic effect through, for example, assessing tumor burden during or following a chemotherapeutic regimen). Detection can be based on detection of a polynucleotide that is differentially expressed in a colon cancer cell, and/or

detection of a polypeptide encoded by a polynucleotide that is differentially expressed in a colon cancer cell ("a polypeptide associated with colon cancer"). The detection methods of the invention can be conducted *in vitro* or *in vivo*, on isolated cells, or in whole tissues or a bodily fluid, *e.g.*, blood, plasma, serum, urine, and the like).

[0083] In general, methods of the invention involving detection of a gene product (*e.g.*, mRNA, cDNA generated from such mRNA, and polypeptides) involve contacting a sample with a probe specific for the gene product of interest. "Probe" as used herein in such methods is meant to refer to a molecule that specifically binds a gene product of interest (*e.g.*, the probe binds to the target gene product with a specificity sufficient to distinguish binding to target over non-specific binding to non-target (background) molecules). "Probes" include, but are not necessarily limited to, nucleic acid probes (*e.g.*, DNA, RNA, modified nucleic acid, and the like), antibodies (*e.g.*, antibodies, antibody fragments that retain binding to a target epitope, single chain antibodies, and the like), or other polypeptide, peptide, or molecule (*e.g.*, receptor ligand) that specifically binds a target gene product of interest.

[0084] The probe and sample suspected of having the gene product of interest are contacted under conditions suitable for binding of the probe to the gene product. For example, contacting is generally for a time sufficient to allow binding of the probe to the gene product (*e.g.*, from several minutes to a few hours), and at a temperature and conditions of osmolarity and the like that provide for binding of the probe to the gene product at a level that is sufficiently distinguishable from background binding of the probe (*e.g.*, under conditions that minimize non-specific binding). Suitable conditions for probe-target gene product binding can be readily determined using controls and other techniques available and known to one of ordinary skill in the art.

[0085] In this embodiment, the probe can be an antibody or other polypeptide, peptide, or molecule (*e.g.*, receptor ligand) that specifically binds a target polypeptide of interest.

[0086] The detection methods can be provided as part of a kit. Thus, the invention further provides kits for detecting the presence and/or a level of a polynucleotide that is differentially expressed in a colon cancer cell (*e.g.*, by detection of an mRNA encoded by

the differentially expressed gene of interest), and/or a polypeptide encoded thereby, in a biological sample. Procedures using these kits can be performed by clinical laboratories, experimental laboratories, medical practitioners, or private individuals. The kits of the invention for detecting a polypeptide encoded by a polynucleotide that is differentially expressed in a colon cancer cell comprise a moiety that specifically binds the polypeptide, which may be a specific antibody. The kits of the invention for detecting a polynucleotide that is differentially expressed in a colon cancer cell comprise a moiety that specifically hybridizes to such a polynucleotide. The kit may optionally provide additional components that are useful in the procedure, including, but not limited to, buffers, developing reagents, labels, reacting surfaces, means for detection, control samples, standards, instructions, and interpretive information.

Detecting a polypeptide encoded by a polynucleotide that is differentially expressed in a colon cancer cell

[0087] In some embodiments, methods are provided for a colon cancer cell by detecting in the cell a polypeptide encoded by a gene differentially expressed in a colon cancer cell. Any of a variety of known methods can be used for detection, including, but not limited to, immunoassay, using antibody specific for the encoded polypeptide, e.g., by enzyme-linked immunosorbent assay (ELISA), radioimmunoassay (RIA), and the like; and functional assays for the encoded polypeptide, e.g., binding activity or enzymatic activity.

[0088] For example, an immunofluorescence assay can be easily performed on cells without first isolating the encoded polypeptide. The cells are first fixed onto a solid support, such as a microscope slide or microtiter well. This fixing step can permeabilize the cell membrane. The permeabilization of the cell membrane permits the polypeptide-specific probe (*e.g.*, antibody) to bind. Alternatively, where the polypeptide is secreted or membrane-bound, or is otherwise accessible at the cell-surface (*e.g.*, receptors, and other molecule stably-associated with the outer cell membrane or otherwise stably associated with the cell membrane, such permeabilization may not be necessary.

[0089] Next, the fixed cells are exposed to an antibody specific for the encoded polypeptide. To increase the sensitivity of the assay, the fixed cells may be further

exposed to a second antibody, which is labeled and binds to the first antibody, which is specific for the encoded polypeptide. Typically, the secondary antibody is detectably labeled, e.g., with a fluorescent marker. The cells which express the encoded polypeptide will be fluorescently labeled and easily visualized under the microscope. See, for example, Hashido *et al.* (1992) *Biochem. Biophys. Res. Comm.* 187:1241-1248.

[0090] As will be readily apparent to the ordinarily skilled artisan upon reading the present specification, the detection methods and other methods described herein can be readily varied. Such variations are within the intended scope of the invention. For example, in the above detection scheme, the probe for use in detection can be immobilized on a solid support, and the test sample contacted with the immobilized probe. Binding of the test sample to the probe can then be detected in a variety of ways, e.g., by detecting a detectable label bound to the test sample to facilitate detection of test sample-immobilized probe complexes.

[0091] The present invention further provides methods for detecting the presence of and/or measuring a level of a polypeptide in a biological sample, which polypeptide is encoded by a polynucleotide that represents a gene differentially expressed in cancer, particularly in a colon cancer cell, using a probe specific for the encoded polypeptide. In this embodiment, the probe can be an antibody or other polypeptide, peptide, or molecule (e.g., receptor ligand) that specifically binds a target polypeptide of interest.

[0092] The methods generally comprise: a) contacting the sample with an antibody specific for a differentially expressed polypeptide in a test cell; and b) detecting binding between the antibody and molecules of the sample. The level of antibody binding (either qualitative or quantitative) indicates the cancerous state of the cell. For example, where the differentially expressed gene is increased in cancerous cells, detection of an increased level of antibody binding to the test sample relative to antibody binding level associated with a normal cell indicates that the test cell is cancerous.

[0093] Suitable controls include a sample known not to contain the encoded polypeptide; and a sample contacted with an antibody not specific for the encoded polypeptide, e.g., an anti-idiotypic antibody. A variety of methods to detect specific antibody-antigen

interactions are known in the art and can be used in the method, including, but not limited to, standard immunohistological methods, immunoprecipitation, an enzyme immunoassay, and a radioimmunoassay.

[0094] In general, the specific antibody will be detectably labeled, either directly or indirectly. Direct labels include radioisotopes; enzymes whose products are detectable (e.g., luciferase, β -galactosidase, and the like); fluorescent labels (e.g., fluorescein isothiocyanate, rhodamine, phycoerythrin, and the like); fluorescence emitting metals, e.g., ^{152}Eu , or others of the lanthanide series, attached to the antibody through metal chelating groups such as EDTA; chemiluminescent compounds, e.g., luminol, isoluminol, acridinium salts, and the like; bioluminescent compounds, e.g., luciferin, aequorin (green fluorescent protein), and the like.

[0095] The antibody may be attached (coupled) to an insoluble support, such as a polystyrene plate or a bead. Indirect labels include second antibodies specific for antibodies specific for the encoded polypeptide ("first specific antibody"), wherein the second antibody is labeled as described above; and members of specific binding pairs, e.g., biotin-avidin, and the like. The biological sample may be brought into contact with and immobilized on a solid support or carrier, such as nitrocellulose, that is capable of immobilizing cells, cell particles, or soluble proteins. The support may then be washed with suitable buffers, followed by contacting with a detectably-labeled first specific antibody. Detection methods are known in the art and will be chosen as appropriate to the signal emitted by the detectable label. Detection is generally accomplished in comparison to suitable controls, and to appropriate standards.

[0096] In some embodiments, the methods are adapted for use *in vivo*, e.g., to locate or identify sites where colon cancer cells are present. In these embodiments, a detectably-labeled moiety, e.g., an antibody, which is specific for a colon cancer-associated polypeptide is administered to an individual (e.g., by injection), and labeled cells are located using standard imaging techniques, including, but not limited to, magnetic resonance imaging, computed tomography scanning, and the like. In this manner, colon cancer cells are differentially labeled.

Detecting a polynucleotide that represents a gene differentially expressed in a colon cancer cell

- [0097] In some embodiments, methods are provided for detecting a colon cancer cell by detecting expression in the cell of a transcript or that is differentially expressed in a colon cancer cell. Any of a variety of known methods can be used for detection, including, but not limited to, detection of a transcript by hybridization with a polynucleotide that hybridizes to a polynucleotide that is differentially expressed in a colon cancer cell; detection of a transcript by a polymerase chain reaction using specific oligonucleotide primers; *in situ* hybridization of a cell using as a probe a polynucleotide that hybridizes to a gene that is differentially expressed in a colon cancer cell.
- [0098] The methods can be used to detect and/or measure mRNA levels of a gene that is differentially expressed in a colon cancer cell. In some embodiments, the methods comprise: a) contacting a sample with a polynucleotide that corresponds to a differentially expressed gene described herein under conditions that allow hybridization; and b) detecting hybridization, if any. Detection of differential hybridization, when compared to a suitable control, is an indication of the presence in the sample of a polynucleotide that is differentially expressed in a colon cancer cell. Appropriate controls include, for example, a sample which is known not to contain a polynucleotide that is differentially expressed in a colon cancer cell, and use of a labeled polynucleotide of the same "sense" as the polynucleotide that is differentially expressed in a colon cancer cell. Conditions that allow hybridization are known in the art, and have been described in more detail above.
- [0099] Detection can also be accomplished by any known method, including, but not limited to, *in situ* hybridization, PCR (polymerase chain reaction), RT-PCR (reverse transcription-PCR), and "Northern" or RNA blotting, or combinations of such techniques, using a suitably labeled polynucleotide. A variety of labels and labeling methods for polynucleotides are known in the art and can be used in the assay methods of the invention. Specific hybridization can be determined by comparison to appropriate controls.

[00100] Polynucleotide generally comprising at least 12 contiguous nt of a polynucleotide provided herein, as shown in the Sequence Listing or of the sequences of the genes corresponding to the polynucleotides of the Sequence Listing, are used for a variety of purposes, such as probes for detection of and/or measurement of, transcription levels of a polynucleotide that is differentially expressed in a colon cancer cell. Additional disclosure about preferred regions of the disclosed polynucleotide sequences is found in the Examples. A probe that hybridizes specifically to a polynucleotide disclosed herein should provide a detection signal at least 2-, 5-, 10-, or 20-fold higher than the background hybridization provided with other unrelated sequences. It should be noted that “probe” as used in this context of detection of nucleic acid is meant to refer to a polynucleotide sequence used to detect a differentially expressed gene product in a test sample. As will be readily appreciated by the ordinarily skilled artisan, the probe can be detectably labeled and contacted with, for example, an array comprising immobilized polynucleotides obtained from a test sample (*e.g.*, mRNA). Alternatively, the probe can be immobilized on an array and the test sample detectably labeled. These and other variations of the methods of the invention are well within the skill in the art and are within the scope of the invention.

[00101] Nucleotide probes are used to detect expression of a gene corresponding to the provided polynucleotide. In Northern blots, mRNA is separated electrophoretically and contacted with a probe. A probe is detected as hybridizing to an mRNA species of a particular size. The amount of hybridization can be quantitated to determine relative amounts of expression, for example under a particular condition. Probes are used for in situ hybridization to cells to detect expression. Probes can also be used *in vivo* for diagnostic detection of hybridizing sequences. Probes are typically labeled with a radioactive isotope. Other types of detectable labels can be used such as chromophores, fluorophores, and enzymes. Other examples of nucleotide hybridization assays are described in WO92/02526 and USPN 5,124,246.

[00102] PCR is another means for detecting small amounts of target nucleic acids (see, *e.g.*, Mullis *et al.*, *Meth. Enzymol.* (1987) 155:335; USPN 4,683,195; and USPN

4,683,202). Two primer polynucleotides nucleotides that hybridize with the target nucleic acids are used to prime the reaction. The primers can be composed of sequence within or 3' and 5' to the polynucleotides of the Sequence Listing. Alternatively, if the primers are 3' and 5' to these polynucleotides, they need not hybridize to them or the complements. After amplification of the target with a thermostable polymerase, the amplified target nucleic acids can be detected by methods known in the art, e.g., Southern blot. mRNA or cDNA can also be detected by traditional blotting techniques (e.g., Southern blot, Northern blot, etc.) described in Sambrook *et al.*, "Molecular Cloning: A Laboratory Manual" (New York, Cold Spring Harbor Laboratory, 1989) (e.g., without PCR amplification). In general, mRNA or cDNA generated from mRNA using a polymerase enzyme can be purified and separated using gel electrophoresis, and transferred to a solid support, such as nitrocellulose. The solid support is exposed to a labeled probe, washed to remove any unhybridized probe, and duplexes containing the labeled probe are detected.

[00103] Methods using PCR amplification can be performed on the DNA from a single cell, although it is convenient to use at least about 10^5 cells. The use of the polymerase chain reaction is described in Saiki et al. (1985) *Science* 239:487, and a review of current techniques may be found in Sambrook, *et al.* Molecular Cloning: A Laboratory Manual, CSH Press 1989, pp.14.2-14.33. A detectable label may be included in the amplification reaction. Suitable detectable labels include fluorochromes, (e.g. fluorescein isothiocyanate (FITC), rhodamine, Texas Red, phycoerythrin, allophycocyanin, 6-carboxyfluorescein (6-FAM), 2',7'-dimethoxy-4',5'-dichloro-6-carboxyfluorescein, 6-carboxy-X-rhodamine (ROX), 6-carboxy-2',4',7',4,7-hexachlorofluorescein (HEX), 5-carboxyfluorescein (5-FAM) or N,N,N',N'-tetramethyl-6-carboxyrhodamine (TAMRA)), radioactive labels, (e.g. ^{32}P , ^{35}S , ^3H , *etc.*), and the like. The label may be a two stage system, where the polynucleotides is conjugated to biotin, haptens, *etc.* having a high affinity binding partner, e.g. avidin, specific antibodies, *etc.*, where the binding partner is conjugated to a detectable label. The label may be conjugated to one or both of the primers. Alternatively, the pool of nucleotides used in the amplification is labeled, so as to

incorporate the label into the amplification product.

Arrays

[00104] Polynucleotide arrays provide a high throughput technique that can assay a large number of polynucleotides or polypeptides in a sample. This technology can be used as a tool to test for differential expression.

[00105] A variety of methods of producing arrays, as well as variations of these methods, are known in the art and contemplated for use in the invention. For example, arrays can be created by spotting polynucleotide probes onto a substrate (*e.g.*, glass, nitrocellulose, *etc.*) in a two-dimensional matrix or array having bound probes. The probes can be bound to the substrate by either covalent bonds or by non-specific interactions, such as hydrophobic interactions.

[00106] Samples of polynucleotides can be detectably labeled (*e.g.*, using radioactive or fluorescent labels) and then hybridized to the probes. Double stranded polynucleotides, comprising the labeled sample polynucleotides bound to probe polynucleotides, can be detected once the unbound portion of the sample is washed away. Alternatively, the polynucleotides of the test sample can be immobilized on the array, and the probes detectably labeled. Techniques for constructing arrays and methods of using these arrays are described in, for example, Schena *et al.* (1996) *Proc Natl Acad Sci U S A.* 93(20):10614-9; Schena *et al.* (1995) *Science* 270(5235):467-70; Shalon *et al.* (1996) *Genome Res.* 6(7):639-45, USPN 5,807,522, EP 799 897; WO 97/29212; WO 97/27317; EP 785 280; WO 97/02357; USPN 5,593,839; USPN 5,578,832; EP 728 520; USPN 5,599,695; EP 721 016; USPN 5,556,752; WO 95/22058; and USPN 5,631,734.

[00107] Arrays can be used to, for example, examine differential expression of genes and can be used to determine gene function. For example, arrays can be used to detect differential expression of a gene corresponding to a polynucleotide described herein, where expression is compared between a test cell and control cell (*e.g.*, cancer cells and normal cells). For example, high expression of a particular message in a cancer cell, which is not observed in a corresponding normal cell, can indicate a cancer specific gene product. Exemplary uses of arrays are further described in, for example, Pappalarado *et*

al., Sem. Radiation Oncol. (1998) 8:217; and Ramsay, *Nature Biotechnol.* (1998) 16:40. Furthermore, many variations on methods of detection using arrays are well within the skill in the art and within the scope of the present invention. For example, rather than immobilizing the probe to a solid support, the test sample can be immobilized on a solid support which is then contacted with the probe.

DIAGNOSIS, PROGNOSIS, ASSESSMENT OF THERAPY (THERAMETRICS), AND MANAGEMENT OF CANCER

- [00108] The polynucleotides described herein, as well as their gene products and corresponding genes and gene products, are of particular interest as genetic or biochemical markers (e.g., in blood or tissues) that will detect the earliest changes along the carcinogenesis pathway and/or to monitor the efficacy of various therapies and preventive interventions.
- [00109] For example, the level of expression of certain polynucleotides can be indicative of a poorer prognosis, and therefore warrant more aggressive chemo- or radio-therapy for a patient or vice versa. The correlation of novel surrogate tumor specific features with response to treatment and outcome in patients can define prognostic indicators that allow the design of tailored therapy based on the molecular profile of the tumor. These therapies include antibody targeting, antagonists (*e.g.*, small molecules), and gene therapy.
- [00110] Determining expression of certain polynucleotides and comparison of a patients profile with known expression in normal tissue and variants of the disease allows a determination of the best possible treatment for a patient, both in terms of specificity of treatment and in terms of comfort level of the patient. Surrogate tumor markers, such as polynucleotide expression, can also be used to better classify, and thus diagnose and treat, different forms and disease states of cancer. Two classifications widely used in oncology that can benefit from identification of the expression levels of the genes corresponding to the polynucleotides described herein are staging of the cancerous disorder, and grading the nature of the cancerous tissue.

[00111] The polynucleotides that correspond to differentially expressed genes, as well as their encoded gene products, can be useful to monitor patients having or susceptible to cancer to detect potentially malignant events at a molecular level before they are detectable at a gross morphological level. In addition, the polynucleotides described herein, as well as the genes corresponding to such polynucleotides, can be useful as therapeutics, *e.g.*, to assess the effectiveness of therapy by using the polynucleotides or their encoded gene products, to assess, for example, tumor burden in the patient before, during, and after therapy.

[00112] Furthermore, a polynucleotide identified as corresponding to a gene that is differentially expressed in, and thus is important for, one type of cancer can also have implications for development or risk of development of other types of cancer, *e.g.*, where a polynucleotide represents a gene differentially expressed across various cancer types. Thus, for example, expression of a polynucleotide corresponding to a gene that has clinical implications for metastatic colon cancer can also have clinical implications for breast cancer, prostate cancer, or ovarian cancer.

[00113] Staging. Staging is a process used by physicians to describe how advanced the cancerous state is in a patient. Staging assists the physician in determining a prognosis, planning treatment and evaluating the results of such treatment. Staging systems vary with the types of cancer, but generally involve the following “TNM” system: the type of tumor, indicated by T; whether the cancer has metastasized to nearby lymph nodes, indicated by N; and whether the cancer has metastasized to more distant parts of the body, indicated by M. Generally, if a cancer is only detectable in the area of the primary lesion without having spread to any lymph nodes it is called Stage I. If it has spread only to the closest lymph nodes, it is called Stage II. In Stage II, the cancer has generally spread to the lymph nodes in near proximity to the site of the primary lesion. Cancers that have spread to a distant part of the body, such as the liver, bone, brain or other site, are Stage IV, the most advanced stage.

[00114] The polynucleotides and corresponding genes and gene products described herein can facilitate fine-tuning of the staging process by identifying markers for the

aggressiveness of a cancer, *e.g.* the metastatic potential, as well as the presence in different areas of the body. Thus, a Stage II cancer with a polynucleotide signifying a high metastatic potential cancer can be used to change a borderline Stage II tumor to a Stage III tumor, justifying more aggressive therapy. Conversely, the presence of a polynucleotide signifying a lower metastatic potential allows more conservative staging of a tumor.

[00115] Grading of cancers. Grade is a term used to describe how closely a tumor resembles normal tissue of its same type. The microscopic appearance of a tumor is used to identify tumor grade based on parameters such as cell morphology, cellular organization, and other markers of differentiation. As a general rule, the grade of a tumor corresponds to its rate of growth or aggressiveness, with undifferentiated or high-grade tumors generally being more aggressive than well-differentiated or low-grade tumors. The following guidelines are generally used for grading tumors: 1) GX Grade cannot be assessed; 2) G1 Well differentiated; G2 Moderately well differentiated; 3) G3 Poorly differentiated; 4) G4 Undifferentiated.

[00116] The polynucleotides of the Sequence Listing, and their corresponding genes and gene products, can be especially valuable in determining the grade of the tumor, as they not only can aid in determining the differentiation status of the cells of a tumor, they can also identify factors other than differentiation that are valuable in determining the aggressiveness of a tumor, such as metastatic potential.

[00117] Assessment of proliferation of cells in tumor. The differential expression level of the polynucleotides described herein can facilitate assessment of the rate of proliferation of tumor cells, and thus provide an indicator of the aggressiveness of the rate of tumor growth. For example, assessment of the relative expression levels of genes involved in cell cycle (*e.g.*, TTK) can provide an indication of cellular proliferation, and thus serve as a marker of proliferation.

[00118] Detection of colon cancer. The polynucleotides corresponding to genes that exhibit the appropriate expression pattern can be used to detect colon cancer in a subject. Colorectal cancer is one of the most common neoplasms in humans and perhaps the most

frequent form of hereditary neoplasia. Prevention and early detection are key factors in controlling and curing colorectal cancer. Colorectal cancer begins as polyps, which are small, benign growths of cells that form on the inner lining of the colon. Over a period of several years, some of these polyps accumulate additional mutations and become cancerous. Multiple familial colorectal cancer disorders have been identified, which are summarized as follows: 1) Familial adenomatous polyposis (FAP); 2) Gardner's syndrome; 3) Hereditary nonpolyposis colon cancer (HNPCC); and 4) Familial colorectal cancer in Ashkenazi Jews.

[00119] The expression of appropriate polynucleotides can be used in the diagnosis, prognosis and management of colorectal cancer. Detection of colon cancer can be determined using expression levels of any of these sequences alone or in combination with the levels of expression. Determination of the aggressive nature and/or the metastatic potential of a colon cancer can be determined by comparing levels of one or more gene products of the genes corresponding to the polynucleotides described herein, and comparing total levels of another sequence known to vary in cancerous tissue, *e.g.*, expression of p53, DCC, ras, FAP (see, *e.g.*, Fearon ER, *et al.*, *Cell* (1990) 61(5):759; Hamilton SR *et al.*, *Cancer* (1993) 72:957; Bodmer W, *et al.*, *Nat Genet.* (1994) 4(3):217; Fearon ER, *Ann N Y Acad Sci.* (1995) 768:101).

[00120] For example, development of colon cancer can be detected by examining the level of expression of a gene corresponding to a polynucleotides described herein to the levels of oncogenes (*e.g.* ras) or tumor suppressor genes (*e.g.* FAP or p53). Thus expression of specific marker polynucleotides can be used to discriminate between normal and cancerous colon tissue, to discriminate between colon cancers with different cells of origin, to discriminate between colon cancers with different potential metastatic rates, etc. For a review of markers of cancer, see, *e.g.*, Hanahan et al. (2000) *Cell* 100:57-70.

Tumor classification and patient stratification

[00121] The invention further provides for methods of classifying tumors, and thus grouping or "stratifying" patients, according to the expression profile of selected differentially expressed genes in a tumor. Differentially expressed genes can be analyzed

for correlation with other differentially expressed genes in a single tumor type or across tumor types. Genes that demonstrate consistent correlation in expression profile in a given cancer cell type (*e.g.*, in a colon cancer cell or type of colon cancer) can be grouped together, *e.g.*, when one gene is overexpressed in a tumor, a second gene is also usually overexpressed. Tumors can then be classified according to the expression profile of one or more genes selected from one or more groups.

[00122] The tumor of each patient in a pool of potential patients can be classified as described above. Patients having similarly classified tumors can then be selected for participation in an investigative or clinical trial of a cancer therapeutic where a homogeneous population is desired. The tumor classification of a patient can also be used in assessing the efficacy of a cancer therapeutic in a heterogeneous patient population. In addition, therapy for a patient having a tumor of a given expression profile can then be selected accordingly.

Treatment of colon cancer

[00123] The invention further provides methods for reducing growth of colon cancer cells. In general, the methods comprise contacting a colon cancer cell with a substance that modulates (1) expression of a polynucleotide corresponding to a gene that is differentially expressed in colon cancer; or (2) a level of and/or an activity of a colon cancer-associated polypeptide. In general, the methods provide for decreasing the expression of a gene that is differentially expressed in a colon cancer cell or decreasing the level of and/or decreasing an activity of a colon cancer-associated polypeptide.

[00124] “Reducing growth of colon cancer cells” includes, but is not limited to, reducing proliferation of colon cancer cells, and reducing the incidence of a non-cancerous colon cell becoming a cancerous colon cell. Whether a reduction in colon cancer cell growth has been achieved can be readily determined using any known assay, including, but not limited to, [³H]-thymidine incorporation; counting cell number over a period of time; detecting and/or measuring a marker associated with colon cancer (*e.g.*, CEA, CA19-9, and LASA).

[00125] The present invention provides methods for treating colon cancer, generally

comprising administering to an individual in need thereof a substance that reduces colon cancer cell growth, in an amount sufficient to reduce colon cancer cell growth and treat the colon cancer. Whether a substance, or a specific amount of the substance, is effective in treating colon cancer can be assessed using any of a variety of known diagnostic assays for colon cancer, including, but not limited to, sigmoidoscopy, proctoscopy, rectal examination, colonoscopy with biopsy, contrast radiographic studies, CAT scans, angiography, and detection of a tumor marker associated with colon cancer in the blood of the individual. The substance can be administered systemically or locally. Thus, in some embodiments, the substance is administered locally, and colon cancer growth is decreased at the site of administration. Local administration may be useful in treating, e.g., a solid tumor.

[00126] A substance that reduces colon cancer cell growth can be targeted to a colon cancer cell. Thus, in some embodiments, the invention provides a method of delivering a drug to a colon cancer cell, comprising administering a drug-antibody complex to a subject, wherein the antibody is specific for a colon cancer-associated polypeptide, and the drug is one that reduces colon cancer cell growth, a variety of which are known in the art. Targeting can be accomplished by coupling (e.g., linking, directly or via a linker molecule, either covalently or non-covalently, so as to form a drug-antibody complex) a drug to an antibody specific for a colon cancer-associated polypeptide. Methods of coupling a drug to an antibody are well known in the art and need not be elaborated upon herein.

[00127] In another embodiment, differentially expressed gene products (e.g., polypeptides or polynucleotides encoding such polypeptides) may be effectively used in treatment through vaccination. The growth of cancer cells is naturally limited in part due to immune surveillance. Stimulation of the immune system using a particular tumor-specific antigen enhances the effect towards the tumor expressing the antigen. An active vaccine comprising a polypeptide encoded by the cDNA of this invention would be appropriately administered to subjects having overabundance of the corresponding RNA, or those predisposed for developing cancer cells with overabundance of the same RNA.

Polypeptide antigens are typically combined with an adjuvant as part of a vaccine composition. The vaccine is preferably administered first as a priming dose, and then again as a boosting dose, usually at least four weeks later. Further boosting doses may be given to enhance the effect. The dose and its timing are usually determined by the person responsible for the treatment.

[00128] The invention also encompasses the selection of a therapeutic regimen based upon the expression profile of differentially expressed genes in the patient's tumor. For example, a tumor can be analyzed for its expression profile of the genes corresponding to SEQ ID NOS:1-1303 as described herein, *e.g.*, the tumor is analyzed to determine which genes are expressed at elevated levels or at decreased levels relative to normal cells of the same tissue type. The expression patterns of the tumor are then compared to the expression patterns of tumors that respond to a selected therapy. Where the expression profiles of the test tumor cell and the expression profile of a tumor cell of known drug responsivity at least substantially match (*e.g.*, selected sets of genes at elevated levels in the tumor of known drug responsivity and are also at elevated levels in the test tumor cell), then the drug selected for therapy is the drug to which tumors with that expression pattern respond.

IDENTIFICATION OF THERAPEUTIC TARGETS AND ANTI-CANCER THERAPEUTIC AGENTS

[00129] The present invention also encompasses methods for identification of agents having the ability to modulate activity of a differentially expressed gene product, as well as methods for identifying a differentially expressed gene product as a therapeutic target for treatment of cancer, especially colon cancer.

Candidate agents

[00130] Identification of compounds that modulate activity of a differentially expressed gene product can be accomplished using any of a variety of drug screening techniques. Such agents are candidates for development of cancer therapies. Of particular interest are screening assays for agents that have tolerable toxicity for normal, non-cancerous human cells. The screening assays of the invention are generally based upon the ability of the

agent to modulate an activity of a differentially expressed gene product and/or to inhibit or suppress phenomenon associated with cancer (*e.g.*, cell proliferation, colony formation, cell cycle arrest, metastasis, and the like).

[00131] The term "agent" as used herein describes any molecule, *e.g.* protein or pharmaceutical, with the capability of modulating a biological activity of a gene product of a differentially expressed gene. Generally a plurality of assay mixtures are run in parallel with different agent concentrations to obtain a differential response to the various concentrations. Typically, one of these concentrations serves as a negative control, *i.e.* at zero concentration or below the level of detection.

[00132] Candidate agents encompass numerous chemical classes, though typically they are organic molecules, preferably small organic compounds having a molecular weight of more than 50 and less than about 2,500 daltons. Candidate agents comprise functional groups necessary for structural interaction with proteins, particularly hydrogen bonding, and typically include at least an amine, carbonyl, hydroxyl or carboxyl group, preferably at least two of the functional chemical groups. The candidate agents often comprise cyclical carbon or heterocyclic structures and/or aromatic or polyaromatic structures substituted with one or more of the above functional groups. Candidate agents are also found among biomolecules including, but not limited to: peptides, saccharides, fatty acids, steroids, purines, pyrimidines, derivatives, structural analogs or combinations thereof.

[00133] Candidate agents are obtained from a wide variety of sources including libraries of synthetic or natural compounds. For example, numerous means are available for random and directed synthesis of a wide variety of organic compounds and biomolecules, including expression of randomized oligonucleotides and oligopeptides. Alternatively, libraries of natural compounds in the form of bacterial, fungal, plant and animal extracts (including extracts from human tissue to identify endogenous factors affecting differentially expressed gene products) are available or readily produced. Additionally, natural or synthetically produced libraries and compounds are readily modified through conventional chemical, physical and biochemical means, and may be used to produce

combinatorial libraries. Known pharmacological agents may be subjected to directed or random chemical modifications, such as acylation, alkylation, esterification, amidification, *etc.* to produce structural analogs.

[00134] Exemplary candidate agents of particular interest include, but are not limited to, antisense polynucleotides, and antibodies, soluble receptors, and the like. Antibodies and soluble receptors are of particular interest as candidate agents where the target differentially expressed gene product is secreted or accessible at the cell-surface (*e.g.*, receptors and other molecule stably-associated with the outer cell membrane).

Screening of candidate agents

[00135] Screening assays can be based upon any of a variety of techniques readily available and known to one of ordinary skill in the art. In general, the screening assays involve contacting a cancerous cell (preferably a cancerous colon cell) with a candidate agent, and assessing the effect upon biological activity of a differentially expressed gene product. The effect upon a biological activity can be detected by, for example, detection of expression of a gene product of a differentially expressed gene (*e.g.*, a decrease in mRNA or polypeptide levels, would in turn cause a decrease in biological activity of the gene product). Alternatively or in addition, the effect of the candidate agent can be assessed by examining the effect of the candidate agent in a functional assay. For example, where the differentially expressed gene product is an enzyme, then the effect upon biological activity can be assessed by detecting a level of enzymatic activity associated with the differentially expressed gene product. The functional assay will be selected according to the differentially expressed gene product. In general, where the differentially expressed gene is increased in expression in a cancerous cell, agents of interest are those that decrease activity of the differentially expressed gene product.

[00136] Assays described *infra* can be readily adapted in the screening assay embodiments of the invention. Exemplary assays useful in screening candidate agents include, but are not limited to, hybridization-based assays (*e.g.*, use of nucleic acid probes or primers to assess expression levels), antibody-based assays (*e.g.*, to assess levels of polypeptide gene products), binding assays (*e.g.*, to detect interaction of a candidate agent with a

differentially expressed polypeptide, which assays may be competitive assays where a natural or synthetic ligand for the polypeptide is available), and the like. Additional exemplary assays include, but are not necessarily limited to, cell proliferation assays, antisense knockout assays, assays to detect inhibition of cell cycle, assays of induction of cell death/apoptosis, and the like. Generally such assays are conducted *in vitro*, but many assays can be adapted for *in vivo* analyses, *e.g.*, in an animal model of the cancer.

Identification of therapeutic targets

[00137] In another embodiment, the invention contemplates identification of differentially expressed genes and gene products as therapeutic targets. In some respects, this is the converse of the assays described above for identification of agents having activity in modulating (*e.g.*, decreasing or increasing) activity of a differentially expressed gene product.

[00138] In this embodiment, therapeutic targets are identified by examining the effect(s) of an agent that can be demonstrated or has been demonstrated to modulate a cancerous phenotype (*e.g.*, inhibit or suppress or prevent development of a cancerous phenotype). Such agents are generally referred to herein as an "anti-cancer agent", which agents encompass chemotherapeutic agents. For example, the agent can be an antisense oligonucleotide that is specific for a selected gene transcript. For example, the antisense oligonucleotide may have a sequence corresponding to a sequence of a differentially expressed gene described herein, *e.g.*, a sequence of one of SEQ ID NOS:1-1303.

[00139] Assays for identification of therapeutic targets can be conducted in a variety of ways using methods that are well known to one of ordinary skill in the art. For example, a test cancerous cell that expresses or overexpresses a differentially expressed gene is contacted with an anti-cancer agent, the effect upon a cancerous phenotype and a biological activity of the candidate gene product assessed. The biological activity of the candidate gene product can be assayed by examining, for example, modulation of expression of a gene encoding the candidate gene product (*e.g.*, as detected by, for example, an increase or decrease in transcript levels or polypeptide levels), or modulation of an enzymatic or other activity of the gene product. The cancerous phenotype can be,

for example, cellular proliferation, loss of contact inhibition of growth (*e.g.*, colony formation), tumor growth (*in vitro* or *in vivo*), and the like. Alternatively or in addition, the effect of modulation of a biological activity of the candidate target gene upon cell death/apoptosis or cell cycle regulation can be assessed.

[00140] Inhibition or suppression of a cancerous phenotype, or an increase in cell/death apoptosis as a result of modulation of biological activity of a candidate gene product indicates that the candidate gene product is a suitable target for cancer therapy. Assays described infra can be readily adapted in for assays for identification of therapeutic targets. Generally such assays are conducted *in vitro*, but many assays can be adapted for *in vivo* analyses, *e.g.*, in an appropriate, art-accepted animal model of the cancer.

USE OF POLYPEPTIDES TO SCREEN FOR PEPTIDE ANALOGS AND ANTAGONISTS

[00141] Polypeptides encoded by differentially expressed genes identified herein can be used to screen peptide libraries to identify binding partners, such as receptors, from among the encoded polypeptides. Peptide libraries can be synthesized according to methods known in the art (*see, e.g.*, USPN 5,010,175 and WO 91/17823).

[00142] Agonists or antagonists of the polypeptides if the invention can be screened using any available method known in the art, such as signal transduction, antibody binding, receptor binding, mitogenic assays, chemotaxis assays, etc. The assay conditions ideally should resemble the conditions under which the native activity is exhibited *in vivo*, that is, under physiologic pH, temperature, and ionic strength. Suitable agonists or antagonists will exhibit strong inhibition or enhancement of the native activity at concentrations that do not cause toxic side effects in the subject. Agonists or antagonists that compete for binding to the native polypeptide can require concentrations equal to or greater than the native concentration, while inhibitors capable of binding irreversibly to the polypeptide can be added in concentrations on the order of the native concentration.

[00143] Such screening and experimentation can lead to identification of a polypeptide binding partner, such as a receptor, encoded by a gene or a cDNA corresponding to a polynucleotide described herein, and at least one peptide agonist or antagonist of the

binding partner. Such agonists and antagonists can be used to modulate, enhance, or inhibit receptor function in cells to which the receptor is native, or in cells that possess the receptor as a result of genetic engineering. Further, if the receptor shares biologically important characteristics with a known receptor, information about agonist/antagonist binding can facilitate development of improved agonists/antagonists of the known receptor.

VACCINES AND USES

[00144] The differentially expressed nucleic acids and polypeptides produced by the nucleic acids of the invention can also be used to modulate primary immune response to prevent or treat cancer. Every immune response is a complex and intricately regulated sequence of events involving several cell types. It is triggered when an antigen enters the body and encounters a specialized class of cells called antigen-presenting cells (APCs). These APCs capture a minute amount of the antigen and display it in a form that can be recognized by antigen-specific helper T lymphocytes. The helper (Th) cells become activated and, in turn, promote the activation of other classes of lymphocytes, such as B cells or cytotoxic T cells. The activated lymphocytes then proliferate and carry out their specific effector functions, which in many cases successfully activate or eliminate the antigen. Thus, activating the immune response to a particular antigen associated with a cancer cell can protect the patient from developing cancer or result in lymphocytes eliminating cancer cells expressing the antigen.

[00145] Gene products, including polypeptides, mRNA (particularly mRNAs having distinct secondary and/or tertiary structures), cDNA, or complete gene, can be prepared and used in vaccines for the treatment or prevention of hyperproliferative disorders and cancers. The nucleic acids and polypeptides can be utilized to enhance the immune response, prevent tumor progression, prevent hyperproliferative cell growth, and the like. Methods for selecting nucleic acids and polypeptides that are capable of enhancing the immune response are known in the art. Preferably, the gene products for use in a vaccine are gene products which are present on the surface of a cell and are recognizable by

lymphocytes and antibodies.

[00146] The gene products may be formulated with pharmaceutically acceptable carriers into pharmaceutical compositions by methods known in the art. The composition is useful as a vaccine to prevent or treat cancer. The composition may further comprise at least one co-immunostimulatory molecule, including but not limited to one or more major histocompatibility complex (MHC) molecules, such as a class I or class II molecule, preferably a class I molecule. The composition may further comprise other stimulator molecules including B7.1, B7.2, ICAM-1, ICAM-2, LFA-1, LFA-3, CD72 and the like, immunostimulatory polynucleotides (which comprise an 5'-CG-3' wherein the cytosine is unmethylated), and cytokines which include but are not limited to IL-1 through IL-15, TNF- α , IFN- γ , RANTES, G-CSF, M-CSF, IFN- α , CTAP III, ENA-78, GRO, I-309, PF-4, IP-10, LD-78, MGSA, MIP-1 α , MIP-1 β , or combination thereof, and the like for immunopotential. In one embodiment, the immunopotential of particular interest are those which facilitate a Th1 immune response.

[00147] The gene products may also be prepared with a carrier that will protect the gene products against rapid elimination from the body, such as a controlled release formulation, including implants and microencapsulated delivery systems. Biodegradable polymers can be used, such as ethylene vinyl acetate, polyanhydrides, polyglycolic acid, collagen, polyorthoesters, polylactic acid, and the like. Methods for preparation of such formulations are known in the art.

[00148] In the methods of preventing or treating cancer, the gene products may be administered via one of several routes including but not limited to transdermal, transmucosal, intravenous, intramuscular, subcutaneous, intradermal, intraperitoneal, intrathecal, intrapleural, intrauterine, rectal, vaginal, topical, intratumor, and the like. For transmucosal or transdermal administration, penetrants appropriate to the barrier to be permeated are used in the formulation. Such penetrants are generally known in the art, and include, for example, administration bile salts and fusidic acid derivatives. In addition, detergents may be used to facilitate permeation. Transmucosal administration may be by nasal sprays or suppositories. For oral administration, the gene products are

formulated into conventional oral administration form such as capsules, tablets and toxics.

[00149] The gene product is administered to a patient in an amount effective to prevent or treat cancer. In general, it is desirable to provide the patient with a dosage of gene product of at least about 1 pg per Kg body weight, preferably at least about 1 ng per Kg body weight, more preferably at least about 1 μ g or greater per Kg body weight of the recipient. A range of from about 1 ng per Kg body weight to about 100 mg per Kg body weight is preferred although a lower or higher dose may be administered. The dose is effective to prime, stimulate and/or cause the clonal expansion of antigen-specific T lymphocytes, preferably cytotoxic T lymphocytes, which in turn are capable of preventing or treating cancer in the recipient. The dose is administered at least once and may be provided as a bolus or a continuous administration. Multiple administrations of the dose over a period of several weeks to months may be preferable. Subsequent doses may be administered as indicated.

[00150] In another method of treatment, autologous cytotoxic lymphocytes or tumor infiltrating lymphocytes may be obtained from a patient with cancer. The lymphocytes are grown in culture, and antigen-specific lymphocytes are expanded by culturing in the presence of the specific gene products alone or in combination with at least one co-immunostimulatory molecule with cytokines. The antigen-specific lymphocytes are then infused back into the patient in an amount effective to reduce or eliminate the tumors in the patient. Cancer vaccines and their uses are further described in USPN 5,961,978; USPN 5,993,829; USPN 6,132,980; and WO 00/38706.

PHARMACEUTICAL COMPOSITIONS AND USES

[00151] Pharmaceutical compositions can comprise polypeptides, receptors that specifically bind a polypeptide produced by a differentially expressed gene (*e.g.*, antibodies, or polynucleotides (including antisense nucleotides and ribozymes) of the claimed invention in a therapeutically effective amount. The compositions can be used to treat primary tumors as well as metastases of primary tumors. In addition, the

pharmaceutical compositions can be used in conjunction with conventional methods of cancer treatment, *e.g.*, to sensitize tumors to radiation or conventional chemotherapy.

[00152] Where the pharmaceutical composition comprises a receptor (such as an antibody) that specifically binds to a gene product encoded by a differentially expressed gene, the receptor can be coupled to a drug for delivery to a treatment site or coupled to a detectable label to facilitate imaging of a site comprising colon cancer cells. Methods for coupling antibodies to drugs and detectable labels are well known in the art, as are methods for imaging using detectable labels.

[00153] The term “therapeutically effective amount” as used herein refers to an amount of a therapeutic agent to treat, ameliorate, or prevent a desired disease or condition, or to exhibit a detectable therapeutic or preventative effect. The effect can be detected by, for example, chemical markers or antigen levels. Therapeutic effects also include reduction in physical symptoms, such as decreased body temperature.

[00154] The precise effective amount for a subject will depend upon the subject's size and health, the nature and extent of the condition, and the therapeutics or combination of therapeutics selected for administration. Thus, it is not useful to specify an exact effective amount in advance. However, the effective amount for a given situation is determined by routine experimentation and is within the judgment of the clinician. For purposes of the present invention, an effective dose will generally be from about 0.01 mg/ kg to 50 mg/kg or 0.05 mg/kg to about 10 mg/kg of the DNA constructs in the individual to which it is administered.

[00155] A pharmaceutical composition can also contain a pharmaceutically acceptable carrier. The term “pharmaceutically acceptable carrier” refers to a carrier for administration of a therapeutic agent, such as antibodies or a polypeptide, genes, and other therapeutic agents. The term refers to any pharmaceutical carrier that does not itself induce the production of antibodies harmful to the individual receiving the composition, and which can be administered without undue toxicity. Suitable carriers can be large, slowly metabolized macromolecules such as proteins, polysaccharides, polylactic acids, polyglycolic acids, polymeric amino acids, amino acid copolymers, and

inactive virus particles. Such carriers are well known to those of ordinary skill in the art. Pharmaceutically acceptable carriers in therapeutic compositions can include liquids such as water, saline, glycerol and ethanol. Auxiliary substances, such as wetting or emulsifying agents, pH buffering substances, and the like, can also be present in such vehicles.

[00156] Typically, the therapeutic compositions are prepared as injectables, either as liquid solutions or suspensions; solid forms suitable for solution in, or suspension in, liquid vehicles prior to injection can also be prepared. Liposomes are included within the definition of a pharmaceutically acceptable carrier. Pharmaceutically acceptable salts can also be present in the pharmaceutical composition, e.g., mineral acid salts such as hydrochlorides, hydrobromides, phosphates, sulfates, and the like; and the salts of organic acids such as acetates, propionates, malonates, benzoates, and the like. A thorough discussion of pharmaceutically acceptable excipients is available in *Remington: The Science and Practice of Pharmacy* (1995) Alfonso Gennaro, Lippincott, Williams, & Wilkins.

DELIVERY METHODS

[00157] Once formulated, the compositions contemplated by the invention can be (1) administered directly to the subject (e.g., as polynucleotide, polypeptides, small molecule agonists or antagonists, and the like); or (2) delivered ex vivo, to cells derived from the subject (e.g., as in *ex vivo* gene therapy). Direct delivery of the compositions will generally be accomplished by parenteral injection, e.g., subcutaneously, intraperitoneally, intravenously or intramuscularly, intratumoral or to the interstitial space of a tissue. Other modes of administration include oral and pulmonary administration, suppositories, and transdermal applications, needles, and gene guns or hyposprays. Dosage treatment can be a single dose schedule or a multiple dose schedule.

[00158] Methods for the ex vivo delivery and reimplantation of transformed cells into a subject are known in the art and described in e.g., International Publication No. WO 93/14778. Examples of cells useful in ex vivo applications include, for example, stem

cells, particularly hematopoietic, lymph cells, macrophages, dendritic cells, or tumor cells. Generally, delivery of nucleic acids for both ex vivo and in vitro applications can be accomplished by, for example, dextran-mediated transfection, calcium phosphate precipitation, polybrene mediated transfection, protoplast fusion, electroporation, encapsulation of the polynucleotide(s) in liposomes, and direct microinjection of the DNA into nuclei, all well known in the art.

[00159] Once differential expression of a gene corresponding to a polynucleotide described herein has been found to correlate with a proliferative disorder, such as neoplasia, dysplasia, and hyperplasia, the disorder can be amenable to treatment by administration of a therapeutic agent based on the provided polynucleotide, corresponding polypeptide or other corresponding molecule (e.g., antisense, ribozyme, etc.). In other embodiments, the disorder can be amenable to treatment by administration of a small molecule drug that, for example, serves as an inhibitor (antagonist) of the function of the encoded gene product of a gene having increased expression in cancerous cells relative to normal cells or as an agonist for gene products that are decreased in expression in cancerous cells (e.g., to promote the activity of gene products that act as tumor suppressors).

[00160] The dose and the means of administration of the inventive pharmaceutical compositions are determined based on the specific qualities of the therapeutic composition, the condition, age, and weight of the patient, the progression of the disease, and other relevant factors. For example, administration of polynucleotide therapeutic composition agents includes local or systemic administration, including injection, oral administration, particle gun or catheterized administration, and topical administration. In general, the therapeutic polynucleotide composition contains an expression construct comprising a promoter operably linked to a polynucleotide of at least 12, 22, 25, 30, or 35 contiguous nt of the polynucleotide disclosed herein. Various methods can be used to administer the therapeutic composition directly to a specific site in the body. For example, a small metastatic lesion is located and the therapeutic composition injected several times in several different locations within the body of tumor. Alternatively,

arteries which serve a tumor are identified, and the therapeutic composition injected into such an artery, in order to deliver the composition directly into the tumor. A tumor that has a necrotic center is aspirated and the composition injected directly into the now empty center of the tumor. The antisense composition is directly administered to the surface of the tumor, for example, by topical application of the composition. X-ray imaging is used to assist in certain of the above delivery methods.

[00161] Targeted delivery of therapeutic compositions containing an antisense polynucleotide, subgenomic polynucleotides, or antibodies to specific tissues can also be used. Receptor-mediated DNA delivery techniques are described in, for example, Findeis *et al.*, *Trends Biotechnol.* (1993) 11:202; Chiou *et al.*, *Gene Therapeutics: Methods And Applications Of Direct Gene Transfer* (J.A. Wolff, ed.) (1994); Wu *et al.*, *J. Biol. Chem.* (1988) 263:621; Wu *et al.*, *J. Biol. Chem.* (1994) 269:542; Zenke *et al.*, *Proc. Natl. Acad. Sci. (USA)* (1990) 87:3655; Wu *et al.*, *J. Biol. Chem.* (1991) 266:338. Therapeutic compositions containing a polynucleotide are administered in a range of about 100 ng to about 200 mg of DNA for local administration in a gene therapy protocol. Concentration ranges of about 500 ng to about 50 mg, about 1 µg to about 2 mg, about 5 µg to about 500 µg, and about 20 µg to about 100 µg of DNA can also be used during a gene therapy protocol. Factors such as method of action (e.g., for enhancing or inhibiting levels of the encoded gene product) and efficacy of transformation and expression are considerations which will affect the dosage required for ultimate efficacy of the antisense subgenomic polynucleotides.

[00162] Where greater expression is desired over a larger area of tissue, larger amounts of antisense subgenomic polynucleotides or the same amounts readministered in a successive protocol of administrations, or several administrations to different adjacent or close tissue portions of, for example, a tumor site, may be required to effect a positive therapeutic outcome. In all cases, routine experimentation in clinical trials will determine specific ranges for optimal therapeutic effect. For polynucleotide related genes encoding polypeptides or proteins with anti-inflammatory activity, suitable use, doses, and administration are described in USPN 5,654,173.

[00163] The therapeutic polynucleotides and polypeptides of the present invention can be delivered using gene delivery vehicles. The gene delivery vehicle can be of viral or non-viral origin (see generally, Jolly, *Cancer Gene Therapy* (1994) 1:51; Kimura, *Human Gene Therapy* (1994) 5:845; Connelly, *Human Gene Therapy* (1995) 1:185; and Kaplitt, *Nature Genetics* (1994) 6:148). Expression of such coding sequences can be induced using endogenous mammalian or heterologous promoters. Expression of the coding sequence can be either constitutive or regulated.

[00164] Viral-based vectors for delivery of a desired polynucleotide and expression in a desired cell are well known in the art. Exemplary viral-based vehicles include, but are not limited to, recombinant retroviruses (see, e.g., WO 90/07936; WO 94/03622; WO 93/25698; WO 93/25234; USPN 5, 219,740; WO 93/11230; WO 93/10218; USPN 4,777,127; GB Patent No. 2,200,651; EP 0 345 242; and WO 91/02805), alphavirus-based vectors (e.g., Sindbis virus vectors, Semliki forest virus (ATCC VR-67; ATCC VR-1247), Ross River virus (ATCC VR-373; ATCC VR-1246) and Venezuelan equine encephalitis virus (ATCC VR-923; ATCC VR-1250; ATCC VR 1249; ATCC VR-532), and adeno-associated virus (AAV) vectors (see, e.g., WO 94/12649, WO 93/03769; WO 93/19191; WO 94/28938; WO 95/11984 and WO 95/00655). Administration of DNA linked to killed adenovirus as described in Curiel, *Hum. Gene Ther.* (1992) 3:147 can also be employed.

[00165] Non-viral delivery vehicles and methods can also be employed, including, but not limited to, polycationic condensed DNA linked or unlinked to killed adenovirus alone (see, e.g., Curiel, *Hum. Gene Ther.* (1992) 3:147); ligand-linked DNA (see, e.g., Wu, *J. Biol. Chem.* (1989) 264:16985); eukaryotic cell delivery vehicles cells (see, e.g., USPN 5,814,482; WO 95/07994; WO 96/17072; WO 95/30763; and WO 97/42338) and nucleic charge neutralization or fusion with cell membranes. Naked DNA can also be employed. Exemplary naked DNA introduction methods are described in WO 90/11092 and USPN 5,580,859. Liposomes that can act as gene delivery vehicles are described in USPN 5,422,120; WO 95/13796; WO 94/23697; WO 91/14445; and EP 0524968. Additional approaches are described in Philip, *Mol. Cell Biol.* (1994) 14:2411, and in Woffendin,

Proc. Natl. Acad. Sci. (1994) 91:1581.

[00166] Further non-viral delivery suitable for use includes mechanical delivery systems such as the approach described in Woffendin *et al.*, *Proc. Natl. Acad. Sci. USA* (1994) 91(24):11581. Moreover, the coding sequence and the product of expression of such can be delivered through deposition of photopolymerized hydrogel materials or use of ionizing radiation (see, e.g., USPN 5,206,152 and WO 92/11033). Other conventional methods for gene delivery that can be used for delivery of the coding sequence include, for example, use of hand-held gene transfer particle gun (see, e.g., USPN 5,149,655); use of ionizing radiation for activating transferred gene (see, e.g., USPN 5,206,152 and WO 92/11033).

EXAMPLES

[00167] The following examples are put forth so as to provide those of ordinary skill in the art with a complete disclosure and description of how to make and use the present invention, and are not intended to limit the scope of what the inventors regard as their invention nor are they intended to represent that the experiments below are all or the only experiments performed. Efforts have been made to ensure accuracy with respect to numbers used (e.g. amounts, temperature, etc.) but some experimental errors and deviations should be accounted for. Unless indicated otherwise, parts are parts by weight, molecular weight is weight average molecular weight, temperature is in degrees Centigrade, and pressure is at or near atmospheric.

EXAMPLE 1: SOURCE OF BIOLOGICAL MATERIALS

[00168] The biological materials used in the experiments that led to the present invention are described below.

Source of patient tissue samples

[00169] Normal and cancerous tissues were collected from patients using laser capture microdissection (LCM) techniques, which techniques are well known in the art (see, e.g., Ohyama *et al.* (2000) *Biotechniques* 29:530-6; Curran *et al.* (2000) *Mol. Pathol.* 53:64-8;

Suarez-Quian *et al.* (1999) *Biotechniques* 26:328-35; Simone *et al.* (1998) *Trends Genet* 14:272-6; Conia *et al.* (1997) *J. Clin. Lab. Anal.* 11:28-38; Emmert-Buck *et al.* (1996) *Science* 274:998-1001). Table 1 (inserted prior to claims) provides information about each patient from which colon tissue samples were isolated, including: the Patient ID ("PT ID") and Path ReportID ("Path ID"), which are numbers assigned to the patient and the pathology reports for identification purposes; the group ("Grp") to which the patients have been assigned; the anatomical location of the tumor ("Anatom Loc"); the primary tumor size ("Size"); the primary tumor grade ("Grade"); the identification of the histopathological grade ("Histo Grade"); a description of local sites to which the tumor had invaded ("Local Invasion"); the presence of lymph node metastases ("Lymph Met"); the incidence of lymph node metastases (provided as a number of lymph nodes positive for metastasis over the number of lymph nodes examined) ("Lymph Met Incid"); the regional lymphnode grade ("Reg Lymph Grade"); the identification or detection of metastases to sites distant to the tumor and their location ("Dist Met & Loc"); the grade of distant metastasis ("Dist Met Grade"); and general comments about the patient or the tumor ("Comments"). Histopathology of all primary tumors indicated the tumor was adenocarcinoma except for Patient ID Nos. 130 (for which no information was provided), 392 (in which greater than 50% of the cells were mucinous carcinoma), and 784 (adenosquamous carcinoma). Extranodal extensions were described in three patients, Patient ID Nos. 784, 789, and 791. Lymphovascular invasion was described in Patient ID Nos. 128, 228, 278, 517, 534, 784, 786, 789, 791, 890, and 892. Crohn's-like infiltrates were described in seven patients, Patient ID Nos. 52, 264, 268, 392, 393, 784, and 791.

Source of polynucleotides on arrays

[00170] Polynucleotides for use on the arrays were obtained from both publicly available sources and from cDNA libraries generated from selected cell lines and patient tissues. Table 2 (inserted prior to claims) provides information about the polynucleotides on the arrays including: (1) the "SEQ ID NO" assigned to each sequence for use in the present specification; (2) the spot identification number ("Spot ID"), an internal reference that serves as a unique identifier for the spot on the array; (3) the "Clone ID" assigned to the

Characterization of sequences

Summary of TeraBLAST Search Results

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("GBHit"); (6) a description of the GenBank sequence ("GBDescription"); and (7) the score of the similarity of the polynucleotide sequence and the GenBank sequence ("GBScore"). The published information for each GenBank and EST description, as well as the corresponding sequence identified by the provided accession number, are incorporated herein by reference.

EXAMPLE 2: DETECTION OF DIFFERENTIAL EXPRESSION USING ARRAYS

- [00174] cDNA probes were prepared from total RNA isolated from the patient cells described above. Since LCM provides for the isolation of specific cell types to provide a substantially homogenous cell sample, this provided for a similarly pure RNA sample.
- [00175] Total RNA was first reverse transcribed into cDNA using a primer containing a T7 RNA polymerase promoter, followed by second strand DNA synthesis. cDNA was then transcribed *in vitro* to produce antisense RNA using the T7 promoter-mediated expression (see, *e.g.*, Luo *et al.* (1999) *Nature Med* 5:117-122), and the antisense RNA was then converted into cDNA. The second set of cDNAs were again transcribed *in vitro*, using the T7 promoter, to provide antisense RNA. Optionally, the RNA was again converted into cDNA, allowing for up to a third round of T7-mediated amplification to produce more antisense RNA. Thus the procedure provided for two or three rounds of *in vitro* transcription to produce the final RNA used for fluorescent labeling.
- [00176] Fluorescent probes were generated by first adding control RNA to the antisense RNA mix, and producing fluorescently labeled cDNA from the RNA starting material. Fluorescently labeled cDNAs prepared from the tumor RNA sample were compared to fluorescently labeled cDNAs prepared from normal cell RNA sample. For example, the cDNA probes from the normal cells were labeled with Cy3 fluorescent dye (green) and the cDNA probes prepared from the tumor cells were labeled with Cy5 fluorescent dye (red), and vice versa.
- [00177] Each array used had an identical spatial layout and control spot set. Each microarray was divided into two areas, each area having an array with, on each half, twelve groupings of 32 x 12 spots, for a total of about 9,216 spots on each array. The two

areas are spotted identically which provide for at least two duplicates of each clone per array.

[00178] Polynucleotides for use on the arrays were obtained from both publicly available sources and from cDNA libraries generated from selected cell lines and patient tissues as described above and in Table 2 (inserted prior to claims). PCR products of from about 0.5kb to 2.0 kb amplified from these sources were spotted onto the array using a Molecular Dynamics Gen III spotter according to the manufacturer's recommendations. The first row of each of the 24 regions on the array had about 32 control spots, including 4 negative control spots and 8 test polynucleotides. The test polynucleotides were spiked into each sample before the labeling reaction with a range of concentrations from 2-600 pg/slide and ratios of 1:1. For each array design, two slides were hybridized with the test samples reverse-labeled in the labeling reaction. This provided for about four duplicate measurements for each clone, two of one color and two of the other, for each sample.

[00179] The differential expression assay was performed by mixing equal amounts of probes from tumor cells and normal cells of the same patient. The arrays were prehybridized by incubation for about 2 hrs at 60°C in 5X SSC/0.2% SDS/1 mM EDTA, and then washed three times in water and twice in isopropanol. Following prehybridization of the array, the probe mixture was then hybridized to the array under conditions of high stringency (overnight at 42°C in 50% formamide, 5X SSC, and 0.2% SDS. After hybridization, the array was washed at 55°C three times as follows: 1) first wash in 1X SSC/0.2% SDS; 2) second wash in 0.1X SSC/0.2% SDS; and 3) third wash in 0.1X SSC.

[00180] The arrays were then scanned for green and red fluorescence using a Molecular Dynamics Generation III dual color laser-scanner/detector. The images were processed using BioDiscovery Autogene software, and the data from each scan set normalized to provide for a ratio of expression relative to normal. Data from the microarray experiments was analyzed according to the algorithms described in U.S. application serial no. 60/252,358, filed November 20, 2000, by E.J. Moler, M.A. Boyle, and F.M. Randazzo, and entitled "Precision and accuracy in cDNA microarray data," which

application is specifically incorporated herein by reference.

[00181] The experiment was repeated, this time labeling the two probes with the opposite color in order to perform the assay in both "color directions." Each experiment was sometimes repeated with two more slides (one in each color direction). The level fluorescence for each sequence on the array expressed as a ratio of the geometric mean of 8 replicate spots/genes from the four arrays or 4 replicate spots/gene from 2 arrays or some other permutation. The data were normalized using the spiked positive controls present in each duplicated area, and the precision of this normalization was included in the final determination of the significance of each differential. The fluorescent intensity of each spot was also compared to the negative controls in each duplicated area to determine which spots have detected significant expression levels in each sample.

[00182] A statistical analysis of the fluorescent intensities was applied to each set of duplicate spots to assess the precision and significance of each differential measurement, resulting in a p-value testing the null hypothesis that there is no differential in the expression level between the tumor and normal samples of each patient. During initial analysis of the microarrays, the hypothesis was accepted if $p > 10^{-3}$, and the differential ratio was set to 1.000 for those spots. All other spots have a significant difference in expression between the tumor and normal sample. If the tumor sample has detectable expression and the normal does not, the ratio is truncated at 1000 since the value for expression in the normal sample would be zero, and the ratio would not be a mathematically useful value (e.g., infinity). If the normal sample has detectable expression and the tumor does not, the ratio is truncated to 0.001, since the value for expression in the tumor sample would be zero and the ratio would not be a mathematically useful value. These latter two situations are referred to herein as "on/off." Database tables were populated using a 95% confidence level ($p > 0.05$).

[00183] Table 4 (inserted prior to the claims) provides the results for gene products that were expressed by at least 2-fold or greater in the colon tumor samples relative to normal tissue samples in at least 20% of the patients tested, or gene products in which expression levels of the gene in colon tumor cells was less than or equal to $\frac{1}{2}$ of the expression level

[00184] Table 4 also includes the results from each patient, identified by the patient ID number (e.g., 10). This data represents the ratio of differential expression for the samples tested from that particular patient's tissues (e.g., "10" is the ratio from the tissue samples of Patient ID no. 10). The ratios of differential expression are expressed as a normalized hybridization signal associated with the tumor probe divided by the normalized hybridization signal with the normal probe. Thus, a ratio greater than 1 indicates that the gene product is increased in expression in cancerous cells relative to normal cells, while a ratio of less than 1 indicates the opposite.

EXAMPLE 3: ANTISENSE REGULATION OF GENE EXPRESSION

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[00187] A number of different oligonucleotides complementary to the mRNA generated by the differentially expressed genes identified herein can be designed as potential antisense oligonucleotides, and tested for their ability to suppress expression of the genes. Sets of antisense oligomers specific to each candidate target are designed using the sequences of the polynucleotides corresponding to a differentially expressed gene and the software program HYBsimulator Version 4 (available for Windows 95/Windows NT or for Power Macintosh, RNature, Inc. 1003 Health Sciences Road, West, Irvine, CA 92612 USA). Factors that are considered when designing antisense oligonucleotides include: 1) the secondary structure of oligonucleotides; 2) the secondary structure of the target gene; 3) the specificity with no or minimum cross-hybridization to other expressed genes; 4) stability; 5) length and 6) terminal GC content. The antisense oligonucleotide is designed so that it will hybridize to its target sequence under conditions of high stringency at physiological temperatures (*e.g.*, an optimal temperature for the cells in culture to provide for hybridization in the cell, *e.g.*, about 37°C), but with minimal formation of homodimers.

[00188] Using the sets of oligomers and the HYBsimulator program, three to ten antisense oligonucleotides and their reverse controls are designed and synthesized for each candidate mRNA transcript, which transcript is obtained from the gene corresponding to the target polynucleotide sequence of interest. Once synthesized and quantitated, the oligomers are screened for efficiency of a transcript knock-out in a panel of cancer cell lines. The efficiency of the knock-out is determined by analyzing mRNA levels using lightcycler quantification. The oligomers that resulted in the highest level of transcript knock-out, wherein the level was at least about 50%, preferably about 80-90%, up to 95% or more up to undetectable message, are selected for use in a cell-based proliferation assay, an anchorage independent growth assay, and an apoptosis assay.

[00189] The ability of each designed antisense oligonucleotide to inhibit gene expression is tested through transfection into SW620 colon carcinoma cells. For each transfection mixture, a carrier molecule (such as a lipid, lipid derivative, lipid-like molecule, cholesterol, cholesterol derivative, or cholesterol-like molecule) is prepared to a working

concentration of 0.5 mM in water, sonicated to yield a uniform solution, and filtered through a 0.45 µm PVDF membrane. The antisense or control oligonucleotide is then prepared to a working concentration of 100 µM in sterile Millipore water. The oligonucleotide is further diluted in OptiMEM™ (Gibco/BRL), in a microfuge tube, to 2 µM, or approximately 20 µg oligo/ml of OptiMEM™. In a separate microfuge tube, the carrier molecule, typically in the amount of about 1.5-2 nmol carrier/µg antisense oligonucleotide, is diluted into the same volume of OptiMEM™ used to dilute the oligonucleotide. The diluted antisense oligonucleotide is immediately added to the diluted carrier and mixed by pipetting up and down. Oligonucleotide is added to the cells to a final concentration of 30 nM.

[00190] The level of target mRNA that corresponds to a target gene of interest in the transfected cells is quantitated in the cancer cell lines using the Roche LightCycler™ real-time PCR machine. Values for the target mRNA are normalized versus an internal control (*e.g.*, beta-actin). For each 20 µl reaction, extracted RNA (generally 0.2-1 µg total) is placed into a sterile 0.5 or 1.5 ml microcentrifuge tube, and water is added to a total volume of 12.5 µl. To each tube is added 7.5 µl of a buffer/enzyme mixture, prepared by mixing (in the order listed) 2.5 µl H₂O, 2.0 µl 10X reaction buffer, 10 µl oligo dT (20 pmol), 1.0 µl dNTP mix (10 mM each), 0.5 µl RNasin® (20u) (Ambion, Inc., Hialeah, FL), and 0.5 µl MMLV reverse transcriptase (50u) (Ambion, Inc.). The contents are mixed by pipetting up and down, and the reaction mixture is incubated at 42°C for 1 hour. The contents of each tube are centrifuged prior to amplification.

[00191] An amplification mixture is prepared by mixing in the following order: 1X PCR buffer II, 3 mM MgCl₂, 140 µM each dNTP, 0.175 pmol each oligo, 1:50,000 dil of SYBR® Green, 0.25 mg/ml BSA, 1 unit *Taq* polymerase, and H₂O to 20 µl. (PCR buffer II is available in 10X concentration from Perkin-Elmer, Norwalk, CT). In 1X concentration it contains 10 mM Tris pH 8.3 and 50 mM KCl. SYBR® Green (Molecular Probes, Eugene, OR) is a dye which fluoresces when bound to double stranded DNA. As double stranded PCR product is produced during amplification, the fluorescence from SYBR® Green increases. To each 20 µl aliquot of amplification

mixture, 2 μ l of template RT is added, and amplification is carried out according to standard protocols. The results are expressed as the percent decrease in expression of the corresponding gene product relative to non-transfected cells, vehicle-only transfected (mock-transfected) cells, or cells transfected with reverse control oligonucleotides.

EXAMPLE 4: EFFECT OF EXPRESSION ON PROLIFERATION

[00192] The effect of gene expression on the inhibition of cell proliferation can be assessed in metastatic breast cancer cell lines (MDA-MB-231 ("231")); SW620 colon colorectal carcinoma cells; SKOV3 cells (a human ovarian carcinoma cell line); or LNCaP, PC3, 22Rv1, MDA-PCA-2b, or DU145 prostate cancer cells.

[00193] Cells are plated to approximately 60-80% confluency in 96-well dishes. Antisense or reverse control oligonucleotide is diluted to 2 μ M in OptiMEM™. The oligonucleotide-OptiMEM™ can then be added to a delivery vehicle, which delivery vehicle can be selected so as to be optimized for the particular cell type to be used in the assay. The oligo/delivery vehicle mixture is then further diluted into medium with serum on the cells. The final concentration of oligonucleotide for all experiments can be about 300 nM.

[00194] Antisense oligonucleotides are prepared as described above (see Example 3). Cells are transfected overnight at 37°C and the transfection mixture is replaced with fresh medium the next morning. Transfection is carried out as described above in Example 3.

[00195] Those antisense oligonucleotides that result in inhibition of proliferation of SW620 cells indicate that the corresponding gene plays a role in production or maintenance of the cancerous phenotype in cancerous colon cells. Those antisense oligonucleotides that inhibit proliferation in SKOV3 cells represent genes that play a role in production or maintenance of the cancerous phenotype in cancerous breast cells. Those antisense oligonucleotides that result in inhibition of proliferation of MDA-MB-231 cells indicate that the corresponding gene plays a role in production or maintenance of the cancerous phenotype in cancerous ovarian cells. Those antisense oligonucleotides that inhibit proliferation in LNCaP, PC3, 22Rv1, MDA-PCA-2b, or DU145 cells

represent genes that play a role in production or maintenance of the cancerous phenotype in cancerous prostate cells.

EXAMPLE 5: EFFECT OF GENE EXPRESSION ON CELL MIGRATION

[00196] The effect of gene expression on the inhibition of cell migration can be assessed in SW620 colon cancer cells using static endothelial cell binding assays, non-static endothelial cell binding assays, and transmigration assays.

[00197] For the static endothelial cell binding assay, antisense oligonucleotides are prepared as described above (see Example 3). Two days prior to use, colon cancer cells (CaP) are plated and transfected with antisense oligonucleotide as described above (see Examples 3 and 4). On the day before use, the medium is replaced with fresh medium, and on the day of use, the medium is replaced with fresh medium containing 2 μ M CellTracker green CMFDA (Molecular Probes, Inc.) and cells are incubated for 30 min. Following incubation, CaP medium is replaced with fresh medium (no CMFDA) and cells are incubated for an additional 30-60 min. CaP cells are detached using CMF PBS/2.5 mM EDTA or trypsin, spun and resuspended in DMEM/1% BSA/ 10 mM HEPES pH 7.0. Finally, CaP cells are counted and resuspended at a concentration of 1×10^6 cells/ml.

[00198] Endothelial cells (EC) are plated onto 96-well plates at 40-50% confluence 3 days prior to use. On the day of use, EC are washed 1X with PBS and 50 λ DMEM/1%BSA/10mM HEPES pH 7 is added to each well. To each well is then added 50K (50 λ) CaP cells in DMEM/1% BSA/ 10mM HEPES pH 7. The plates are incubated for an additional 30 min and washed 5X with PBS containing Ca^{++} and Mg^{++} . After the final wash, 100 μ L PBS is added to each well and fluorescence is read on a fluorescent plate reader (Ab492/Em 516 nm).

[00199] For the non-static endothelial cell binding assay, CaP are prepared as described above. EC are plated onto 24-well plates at 30-40% confluence 3 days prior to use. On the day of use, a subset of EC are treated with cytokine for 6 hours then washed 2X with PBS. To each well is then added 150-200K CaP cells in DMEM/1% BSA/ 10mM

HEPES pH 7. Plates are placed on a rotating shaker (70 RPM) for 30 min and then washed 3X with PBS containing Ca^{++} and Mg^{++} . After the final wash, 500 μL PBS is added to each well and fluorescence is read on a fluorescent plate reader (Ab492/Em 516 nm).

[00200] For the transmigration assay, CaP are prepared as described above with the following changes. On the day of use, CaP medium is replaced with fresh medium containing 5 μM CellTracker green CMFDA (Molecular Probes, Inc.) and cells are incubated for 30 min. Following incubation, CaP medium is replaced with fresh medium (no CMFDA) and cells are incubated for an additional 30-60 min. CaP cells are detached using CMF PBS/2.5 mM EDTA or trypsin, spun and resuspended in EGM-2-MV medium. Finally, CaP cells are counted and resuspended at a concentration of 1×10^6 cells/ml.

[00201] EC are plated onto FluorBlok transwells (BD Biosciences) at 30-40% confluence 5-7 days before use. Medium is replaced with fresh medium 3 days before use and on the day of use. To each transwell is then added 50K labeled CaP. 30 min prior to the first fluorescence reading, 10 μg of FITC-dextran (10K MW) is added to the EC plated filter. Fluorescence is then read at multiple time points on a fluorescent plate reader (Ab492/Em 516 nm).

[00202] Those antisense oligonucleotides that result in inhibition of binding of SW620 colon cancer cells to endothelial cells indicate that the corresponding gene plays a role in the production or maintenance of the cancerous phenotype in cancerous colon cells. Those antisense oligonucleotides that result in inhibition of endothelial cell transmigration by SW620 colon cancer cells indicate that the corresponding gene plays a role in the production or maintenance of the cancerous phenotype in cancerous colon cells.

EXAMPLE 6: EFFECT OF GENE EXPRESSION ON COLONY FORMATION

[00203] The effect of gene expression upon colony formation of SW620 cells, SKOV3 cells, MD-MBA-231 cells, LNCaP cells, PC3 cells, 22Rv1 cells, MDA-PCA-2b cells,

and DU145 cells can be tested in a soft agar assay. Soft agar assays are conducted by first establishing a bottom layer of 2 ml of 0.6% agar in media plated fresh within a few hours of layering on the cells. The cell layer is formed on the bottom layer by removing cells transfected as described above from plates using 0.05% trypsin and washing twice in media. The cells are counted in a Coulter counter, and resuspended to 10^6 per ml in media. 10 μ l aliquots are placed with media in 96-well plates (to check counting with WST1), or diluted further for the soft agar assay. 2000 cells are plated in 800 μ l 0.4% agar in duplicate wells above 0.6% agar bottom layer. After the cell layer agar solidifies, 2 ml of media is dribbled on top and antisense or reverse control oligo (produced as described in Example 3) is added without delivery vehicles. Fresh media and oligos are added every 3-4 days. Colonies form in 10 days to 3 weeks. Fields of colonies are counted by eye. Wst-1 metabolism values can be used to compensate for small differences in starting cell number. Larger fields can be scanned for visual record of differences.

[00204] Those antisense oligonucleotides that result in inhibition of colony formation of SW620 cells indicate that the corresponding gene plays a role in production or maintenance of the cancerous phenotype in cancerous colon cells. Those antisense oligonucleotides that inhibit colony formation in SKOV3 cells represent genes that play a role in production or maintenance of the cancerous phenotype in cancerous breast cells. Those antisense oligonucleotides that result in inhibition of colony formation of MDA-MB-231 cells indicate that the corresponding gene plays a role in production or maintenance of the cancerous phenotype in cancerous ovarian cells. Those antisense oligonucleotides that inhibit colony formation in LNCaP, PC3, 22Rv1, MDA-PCA-2b, or DU145 cells represent genes that play a role in production or maintenance of the cancerous phenotype in cancerous prostate cells.

EXAMPLE 7: INDUCTION OF CELL DEATH UPON DEPLETION OF POLYPEPTIDES BY DEPLETION OF MRNA ("ANTISENSE KNOCKOUT")

[00205] In order to assess the effect of depletion of a target message upon cell death,

SW620 cells, or other cells derived from a cancer of interest, can be transfected for proliferation assays. For cytotoxic effect in the presence of cisplatin (cis), the same protocol is followed but cells are left in the presence of 2 μ M drug. Each day, cytotoxicity is monitored by measuring the amount of LDH enzyme released in the medium due to membrane damage. The activity of LDH is measured using the Cytotoxicity Detection Kit from Roche Molecular Biochemicals. The data is provided as a ratio of LDH released in the medium vs. the total LDH present in the well at the same time point and treatment (rLDH/tLDH). A positive control using antisense and reverse control oligonucleotides for BCL2 (a known anti-apoptotic gene) is included; loss of message for BCL2 leads to an increase in cell death compared with treatment with the control oligonucleotide (background cytotoxicity due to transfection).

EXAMPLE 8: FUNCTIONAL ANALYSIS OF GENE PRODUCTS DIFFERENTIALLY EXPRESSED IN COLON CANCER IN PATIENTS

[00206] The gene products of sequences of a gene differentially expressed in cancerous cells can be further analyzed to confirm the role and function of the gene product in tumorigenesis, *e.g.*, in promoting or inhibiting development of a metastatic phenotype. For example, the function of gene products corresponding to genes identified herein can be assessed by blocking function of the gene products in the cell. For example, where the gene product is secreted or associated with a cell surface membrane, blocking antibodies can be generated and added to cells to examine the effect upon the cell phenotype in the context of, for example, the transformation of the cell to a cancerous, particularly a metastatic, phenotype. In order to generate antibodies, a clone corresponding to a selected gene product is selected, and a sequence that represents a partial or complete coding sequence is obtained. The resulting clone is expressed, the polypeptide produced isolated, and antibodies generated. The antibodies are then combined with cells and the effect upon tumorigenesis assessed.

[00207] Where the gene product of the differentially expressed genes identified herein exhibits sequence homology to a protein of known function (*e.g.*, to a specific kinase or

[00208] Additional functional assays include, but are not necessarily limited to, those that analyze the effect of expression of the corresponding gene upon cell cycle and cell migration. Methods for performing such assays are well known in the art.

[00209] The sequences of the polynucleotides provided in the present invention can be used to extend the sequence information of the gene to which the polynucleotides correspond (*e.g.*, a gene, or mRNA encoded by the gene, having a sequence of the polynucleotide described herein). This expanded sequence information can in turn be used to further characterize the corresponding gene, which in turn provides additional information about the nature of the gene product (*e.g.*, the normal function of the gene product). The additional information can serve to provide additional evidence of the gene product's use as a therapeutic target, and provide further guidance as to the types of agents that can modulate its activity.

[00211] The contig is assembled using the software program Sequencher, version 4.05, according to the manufacturer's instructions and an overview alignment of the contiged sequences is produced. The sequence information obtained in the contig assembly can then be used to obtain a consensus sequence derived from the contig using the

Sequencher program. The consensus sequence is used as a query sequence in a TeraBLASTN search of the DGTI DoubleTwist Gene Index (DoubleTwist, Inc., Oakland, CA), which contains all the EST and non-redundant sequence in public databases.

[00212] Through contig assembly and the use of homology searching software programs, the sequence information provided herein can be readily extended to confirm, or confirm a predicted, gene having the sequence of the polynucleotides described in the present invention. Further the information obtained can be used to identify the function of the gene product of the gene corresponding to the polynucleotides described herein. While not necessary to the practice of the invention, identification of the function of the corresponding gene, can provide guidance in the design of therapeutics that target the gene to modulate its activity and modulate the cancerous phenotype (*e.g.*, inhibit metastasis, proliferation, and the like).

[00213] While the present invention has been described with reference to the specific embodiments thereof, it should be understood by those skilled in the art that various changes may be made and equivalents may be substituted without departing from the true spirit and scope of the invention. In addition, many modifications may be made to adapt a particular situation, material, composition of matter, process, process step or steps, to the objective, spirit and scope of the present invention. All such modifications are intended to be within the scope of the claims appended hereto.

Table 1

| Pt ID | Path ID | Grp | Anatom Loc | Size | Grade | Histo Grade | Local Invasion | Lymph Met | Lymph Met Incid | Reg Lymph Grade | Dist Met & Loc | Dist Met Grade | Comment |
|-------|---------|-----|-----------------|------|-------|-------------|--|-----------|-----------------|-----------------|----------------|----------------|---|
| 10 | 16 | III | Cecum | 8.5 | T3 | G2 | through muscularis propria approaching pericolic fat, but not at serosal surface | Pos | 1/17 | N1 | Neg | M0 | Moderately differentiated |
| 15 | 21 | III | Ascending colon | 4.0 | T3 | G2 | Extending into subserosal adipose tissue | Pos | 3/8 | N1 | Neg | MX | invasive adenocarcinoma, moderately differentiated; focal perineural invasion is seen |
| 52 | 71 | II | Cecum | 9.0 | T3 | G3 | Invasion through muscularis propria, subserosal involvement; ileocecal valve involvement | Neg | 0/12 | N0 | Neg | M0 | Hyperplastic polyp in appendix. |
| 121 | 140 | II | Sigmoid | 6 | T4 | G2 | Invasion of muscularis propria into serosa, involving submucosa of urinary bladder | Neg | 0/34 | N0 | Neg | M0 | Perineural invasion; donut anastomosis Neg. One tubulovillous and one tubular adenoma with no high grade dysplasia. |

Table 1

| Pt ID | Path ID | Grp | Anatom Loc | Size | Grade | Histo Grade | Local Invasion | Lymph Met | Lymph Met Incid | Reg Lymph Grade | Dist Met & Loc | Dist Met Grade | Comment |
|-------|---------|-----|------------------|------|-------|-------------|---|-----------|-----------------|-----------------|----------------|----------------|--|
| 125 | 144 | II | Cecum | 6 | T3 | G2 | Invasion through the muscularis propria into subserosal adipose tissue. Ileocecal junction. | Neg | 0/19 | N0 | Neg | M0 | patient history of metastatic melanoma |
| 128 | 147 | III | Transverse colon | 5.0 | T3 | G2 | Invasion of muscularis propria into pericolonic fat | Pos | 1/5 | N1 | Neg | M0 | |
| 130 | 149 | | Splenic flexure | 5.5 | T3 | | through wall and into surrounding adipose tissue | Pos | 10/24 | N2 | Neg | M1 | |
| 133 | 152 | II | Rectum | 5.0 | T3 | G2 | Invasion through muscularis propria into non-peritonealized pericolonic tissue; gross configuration is annular. | Neg | 0/9 | N0 | Neg | M0 | Small separate tubular adenoma (0.4 cm) |
| 141 | 160 | IV | Cecum | 5.5 | T3 | G2 | Invasion of muscularis propria into pericolonic adipose tissue, but not through serosa. Arising from tubular adenoma. | Pos | 7/21 | N2 | Pos - Liver | M1 | Perineural invasion identified adjacent to metastatic adenocarcinoma. ^a |

Table 1

| Pt ID | Path ID | Grp | Anatom Loc | Size | Grade | Histo Grade | Local Invasion | Lymph Met | Lymph Met Incid | Reg Lymph Grade | Dist Met & Loc | Dist Met Grade | Comment |
|-------|---------|-----|------------------|------|-------|-------------|--|-----------|-----------------|-----------------|--------------------------|----------------|---|
| 156 | 175 | III | Hepatic flexure | 3.8 | T3 | G2 | Invasion through muscularis propria into subserosa/pericolonic adipose, no serosal involvement. Gross configuration annular. | Pos | 2/13 | N1 | Neg | M0 | Separate tubulovillous and tubular adenomas |
| 228 | 247 | III | Rectum | 5.8 | T3 | G2 to G3 | Invasion through muscularis propria to involve subserosal, perirectal adipose, and serosa | Pos | 1/8 | N1 | Neg | MX | Hyperplastic polyps |
| 264 | 283 | II | Ascending colon | 5.5 | T3 | G2 | Invasion through muscularis propria into subserosal adipose tissue. | Neg | 0/10 | N0 | Neg | M0 | Tubulovillous adenoma with high grade dysplasia |
| 266 | 285 | III | Transverse colon | 9 | T3 | G2 | Invades through muscularis propria to involve pericolonic adipose, extends to serosa. | Neg | 0/15 | N1 | Pos - Mesenteric deposit | MX | |
| 267 | 286 | III | Ileocecal | 4.5 | T2 | G2 | Confined to muscularis propria | Pos | 2/12 | N1 | Neg | M0 | |

Table 1

| Pt ID | Path ID | Grp | Anatom Loc | Size | Grade | Histo Grade | Local Invasion | Lymph Met | Lymph Met Incid | Reg Lymph Grade | Dist Met & Loc | Dist Met Grade | Comment |
|-------|---------|-----|------------------|------|-------|-------------|---|-----------|-----------------|-----------------|----------------|----------------|---|
| 268 | 287 | I | Cecum | 6.5 | T2 | G2 | Invades full thickness of muscularis propria, but mesenteric adipose free of malignancy | Neg | 0/12 | N0 | Neg | M0 | |
| 278 | 297 | III | Rectum | 4 | T3 | G2 | Invasion into perirectal adipose tissue. | Pos | 7/10 | N2 | Neg | M0 | Descending colon polyps, no HGD or carcinoma identified.. |
| 295 | 314 | II | Ascending colon | 5.0 | T3 | G2 | Invasion through muscularis propria into pericolic adipose tissue. | Neg | 0/12 | N0 | Neg | M0 | Melanosis coli and diverticular disease. |
| 296 | 315 | III | Cecum | 5.5 | T3 | G2 | Invasion through muscularis propria and invades pericolic adipose tissue. Ileocecal junction. | Pos | 2/12 | N1 | Neg | M0 | Tubulovillous adenoma (2.0 cm) with no high grade dysplasia. Neg. liver biopsy. |
| 300 | 319 | III | Descending colon | 5.2 | T2 | G2 | through the muscularis propria into pericolic fat | Pos | 2/2 | N1 | Neg | M0 | |
| 322 | 341 | II | Sigmoid | 7 | T3 | G2 | through the muscularis propria into pericolic fat | Neg | 0/5 | N0 | Neg | M0 | vascular invasion is identified |
| 339 | 358 | II | Rectosigmoid | 6 | T3 | G2 | Extends into perirectal fat but does not reach serosa | Neg | 0/6 | N0 | Neg | M0 | 1 hyperplastic polyp identified |

Table 1

| Pt ID | Path ID | Grp | Anatom Loc | Size | Grade | Histo Grade | Local Invasion | Lymph Met | Lymph Met Incid | Reg Lymph Grade | Dist Met & Loc | Dist Met Grade | Comment |
|-------|---------|-----|-----------------|---------------|-------|-------------|--|-----------|-----------------|-----------------|----------------|----------------|---|
| 341 | 360 | II | Ascending colon | 2 cm invasive | T3 | G2 | Invasion through muscularis propria to involve pericolonic fat. Arising from villous adenoma. | Neg | 0/4 | N0 | Neg | MX | |
| 356 | 375 | II | Sigmoid | 6.5 | T3 | G2 | Through colon wall into subserosal adipose tissue. No serosal spread seen. | Neg | 0/4 | N0 | Neg | M0 | |
| 360 | 412 | III | Ascending colon | 4.3 | T3 | G2 | Invasion thru muscularis propria to pericolonic fat | Pos | 1/5 | N1 | Neg | M0 | Two mucosal polyps |
| 392 | 444 | IV | Ascending colon | 2 | T3 | G2 | Invasion through muscularis propria into subserosal adipose tissue, not serosa. | Pos | 1/6 | N1 | Pos - Liver | M1 | Tumor arising at prior ileocolic surgical anastomosis. |
| 393 | 445 | II | Cecum | 6.0 | T3 | G2 | Cecum, invades through muscularis propria to involve subserosal adipose tissue but not serosa. | Neg | 0/21 | N0 | Neg | M0 | |
| 413 | 465 | IV | Cecum | 4.8 | T3 | G2 | Invasive through muscularis to involve periserosal fat; abutting ileocecal junction. | Neg | 0/7 | N0 | Pos - Liver | M1 | redagnosis of oophorectomy path to metastatic colon cancer. |

Table 1

| Pt ID | Path ID | Grp | Anatom Loc | Size | Grade | Histo Grade | Local Invasion | Lymph Met | Lymph Met Incid | Reg Lymph Grade | Dist Met & Loc | Dist Met Grade | Comment |
|-------|---------|-----|-----------------|------|-------|-------------|---|-----------|-----------------|-----------------|----------------|----------------|--|
| 452 | 504 | II | Ascending colon | 4 | T3 | G2 | through muscularis propria approaching pericolic fat, but not at serosal surface | Neg | 0/39 | N0 | Neg | M0 | |
| 505 | 383 | IV | | 7.5 | T3 | G2 | Invasion through muscularis propria involving pericolic adipose, serosal surface uninvolved | Pos | 2/17 | N1 | Pos - Liver | M1 | Anatomical location of primary not notated in report. Evidence of chronic colitis. |
| 517 | 395 | IV | Sigmoid | 3 | T3 | G2 | penetrates muscularis propria, involves pericolic fat. | Pos | 6/6 | N2 | Neg | M0 | No mention of distant met in report |
| 534 | 553 | II | Ascending colon | 12 | T3 | G3 | Invasion through the muscularis propria involving pericolic fat. Serosa free of tumor. | Neg | 0/8 | N0 | Neg | M0 | Omentum with fibrosis and fat necrosis. Small bowel with acute and chronic serositis, focal abscess and adhesions. |

Table 1

| Pt ID | Path ID | Grp | Anatom Loc | Size | Grade | Histo Grade | Local Invasion | Lymph Met | Lymph Met Incid | Reg Lymph Grade | Dist Met & Loc | Dist Met Grade | Comment |
|-------|---------|-----|-----------------|------|-------|-------------|---|-----------|-----------------|-----------------|----------------|----------------|---|
| 546 | 565 | IV | Ascending colon | 5.5 | T3 | G2 | Invasion through muscularis propria extensively through submucosal and extending to serosa. | Pos | 6/12 | N2 | Pos - Liver | M1 | |
| 577 | 596 | II | Cecum | 11.5 | T3 | G2 | Invasion through the bowel wall, into subserosal adipose. Serosal surface free of tumor. | Neg | 0/58 | N0 | Neg | M0 | Appendix dilated and fibrotic, but not involved by tumor |
| 695 | 714 | II | Cecum | 14.0 | T3 | G2 | extending through bowel wall into serosal fat | Neg | 0/22 | N0 | Neg | MX | moderately differentiated adenocarcinoma with mucinous differentiation (% not stated), tubular adenoma and hyperplastic polyps present, |
| 784 | 803 | IV | Ascending colon | 3.5 | T3 | G3 | through muscularis propria into pericolic soft tissues | Pos | 5/17 | N2 | Pos - Liver | M1 | invasive poorly differentiated adenosquamous carcinoma |

Table 1

| Pt ID | Path ID | Grp | Anatom Loc | Size | Grade | Histo Grade | Local Invasion | Lymph Met | Lymph Met Incid | Reg Lymph Grade | Dist Met & Loc | Dist Met Grade | Comment |
|-------|---------|-----|------------------|------|-------|-------------|---|-----------|-----------------|-----------------|----------------|----------------|---|
| 786 | 805 | IV | Descending colon | 9.5 | T3 | G2 | through muscularis propria into pericolic fat, but not at serosal surface | Neg | 0/12 | N0 | Pos - Liver | M1 | moderately differentiated invasive adenocarcinoma ^a |
| 787 | 806 | II | Rectosigmoid | 2.5 | T3 | G2-G3 | Invasion of muscularis propria into soft tissue | Neg | | N0 | Neg | MX | Peritumoral lymphocytic response; 5 LN examined in pericolic fat, no metastases observed. |
| 789 | 808 | IV | Cecum | 5.0 | T3 | G2-G3 | Extending through muscularis propria into pericolic fat | Pos | 5/10 | N2 | Pos - Liver | M1 | Three fungating lesions examined. |
| 790 | 809 | IV | Rectum | 6.8 | T3 | G1-G2 | Invading through muscularis propria into perirectal fat | Pos | 3/13 | N1 | Pos - Liver | M1 | |
| 791 | 810 | IV | Ascending colon | 5.8 | T3 | G3 | Through the muscularis propria into pericolic fat | Pos | 13/25 | N2 | Pos - Liver | M1 | poorly differentiated invasive colonic adenocarcinoma ^a |

Table 1

| Pt ID | Path ID | Grp | Anatom Loc | Size | Grade | Histo Grade | Local Invasion | Lymph Met | Lymph Met Incid | Reg Lymph Grade | Dist Met & Loc | Dist Met Grade | Comment |
|-------|---------|-----|-----------------|------|-------|-------------|--|-----------|-----------------|-----------------|---|----------------|--|
| 888 | 908 | IV | Ascending colon | 2.0 | T2 | G1 | Into muscularis propria | Pos | 3/21 | N0 | Pos - Liver | M1 | well to moderately differentiated adenocarcinoma; this patient has tumors of the ascending colon and the sigmoid colon |
| 889 | 909 | IV | Cecum | 4.8 | T3 | G2 | Through muscularis propria into subserosal tissue | Pos | 1/4 | N1 | Pos - Liver | M1 | moderately differentiated adenocarcinoma |
| 890 | 910 | IV | Ascending colon | | T3 | G2 | Through muscularis propria into subserosa. | Pos | 11/15 | N2 | Pos - Liver | M1 | |
| 891 | 911 | IV | Rectum | 5.2 | T3 | G2 | Invasion through muscularis propria into perirectal soft tissue | Pos | 4/15 | N2 | Pos - Liver | M1 | Perineural invasion present. |
| 892 | 912 | IV | Sigmoid | 5.0 | T3 | G2 | Invasion into pericolic sort tissue. Tumor focally invading skeletal muscle attached to colon. | Pos | 1/28 | N1 | Pos - Liver, left and right lobe, omentum | M1 | Perineural invasion present, extensive. Patient with a history of colon cancer. |

Table 1

| Pt ID | Path ID | Grp | Anatom Loc | Size | Grade | Histo Grade | Local Invasion | Lymph Met | Lymph Met Incid | Reg Lymph Grade | Dist Met & Loc | Dist Met Grade | Comment |
|-------|---------|-----|------------------|------|-------|-------------|--|-----------|-----------------|-----------------|----------------|----------------|--|
| 893 | 913 | IV | Transverse colon | 6.0 | T3 | G2-G3 | Through muscularis propria into pericolic fat | Pos | 14/17 | N2 | Pos - Liver | M1 | Perineural invasion focally present. Omentum mass, but resection with no tumor identified. |
| 989 | 1009 | IV | Sigmoid | 6.0 | T3 | G2 | Invasion through colon wall and focally involving subserosal tissue. | Pos | 1/7 | N1 | Pos - Liver | M1 | Primary adenocarcinoma arising from tubulovillous adenoma. |

Table 2

| SEQ ID NO | Spot ID | Clone ID | MAClone ID |
|-----------|---------|----------------|------------|
| 1 | 18 | M00026919B:A10 | MA40:F01 |
| 2 | 20 | M00026919B:E07 | MA40:G01 |
| 3 | 22 | M00026919D:F04 | MA40:H01 |
| 4 | 54 | M00026914D:G06 | MA40:A01 |
| 5 | 56 | M00026950A:A09 | MA40:D07 |
| 6 | 67 | M00003820C:A09 | MA244:B01 |
| 7 | 73 | M00001673A:G03 | MA244:E01 |
| 8 | 115 | M00007939A:A12 | MA27:B07 |
| 9 | 119 | M00007939A:B11 | MA27:D07 |
| 10 | 127 | M00007939B:G03 | MA27:H07 |
| 11 | 166 | M00007997D:G08 | MA29:C01 |
| 12 | 220 | M00026894C:E11 | MA39:F07 |
| 13 | 238 | M00001391A:C05 | MA15:G01 |
| 14 | 294 | M00006818A:A06 | MA240:C01 |
| 15 | 393 | M00023278A:F09 | MA36:E01 |
| 16 | 405 | M00023299A:G01 | MA36:C07 |
| 17 | 411 | M00023301A:A11 | MA36:F07 |
| 18 | 453 | M00008050A:D12 | MA30:C01 |
| 19 | 460 | M00022135A:C04 | MA35:F01 |
| 20 | 462 | M00022137A:A05 | MA35:G01 |
| 21 | 466 | M00022176C:A07 | MA35:A07 |
| 22 | 471 | M00008077B:A08 | MA30:D07 |
| 23 | 477 | M00008077C:D09 | MA30:G07 |
| 24 | 492 | M00022081C:E09 | MA34:F01 |
| 25 | 495 | M00001662A:G06 | MA24:H01 |
| 26 | 504 | M00022102B:B11 | MA34:D07 |
| 27 | 506 | M00022102B:E08 | MA34:E07 |
| 28 | 556 | M00022569D:G06 | MA22:F01 |
| 29 | 577 | M00001358B:B11 | MA14:A01 |
| 30 | 578 | M00001429A:G04 | MA16:A01 |
| 31 | 579 | M00001358B:F05 | MA14:B01 |
| 32 | 582 | M00001429C:C03 | MA16:C01 |
| 33 | 585 | M00001359D:B04 | MA14:E01 |
| 34 | 587 | M00001360A:E10 | MA14:F01 |
| 35 | 589 | M00001360C:B05 | MA14:G01 |
| 36 | 590 | M00001430B:F01 | MA16:G01 |
| 37 | 592 | M00001430C:A02 | MA16:H01 |
| 38 | 594 | M00001445C:H05 | MA16:A07 |
| 39 | 596 | M00001445D:D07 | MA16:B07 |
| 40 | 605 | M00001374D:D10 | MA14:G07 |
| 41 | 607 | M00001375A:A08 | MA14:H07 |
| 42 | 643 | M00006600A:E07 | MA241:B01 |
| 43 | 661 | M00006690A:F06 | MA241:C07 |
| 44 | 739 | M00023325D:A08 | MA37:B02 |
| 45 | 742 | M00026921D:F12 | MA40:C02 |
| 46 | 743 | M00023325D:F06 | MA37:D02 |
| 47 | 750 | M00026924A:E09 | MA40:G02 |
| 48 | 823 | M00007940C:A04 | MA27:D08 |
| 49 | 827 | M00007941C:H03 | MA27:F08 |
| 50 | 828 | M00021638B:F03 | MA31:F08 |

Table 2

| SEQ ID NO | Spot ID | Clone ID | MAClone ID |
|-----------|---------|----------------|------------|
| 51 | 831 | M00007941D:C04 | MA27:H08 |
| 52 | 842 | M00004054D:D02 | |
| 53 | 857 | M00001507A:A10 | MA23:E08 |
| 54 | 858 | M00004198D:A01 | |
| 55 | 861 | M00001528C:B08 | MA23:G08 |
| 56 | 868 | M00008002C:A05 | MA29:B03 |
| 57 | 880 | M00008006C:H05 | MA29:H03 |
| 58 | 898 | M00026850C:A01 | MA39:A02 |
| 59 | 908 | M00026853D:C07 | MA39:F02 |
| 60 | 920 | M00026896A:C09 | MA39:D08 |
| 61 | 934 | M00001391B:D02 | MA15:C02 |
| 62 | 938 | M00001391B:H05 | MA15:E02 |
| 63 | 940 | M00001391D:C07 | MA15:F02 |
| 64 | 942 | M00001392B:B01 | MA15:G02 |
| 65 | 954 | M00001407B:C03 | MA15:E08 |
| 66 | 1011 | M00005635B:E02 | MA242:B08 |
| 67 | 1017 | M00005636B:B06 | MA242:E08 |
| 68 | 1018 | M00006971A:E06 | MA240:E08 |
| 69 | 1019 | M00005636D:B08 | MA242:F08 |
| 70 | 1107 | M00023302C:A04 | MA36:B08 |
| 71 | 1117 | M00023305A:C02 | MA36:G08 |
| 72 | 1172 | M00022180A:E08 | MA35:B08 |
| 73 | 1178 | M00022181C:H11 | MA35:E08 |
| 74 | 1193 | M00001673A:C11 | |
| 75 | 1201 | M00003853B:C07 | |
| 76 | 1204 | M00022106B:D04 | MA34:B08 |
| 77 | 1209 | M00003858B:G01 | MA24:E08 |
| 78 | 1214 | M00022109B:A11 | MA34:G08 |
| 79 | 1260 | M00022921A:H05 | MA22:F02 |
| 80 | 1282 | M00001430D:H07 | MA16:A02 |
| 81 | 1283 | M00001360D:H10 | MA14:B02 |
| 82 | 1284 | M00001431A:E01 | MA16:B02 |
| 83 | 1285 | M00001361A:A02 | MA14:C02 |
| 84 | 1295 | M00001362A:B03 | MA14:H02 |
| 85 | 1297 | M00001376C:C01 | MA14:A08 |
| 86 | 1300 | M00001449A:D02 | MA16:B08 |
| 87 | 1301 | M00001378B:A02 | MA14:C08 |
| 88 | 1302 | M00001450A:D12 | MA16:C08 |
| 89 | 1303 | M00001378C:D08 | MA14:D08 |
| 90 | 1310 | M00001451D:F01 | MA16:G08 |
| 91 | 1349 | M00006628B:A02 | MA241:C02 |
| 92 | 1444 | M00026926C:F03 | MA40:B03 |
| 93 | 1458 | M00026963B:H03 | MA40:A09 |
| 94 | 1464 | M00026964A:E10 | MA40:D09 |
| 95 | 1468 | M00026965C:A11 | MA40:F09 |
| 96 | 1493 | M00001398A:D11 | MA244:C09 |
| 97 | 1512 | M00008095C:H08 | MA31:D03 |
| 98 | 1523 | M00007942A:F12 | MA27:B09 |
| 99 | 1554 | M00004212B:B12 | MA25:A09 |
| 100 | 1576 | M00008014C:E11 | MA29:D05 |

Table 2

| SEQ ID NO | Spot ID | Clone ID | MAClone ID |
|-----------|---------|----------------|------------|
| 101 | 1578 | M00008015A:B05 | MA29:E05 |
| 102 | 1586 | M00022049A:B08 | MA33:A05 |
| 103 | 1602 | M00026856B:F08 | MA39:A03 |
| 104 | 1604 | M00026856C:H12 | MA39:B03 |
| 105 | 1628 | M00026900D:A03 | MA39:F09 |
| 106 | 1630 | M00026900D:C12 | MA39:G09 |
| 107 | 1632 | M00026901D:A03 | MA39:H09 |
| 108 | 1642 | M00001393A:G03 | MA15:E03 |
| 109 | 1656 | M00001409B:D03 | MA15:D09 |
| 110 | 1658 | M00001409B:G01 | MA15:E09 |
| 111 | 1660 | M00001410C:C09 | MA15:F09 |
| 112 | 1662 | M00001410D:A03 | MA15:G09 |
| 113 | 1697 | M00005504D:F06 | MA242:A03 |
| 114 | 1709 | M00005510D:H10 | MA242:G03 |
| 115 | 1726 | M00006990D:D06 | MA240:G09 |
| 116 | 1761 | SL146 | MA248:A03 |
| 117 | 1775 | SL153 | MA248:H03 |
| 118 | 1785 | SL198 | MA248:E09 |
| 119 | 1787 | SL199 | MA248:F09 |
| 120 | 1789 | SL200 | MA248:G09 |
| 121 | 1797 | M00023283D:C03 | MA36:C03 |
| 122 | 1799 | M00023283D:D03 | MA36:D03 |
| 123 | 1801 | M00023284A:D09 | MA36:E03 |
| 124 | 1807 | M00023285D:C05 | MA36:H03 |
| 125 | 1809 | M00023306C:H11 | MA36:A09 |
| 126 | 1813 | M00023308D:B06 | MA36:C09 |
| 127 | 1817 | M00023309D:H04 | MA36:E09 |
| 128 | 1819 | M00023310A:D07 | MA36:F09 |
| 129 | 1875 | M00008079C:H04 | MA30:B09 |
| 130 | 1883 | M00008080B:B10 | MA30:F09 |
| 131 | 1884 | M00022198D:C02 | MA35:F09 |
| 132 | 1886 | M00022198D:G03 | MA35:G09 |
| 133 | 1895 | M00003768B:B09 | MA24:D03 |
| 134 | 1910 | M00022110C:A08 | MA34:C09 |
| 135 | 1913 | M00003886C:H08 | MA24:E09 |
| 136 | 1960 | M00023297B:A10 | MA22:D03 |
| 137 | 1966 | M00023314C:G05 | MA22:G03 |
| 138 | 1991 | M00001363B:C04 | MA14:D03 |
| 139 | 1992 | M00001434D:F08 | MA16:D03 |
| 140 | 1994 | M00001435B:A04 | MA16:E03 |
| 141 | 1996 | M00001435B:B09 | MA16:F03 |
| 142 | 2000 | M00001435C:F08 | MA16:H03 |
| 143 | 2001 | M00001381A:F03 | MA14:A09 |
| 144 | 2004 | M00001453B:E11 | MA16:B09 |
| 145 | 2008 | M00001453C:D02 | MA16:D09 |
| 146 | 2050 | M00007121D:A05 | MA243:A03 |
| 147 | 2052 | M00007122C:F03 | MA243:B03 |
| 148 | 2053 | M00006638A:G02 | MA241:C03 |
| 149 | 2059 | M00006639B:H09 | MA241:F03 |
| 150 | 2064 | M00007127C:C11 | MA243:H03 |

Table 2

| SEQ ID NO | Spot ID | Clone ID | MAClone ID |
|-----------|---------|----------------|------------|
| 151 | 2073 | M00006720D:C11 | MA241:E09 |
| 152 | 2075 | M00006728C:E07 | MA241:F09 |
| 153 | 2156 | M00026931D:E08 | MA40:F04 |
| 154 | 2158 | M00026932D:B08 | MA40:G04 |
| 155 | 2168 | M00026969D:D02 | MA40:D10 |
| 156 | 2169 | M00023393B:E02 | MA37:E10 |
| 157 | 2185 | M00003782D:D06 | MA244:E04 |
| 158 | 2189 | M00004105D:B04 | MA244:G04 |
| 159 | 2199 | M00001556D:B11 | MA244:D10 |
| 160 | 2234 | M00021664B:G03 | MA31:E10 |
| 161 | 2242 | M00004078A:A07 | |
| 162 | 2263 | M00001561A:B03 | MA23:D10 |
| 163 | 2284 | M00008023C:A06 | MA29:F07 |
| 164 | 2286 | M00008024C:F02 | MA29:G07 |
| 165 | 2288 | M00008024C:G06 | MA29:H07 |
| 166 | 2292 | M00022057C:H10 | MA33:B07 |
| 167 | 2294 | M00022059B:B06 | MA33:C07 |
| 168 | 2324 | M00026902B:F10 | MA39:B10 |
| 169 | 2342 | M00001394D:B08 | MA15:C04 |
| 170 | 2354 | M00001415A:G05 | MA15:A10 |
| 171 | 2356 | M00001416B:E03 | MA15:B10 |
| 172 | 2368 | M00001421B:B12 | MA15:H10 |
| 173 | 2413 | M00005528C:E02 | MA242:G04 |
| 174 | 2513 | M00023312D:F10 | MA36:A10 |
| 175 | 2566 | M00022157A:C06 | MA35:C04 |
| 176 | 2576 | M00022165A:A11 | MA35:H04 |
| 177 | 2584 | M00022206A:B10 | MA35:D10 |
| 178 | 2601 | M00003811B:F09 | |
| 179 | 2605 | M00003812D:A11 | |
| 180 | 2606 | M00022088D:C10 | MA34:G04 |
| 181 | 2613 | M00003910B:C12 | |
| 182 | 2689 | M00001366A:F06 | MA14:A04 |
| 183 | 2692 | M00001435C:F12 | MA16:B04 |
| 184 | 2694 | M00001436B:E11 | MA16:C04 |
| 185 | 2695 | M00001366B:E01 | MA14:D04 |
| 186 | 2696 | M00001436C:C03 | MA16:D04 |
| 187 | 2700 | M00001437A:B01 | MA16:F04 |
| 188 | 2702 | M00001437B:B08 | MA16:G04 |
| 189 | 2712 | M00001467B:H05 | |
| 190 | 2716 | M00001468A:D02 | MA16:F10 |
| 191 | 2756 | M00007131B:B11 | MA243:B04 |
| 192 | 2761 | M00006650A:A10 | MA241:E04 |
| 193 | 2765 | M00006653C:B09 | MA241:G04 |
| 194 | 2766 | M00007154B:H08 | MA243:G04 |
| 195 | 2769 | M00006740A:E02 | MA241:A10 |
| 196 | 2770 | M00021621A:D04 | MA243:A10 |
| 197 | 2771 | M00006740B:F11 | MA241:B10 |
| 198 | 2773 | M00006741C:A01 | MA241:C10 |
| 199 | 2780 | M00022171C:A04 | MA243:F10 |
| 200 | 2858 | M00026937C:B08 | MA40:E05 |

Table 2

| SEQ ID NO | Spot ID | Clone ID | MAClone ID |
|-----------|---------|----------------|------------|
| 201 | 2861 | M00023367A:H06 | MA37:G05 |
| 202 | 2876 | M00026985C:E12 | MA40:F11 |
| 203 | 2916 | M00008100A:A07 | MA31:B05 |
| 204 | 2921 | M00007936B:H07 | MA27:E05 |
| 205 | 2924 | M00008100C:E05 | MA31:F05 |
| 206 | 2937 | M00007947B:B02 | MA27:E11 |
| 207 | 2956 | M00004105A:C09 | MA25:F05 |
| 208 | 2957 | M00001433C:D09 | MA23:G05 |
| 209 | 2980 | M00008027B:D09 | MA29:B09 |
| 210 | 2984 | M00008028D:B01 | MA29:D09 |
| 211 | 2988 | M00008039A:C09 | MA29:F09 |
| 212 | 3026 | M00026905A:A10 | MA39:A11 |
| 213 | 3030 | M00026905D:C05 | MA39:C11 |
| 214 | 3054 | M00001401B:A06 | MA15:G05 |
| 215 | 3056 | M00001402A:A08 | MA15:H05 |
| 216 | 3105 | M00005534C:E12 | MA242:A05 |
| 217 | 3111 | M00005542A:D09 | MA242:D05 |
| 218 | 3132 | M00007031D:E02 | MA240:F11 |
| 219 | 3134 | M00007032A:D04 | MA240:G11 |
| 220 | 3135 | M00005813C:F12 | MA242:H11 |
| 221 | 3171 | SL163 | MA248:B05 |
| 222 | 3173 | SL164 | MA248:C05 |
| 223 | 3179 | SL167 | MA248:F05 |
| 224 | 3181 | SL168 | MA248:G05 |
| 225 | 3183 | SL169 | MA248:H05 |
| 226 | 3231 | M00023320B:A03 | MA36:H11 |
| 227 | 3238 | M00005350B:F10 | MA246:C05 |
| 228 | 3267 | M00008069D:F01 | MA30:B05 |
| 229 | 3268 | M00022165B:C08 | MA35:B05 |
| 230 | 3272 | M00022165C:E12 | MA35:D05 |
| 231 | 3274 | M00022166C:E07 | MA35:E05 |
| 232 | 3275 | M00008072D:E12 | MA30:F05 |
| 233 | 3282 | M00022211B:D05 | MA35:A11 |
| 234 | 3293 | M00008089A:E09 | MA30:G11 |
| 235 | 3317 | M00003974D:E04 | MA24:C11 |
| 236 | 3323 | M00003980D:F10 | MA24:F11 |
| 237 | 3327 | M00003984D:C08 | MA24:H11 |
| 238 | 3370 | M00023373D:A01 | MA22:E05 |
| 239 | 3376 | M00023396D:D01 | MA22:H05 |
| 240 | 3394 | M00001437D:E12 | MA16:A05 |
| 241 | 3396 | M00001438A:B09 | MA16:B05 |
| 242 | 3401 | M00001369A:C07 | MA14:E05 |
| 243 | 3404 | M00001439C:A07 | MA16:F05 |
| 244 | 3407 | M00001369C:A05 | MA14:H05 |
| 245 | 3410 | M00001468D:B11 | MA16:A11 |
| 246 | 3411 | M00001386B:F08 | MA14:B11 |
| 247 | 3419 | M00001387A:A08 | MA14:F11 |
| 248 | 3460 | M00007163A:B10 | MA243:B05 |
| 249 | 3465 | M00006675C:A06 | MA241:E05 |
| 250 | 3470 | M00007191C:A06 | MA243:G05 |

Table 2

| SEQ ID NO | Spot ID | Clone ID | MAClone ID |
|-----------|---------|---------------------|------------|
| 251 | 3471 | M00006678A:D02 | MA241:H05 |
| 252 | 3562 | M00026941C:A12 | MA40:E06 |
| 253 | 3578 | M00026996A:E01 | MA40:E12 |
| 254 | 3581 | M00023401B:E06 | MA37:G12 |
| 255 | 3584 | M00027005B:D03 | MA40:H12 |
| 256 | 3621 | M00007937B:A02 | MA27:C06 |
| 257 | 3622 | M00021612C:E11 | MA31:C06 |
| 258 | 3629 | M00007938C:C12 | MA27:G06 |
| 259 | 3675 | M00001623C:A06 | MA23:F12 |
| 260 | 3677 | M00001630D:A11 | MA23:G12 |
| 261 | 3682 | M00008044B:E11 | MA29:A11 |
| 262 | 3684 | M00008044C:C10 | MA29:B11 |
| 263 | 3686 | M00008044D:B08 | MA29:C11 |
| 264 | 3688 | M00008044D:C05 | MA29:D11 |
| 265 | 3706 | M00022074C:A04 | MA33:E11 |
| 266 | 3738 | M00026910C:D12 | MA39:E12 |
| 267 | 3742 | M00026913A:D06 | MA39:G12 |
| 268 | 3752 | M00001402C:H08 | MA15:D06 |
| 269 | 3756 | M00001404C:C11 | MA15:F06 |
| 270 | 3813 | M00005587B:G05 | MA242:C06 |
| 271 | 3814 | M00006934D:D10 | MA240:C06 |
| 272 | 3885 | SL176 | MA248:G06 |
| 273 | 3905 | M00023295D:E05 | MA36:A06 |
| 274 | 3921 | M00023320B:C02 | MA36:A12 |
| 275 | 3956 | M00005401B:F12 | MA246:B12 |
| 276 | 3979 | M00008074D:C05 | MA30:F06 |
| 277 | 3982 | M00022175B:F06 | MA35:G06 |
| 278 | 3998 | M00022230B:C10 | MA35:G12 |
| 279 | 4006 | M00022093C:C08 | MA34:C06 |
| 280 | 4008 | M00022093C:C12 | MA34:D06 |
| 281 | 4028 | M00022132A:H07 | MA34:F12 |
| 282 | 4066 | M00023397B:D04 | MA22:A06 |
| 283 | 4074 | M00023399D:G04 | MA22:E06 |
| 284 | 4098 | M00001439D:C09 | MA16:A06 |
| 285 | 4100 | M00001441A:A09 | MA16:B06 |
| 286 | 4101 | M00001369D:E02 | MA14:C06 |
| 287 | 4105 | M00001371D:H10 | MA14:E06 |
| 288 | 4107 | M00001372A:D01 | MA14:F06 |
| 289 | 4110 | M00001444C:F03 | MA16:G06 |
| 290 | 4112 | M00001445A:B02 | |
| 291 | 4119 | M00001388D:F11 | MA14:D12 |
| 292 | 4124 | M00001481C:A12 | MA16:F12 |
| 293 | 4125 | M00001389B:B05 | MA14:G12 |
| 294 | 4127 | M00001389C:G01 | MA14:H12 |
| 295 | 4128 | M00001482D:D11 | MA16:H12 |
| 296 | 4183 | M00006809B:F04 | MA241:D12 |
| 297 | 8513 | I:3325119:07A01:A01 | MA127:A01 |
| 298 | 8517 | I:3033345:07A01:C01 | MA127:C01 |
| 299 | 8537 | I:3176222:07A01:E07 | MA127:E07 |
| 300 | 8542 | I:2510627:07B01:G07 | MA129:G07 |

Table 2

| SEQ ID NO | Spot ID | Clone ID | MAClone ID |
|-----------|---------|---------------------|------------|
| 301 | 8546 | I:1705208:06B01:A01 | MA125:A01 |
| 302 | 8566 | I:1672781:06B01:C07 | MA125:C07 |
| 303 | 8568 | I:1712888:06B01:D07 | MA125:D07 |
| 304 | 8570 | I:1696224:06B01:E07 | MA125:E07 |
| 305 | 8576 | I:3935034:06B01:H07 | MA125:H07 |
| 306 | 8617 | I:1800114:03A01:E01 | MA111:E01 |
| 307 | 8631 | I:1976029:03A01:D07 | MA111:D07 |
| 308 | 8634 | I:1439934:03B01:E07 | MA113:E07 |
| 309 | 8645 | I:2512879:01A01:C01 | MA103:C01 |
| 310 | 8660 | I:2900277:01B01:B07 | MA105:B07 |
| 311 | 8661 | I:1479255:01A01:C07 | MA103:C07 |
| 312 | 8738 | I:2648612:04B01:A01 | MA117:A01 |
| 313 | 8741 | I:1889867:04A01:C01 | MA115:C01 |
| 314 | 8743 | I:1858905:04A01:D01 | MA115:D01 |
| 315 | 8752 | I:2591494:04B01:H01 | MA117:H01 |
| 316 | 8754 | I:2916261:04B01:A07 | MA117:A07 |
| 317 | 8756 | I:2397815:04B01:B07 | MA117:B07 |
| 318 | 8760 | I:2182095:04B01:D07 | MA117:D07 |
| 319 | 8769 | I:2506194:02A01:A01 | MA107:A01 |
| 320 | 8773 | I:1806219:02A01:C01 | MA107:C01 |
| 321 | 8797 | I:1729724:02A01:G07 | MA107:G07 |
| 322 | 8845 | I:1886842:05A02:G01 | MA120:G01 |
| 323 | 8851 | I:1352669:05A02:B07 | MA120:B07 |
| 324 | 8854 | I:1755847:05B02:C07 | MA122:C07 |
| 325 | 8856 | I:1803418:05B02:D07 | MA122:D07 |
| 326 | 8860 | I:1568725:05B02:F07 | MA122:F07 |
| 327 | 8861 | I:1857708:05A02:G07 | MA120:G07 |
| 328 | 8862 | I:1687060:05B02:G07 | MA122:G07 |
| 329 | 8881 | I:3407289:07A02:A07 | MA128:A07 |
| 330 | 8883 | I:1235535:07A02:B07 | MA128:B07 |
| 331 | 8984 | I:1525795:03B02:D07 | MA114:D07 |
| 332 | 8991 | I:3744592:03A02:H07 | MA112:H07 |
| 333 | 8995 | I:1485817:01A02:B01 | MA104:B01 |
| 334 | 8996 | I:2365149:01B02:B01 | MA106:B01 |
| 335 | 8999 | I:1439677:01A02:D01 | MA104:D01 |
| 336 | 9006 | I:2372275:01B02:G01 | MA106:G01 |
| 337 | 9008 | I:3211615:01B02:H01 | MA106:H01 |
| 338 | 9012 | I:2368282:01B02:B07 | MA106:B07 |
| 339 | 9095 | I:1737833:04A02:D01 | MA116:D01 |
| 340 | 9100 | I:2382192:04B02:F01 | MA118:F01 |
| 341 | 9111 | I:1958902:04A02:D07 | MA116:D07 |
| 342 | 9118 | I:1704472:04B02:G07 | MA118:G07 |
| 343 | 9119 | I:1903767:04A02:H07 | MA116:H07 |
| 344 | 9125 | I:1268080:02A02:C01 | MA108:C01 |
| 345 | 9141 | I:1347384:02A02:C07 | MA108:C07 |
| 346 | 9168 | I:2344817:08B01:H02 | MA133:H02 |
| 347 | 9171 | I:3236109:08A01:B08 | MA131:B08 |
| 348 | 9247 | I:2832506:07A01:H08 | MA127:H08 |
| 349 | 9252 | I:1673876:06B01:B02 | MA125:B02 |
| 350 | 9258 | I:3686211:06B01:E02 | MA125:E02 |

Table 2

| SEQ ID NO | Spot ID | Clone ID | MAClone ID |
|-----------|---------|---------------------|------------|
| 351 | 9264 | I:2449837:06B01:H02 | MA125:H02 |
| 352 | 9270 | I:1613874:06B01:C08 | MA125:C08 |
| 353 | 9317 | I:1813409:03A01:C02 | MA111:C02 |
| 354 | 9329 | I:1975514:03A01:A08 | MA111:A08 |
| 355 | 9347 | I:1403294:01A01:B02 | MA103:B02 |
| 356 | 9352 | I:2414624:01B01:D02 | MA105:D02 |
| 357 | 9360 | I:2901811:01B01:H02 | MA105:H02 |
| 358 | 9364 | I:2683564:01B01:B08 | MA105:B08 |
| 359 | 9366 | I:2725511:01B01:C08 | MA105:C08 |
| 360 | 9441 | I:1431273:04A01:A02 | MA115:A02 |
| 361 | 9442 | I:1636639:04B01:A02 | MA117:A02 |
| 362 | 9448 | I:2455617:04B01:D02 | MA117:D02 |
| 363 | 9452 | I:2952504:04B01:F02 | MA117:F02 |
| 364 | 9457 | I:1483847:04A01:A08 | MA115:A08 |
| 365 | 9460 | I:2923150:04B01:B08 | MA117:B08 |
| 366 | 9467 | I:1813133:04A01:F08 | MA115:F08 |
| 367 | 9472 | I:2510171:04B01:H08 | MA117:H08 |
| 368 | 9487 | I:2190284:02A01:H02 | MA107:H02 |
| 369 | 9540 | I:1522716:05B02:B02 | MA122:B02 |
| 370 | 9549 | I:1901271:05A02:G02 | MA120:G02 |
| 371 | 9552 | I:1820522:05B02:H02 | MA122:H02 |
| 372 | 9553 | I:2365295:05A02:A08 | MA120:A08 |
| 373 | 9557 | I:1335140:05A02:C08 | MA120:C08 |
| 374 | 9560 | I:1822577:05B02:D08 | MA122:D08 |
| 375 | 9618 | I:1306814:06B02:A08 | MA126:A08 |
| 376 | 9624 | I:3034694:06B02:D08 | MA126:D08 |
| 377 | 9666 | I:1453049:03B02:A02 | MA114:A02 |
| 378 | 9672 | I:1453748:03B02:D02 | MA114:D02 |
| 379 | 9677 | I:3001492:03A02:G02 | MA112:G02 |
| 380 | 9685 | I:3876715:03A02:C08 | MA112:C08 |
| 381 | 9687 | I:2992851:03A02:D08 | MA112:D08 |
| 382 | 9694 | I:1500649:03B02:G08 | MA114:G08 |
| 383 | 9699 | I:1512943:01A02:B02 | MA104:B02 |
| 384 | 9703 | I:1467565:01A02:D02 | MA104:D02 |
| 385 | 9720 | I:2455118:01B02:D08 | MA106:D08 |
| 386 | 9722 | I:2840251:01B02:E08 | MA106:E08 |
| 387 | 9770 | I:2911347:10B02:E02 | MA67:E02 |
| 388 | 9790 | I:1812030:10B02:G08 | MA67:G08 |
| 389 | 9820 | I:2663606:04B02:F08 | MA118:F08 |
| 390 | 9833 | I:1308333:02A02:E02 | MA108:E02 |
| 391 | 9834 | I:1578941:02B02:E02 | MA110:E02 |
| 392 | 9847 | I:1535439:02A02:D08 | MA108:D08 |
| 393 | 9856 | I:1857475:02B02:H08 | MA110:H08 |
| 394 | 9884 | I:2908878:08B01:F09 | MA133:F09 |
| 395 | 9925 | I:2830575:07A01:C03 | MA127:C03 |
| 396 | 9934 | I:1557906:07B01:G03 | MA129:G03 |
| 397 | 9964 | I:2200604:06B01:F03 | MA125:F03 |
| 398 | 9973 | I:1653326:06A01:C09 | MA123:C09 |
| 399 | 9981 | I:1720149:06A01:G09 | MA123:G09 |
| 400 | 10030 | I:1560987:03B01:G03 | MA113:G03 |

Table 2

| SEQ ID NO | Spot ID | Clone ID | MAClone ID |
|-----------|---------|---------------------|------------|
| 401 | 10046 | I:1510714:03B01:G09 | MA113:G09 |
| 402 | 10050 | I:2501484:01B01:A03 | MA105:A03 |
| 403 | 10051 | I:1379063:01A01:B03 | MA103:B03 |
| 404 | 10054 | I:2797902:01B01:C03 | MA105:C03 |
| 405 | 10062 | I:1805613:01B01:G03 | MA105:G03 |
| 406 | 10063 | I:1524885:01A01:H03 | MA103:H03 |
| 407 | 10064 | I:2888464:01B01:H03 | MA105:H03 |
| 408 | 10148 | I:1992788:04B01:B03 | MA117:B03 |
| 409 | 10155 | I:1413451:04A01:F03 | MA115:F03 |
| 410 | 10166 | I:2779515:04B01:C09 | MA117:C09 |
| 411 | 10206 | I:1583076:02B01:G09 | MA109:G09 |
| 412 | 10243 | I:3070110:05A02:B03 | MA120:B03 |
| 413 | 10255 | I:1904493:05A02:H03 | MA120:H03 |
| 414 | 10257 | I:2860815:05A02:A09 | MA120:A09 |
| 415 | 10285 | I:1930135:07A02:G03 | MA128:G03 |
| 416 | 10318 | I:3747901:06B02:G03 | MA126:G03 |
| 417 | 10321 | I:1720946:06A02:A09 | MA124:A09 |
| 418 | 10328 | I:2877413:06B02:D09 | MA126:D09 |
| 419 | 10330 | I:3035279:06B02:E09 | MA126:E09 |
| 420 | 10393 | I:2503913:03A02:E09 | MA112:E09 |
| 421 | 10403 | I:1517380:01A02:B03 | MA104:B03 |
| 422 | 10406 | I:3138128:01B02:C03 | MA106:C03 |
| 423 | 10409 | I:2453722:01A02:E03 | MA104:E03 |
| 424 | 10417 | I:1414260:01A02:A09 | MA104:A09 |
| 425 | 10418 | I:2891247:01B02:A09 | MA106:A09 |
| 426 | 10427 | I:1682176:01A02:F09 | MA104:F09 |
| 427 | 10503 | I:2739076:04A02:D03 | MA116:D03 |
| 428 | 10508 | I:1900378:04B02:F03 | MA118:F03 |
| 429 | 10509 | I:1603391:04A02:G03 | MA116:G03 |
| 430 | 10517 | I:2018222:04A02:C09 | MA116:C09 |
| 431 | 10523 | I:1327263:04A02:F09 | MA116:F09 |
| 432 | 10547 | I:1734393:02A02:B09 | MA108:B09 |
| 433 | 10553 | I:2190607:02A02:E09 | MA108:E09 |
| 434 | 10569 | I:2447969:08A01:E04 | MA131:E04 |
| 435 | 10592 | I:1753033:08B01:H10 | MA133:H10 |
| 436 | 10650 | I:2456393:07B01:E10 | MA129:E10 |
| 437 | 10658 | I:1719920:06B01:A04 | MA125:A04 |
| 438 | 10672 | I:2927362:06B01:H04 | MA125:H04 |
| 439 | 10684 | I:4082816:06B01:F10 | MA125:F10 |
| 440 | 10721 | I:1803446:03A01:A04 | MA111:A04 |
| 441 | 10725 | I:1557490:03A01:C04 | MA111:C04 |
| 442 | 10746 | I:1445895:03B01:E10 | MA113:E10 |
| 443 | 10767 | I:1336836:01A01:H04 | MA103:H04 |
| 444 | 10778 | I:1802745:01B01:E10 | MA105:E10 |
| 445 | 10784 | I:2503003:01B01:H10 | MA105:H10 |
| 446 | 10827 | I:1655377:10A01:F04 | MA64:F04 |
| 447 | 10849 | I:1430662:04A01:A04 | MA115:A04 |
| 448 | 10861 | I:3335055:04A01:G04 | MA115:G04 |
| 449 | 10868 | I:2457671:04B01:B10 | MA117:B10 |
| 450 | 10901 | I:1641421:02A01:C10 | MA107:C10 |

Table 2

| SEQ ID NO | Spot ID | Clone ID | MAClone ID |
|-----------|---------|---------------------|------------|
| 451 | 10906 | I:1655225:02B01:E10 | MA109:E10 |
| 452 | 10947 | I:1313325:05A02:B04 | MA120:B04 |
| 453 | 10962 | I:1558081:05B02:A10 | MA122:A10 |
| 454 | 10975 | I:1889191:05A02:H10 | MA120:H10 |
| 455 | 10997 | I:3495906:07A02:C10 | MA128:C10 |
| 456 | 11095 | I:3704132:03A02:D10 | MA112:D10 |
| 457 | 11100 | I:1636553:03B02:F10 | MA114:F10 |
| 458 | 11104 | I:1402228:03B02:H10 | MA114:H10 |
| 459 | 11107 | I:1361963:01A02:B04 | MA104:B04 |
| 460 | 11111 | I:1510424:01A02:D04 | MA104:D04 |
| 461 | 11112 | I:2918558:01B02:D04 | MA106:D04 |
| 462 | 11127 | I:1731061:01A02:D10 | MA104:D10 |
| 463 | 11201 | I:2579602:04A02:A04 | MA116:A04 |
| 464 | 11202 | I:2824181:04B02:A04 | MA118:A04 |
| 465 | 11203 | I:2123183:04A02:B04 | MA116:B04 |
| 466 | 11221 | I:1958560:04A02:C10 | MA116:C10 |
| 467 | 11229 | I:1447903:04A02:G10 | MA116:G10 |
| 468 | 11257 | I:1875576:02A02:E10 | MA108:E10 |
| 469 | 11262 | I:1709457:02B02:G10 | MA110:G10 |
| 470 | 11278 | I:2155675:08B01:G05 | MA133:G05 |
| 471 | 11329 | I:1635069:07A01:A05 | MA127:A05 |
| 472 | 11341 | I:1453445:07A01:G05 | MA127:G05 |
| 473 | 11351 | I:3002566:07A01:D11 | MA127:D11 |
| 474 | 11365 | I:1631511:06A01:C05 | MA123:C05 |
| 475 | 11375 | I:1610523:06A01:H05 | MA123:H05 |
| 476 | 11386 | I:3297656:06B01:E11 | MA125:E11 |
| 477 | 11392 | I:2509730:06B01:H11 | MA125:H11 |
| 478 | 11432 | I:2121863:03B01:D05 | MA113:D05 |
| 479 | 11434 | I:1413704:03B01:E05 | MA113:E05 |
| 480 | 11441 | I:1626232:03A01:A11 | MA111:A11 |
| 481 | 11460 | I:2354446:01B01:B05 | MA105:B05 |
| 482 | 11466 | I:2916753:01B01:E05 | MA105:E05 |
| 483 | 11473 | I:2555034:01A01:A11 | MA103:A11 |
| 484 | 11480 | I:2804190:01B01:D11 | MA105:D11 |
| 485 | 11481 | I:1814488:01A01:E11 | MA103:E11 |
| 486 | 11482 | I:2474163:01B01:E11 | MA105:E11 |
| 487 | 11485 | I:1402967:01A01:G11 | MA103:G11 |
| 488 | 11543 | I:2821541:10A01:D11 | MA64:D11 |
| 489 | 11554 | I:2888814:04B01:A05 | MA117:A05 |
| 490 | 11557 | I:1451005:04A01:C05 | MA115:C05 |
| 491 | 11567 | I:1457726:04A01:H05 | MA115:H05 |
| 492 | 11568 | I:2883195:04B01:H05 | MA117:H05 |
| 493 | 11581 | I:1603605:04A01:G11 | MA115:G11 |
| 494 | 11583 | I:2832224:04A01:H11 | MA115:H11 |
| 495 | 11585 | I:2231364:02A01:A05 | MA107:A05 |
| 496 | 11612 | I:1595081:02B01:F11 | MA109:F11 |
| 497 | 11654 | I:1877913:05B02:C05 | MA122:C05 |
| 498 | 11660 | I:1666130:05B02:F05 | MA122:F05 |
| 499 | 11664 | I:1709995:05B02:H05 | MA122:H05 |
| 500 | 11683 | I:3872557:07A02:B05 | MA128:B05 |

Table 2

| SEQ ID NO | Spot ID | Clone ID | MAClone ID |
|-----------|---------|---------------------|------------|
| 501 | 11705 | I:2734906:07A02:E11 | MA128:E11 |
| 502 | 11715 | I:1798585:06A02:B05 | MA124:B05 |
| 503 | 11723 | I:1683389:06A02:F05 | MA124:F05 |
| 504 | 11725 | I:1704517:06A02:G05 | MA124:G05 |
| 505 | 11728 | I:2792982:06B02:H05 | MA126:H05 |
| 506 | 11736 | I:3511355:06B02:D11 | MA126:D11 |
| 507 | 11777 | I:1738060:03A02:A05 | MA112:A05 |
| 508 | 11780 | I:1810821:03B02:B05 | MA114:B05 |
| 509 | 11785 | I:2451279:03A02:E05 | MA112:E05 |
| 510 | 11786 | I:1431166:03B02:E05 | MA114:E05 |
| 511 | 11794 | I:2949427:03B02:A11 | MA114:A11 |
| 512 | 11802 | I:1458366:03B02:E11 | MA114:E11 |
| 513 | 11806 | I:1525881:03B02:G11 | MA114:G11 |
| 514 | 11817 | I:2071473:01A02:E05 | MA104:E05 |
| 515 | 11829 | I:2481012:01A02:C11 | MA104:C11 |
| 516 | 11830 | I:2816931:01B02:C11 | MA106:C11 |
| 517 | 11836 | I:1806769:01B02:F11 | MA106:F11 |
| 518 | 11922 | I:2636634:04B02:A11 | MA118:A11 |
| 519 | 11962 | I:1649959:02B02:E11 | MA110:E11 |
| 520 | 11964 | I:1633719:02B02:F11 | MA110:F11 |
| 521 | 11966 | I:1901035:02B02:G11 | MA110:G11 |
| 522 | 11990 | I:2503879:08B01:C12 | MA133:C12 |
| 523 | 12036 | I:2383065:07B01:B06 | MA129:B06 |
| 524 | 12043 | I:3357245:07A01:F06 | MA127:F06 |
| 525 | 12045 | I:2832314:07A01:G06 | MA127:G06 |
| 526 | 12055 | I:3667096:07A01:D12 | MA127:D12 |
| 527 | 12071 | I:1798283:06A01:D06 | MA123:D06 |
| 528 | 12131 | I:1648206:03A01:B06 | MA111:B06 |
| 529 | 12148 | I:3360476:03B01:B12 | MA113:B12 |
| 530 | 12150 | I:2500511:03B01:C12 | MA113:C12 |
| 531 | 12152 | I:1730806:03B01:D12 | MA113:D12 |
| 532 | 12166 | I:2479074:01B01:C06 | MA105:C06 |
| 533 | 12170 | I:1635004:01B01:E06 | MA105:E06 |
| 534 | 12174 | I:2378569:01B01:G06 | MA105:G06 |
| 535 | 12183 | I:2207849:01A01:D12 | MA103:D12 |
| 536 | 12187 | I:1504554:01A01:F12 | MA103:F12 |
| 537 | 12258 | I:2989991:04B01:A06 | MA117:A06 |
| 538 | 12260 | I:2852561:04B01:B06 | MA117:B06 |
| 539 | 12277 | I:2832839:04A01:C12 | MA115:C12 |
| 540 | 12282 | I:2845548:04B01:E12 | MA117:E12 |
| 541 | 12292 | I:1251819:02B01:B06 | MA109:B06 |
| 542 | 12296 | I:1672930:02B01:D06 | MA109:D06 |
| 543 | 12298 | I:2122820:02B01:E06 | MA109:E06 |
| 544 | 12303 | I:2174920:02A01:H06 | MA107:H06 |
| 545 | 12362 | I:1875994:05B02:E06 | MA122:E06 |
| 546 | 12365 | I:1858644:05A02:G06 | MA120:G06 |
| 547 | 12425 | I:1700047:06A02:E06 | MA124:E06 |
| 548 | 12426 | I:1718257:06B02:E06 | MA126:E06 |
| 549 | 12427 | I:1612306:06A02:F06 | MA124:F06 |
| 550 | 12443 | I:1637427:06A02:F12 | MA124:F12 |

Table 2

| SEQ ID NO | Spot ID | Clone ID | MAClone ID |
|-----------|---------|----------------------|------------|
| 551 | 12499 | I:2513883:03A02:B12 | MA112:B12 |
| 552 | 12525 | I:2645840:01A02:G06 | MA104:G06 |
| 553 | 12529 | I:1737403:01A02:A12 | MA104:A12 |
| 554 | 12544 | I:1733522:01B02:H12 | MA106:H12 |
| 555 | 17049 | RG:160664:10006:E07 | MA155:E07 |
| 556 | 17065 | I:747335:16A01:E01 | MA87:E01 |
| 557 | 17071 | I:2085191:16A01:H01 | MA87:H01 |
| 558 | 17081 | I:1211126:16A01:E07 | MA87:E07 |
| 559 | 17157 | RG:669310:10010:C01 | MA159:C01 |
| 560 | 17167 | RG:730402:10010:H01 | MA159:H01 |
| 561 | 17174 | RG:1047541:10012:C07 | MA161:C07 |
| 562 | 17178 | RG:1161753:10012:E07 | MA161:E07 |
| 563 | 17194 | I:1218464:17B01:E01 | MA93:E01 |
| 564 | 17214 | I:958633:17B01:G07 | MA93:G07 |
| 565 | 17236 | I:1602726:09B01:B07 | MA137:B07 |
| 566 | 17379 | RG:205212:10007:B01 | MA156:B01 |
| 567 | 17395 | RG:207395:10007:B07 | MA156:B07 |
| 568 | 17422 | I:349535:16B02:G01 | MA90:G01 |
| 569 | 17423 | I:2323525:16A02:H01 | MA88:H01 |
| 570 | 17432 | I:1965049:16B02:D07 | MA90:D07 |
| 571 | 17437 | I:2054436:16A02:G07 | MA88:G07 |
| 572 | 17515 | RG:1506197:10013:F01 | MA162:F01 |
| 573 | 17518 | RG:1871436:10015:G01 | MA164:G01 |
| 574 | 17524 | RG:1705470:10015:B07 | MA164:B07 |
| 575 | 17556 | I:546910:17B02:B07 | MA94:B07 |
| 576 | 17580 | I:1799023:09B02:F01 | MA138:F01 |
| 577 | 17584 | I:2380380:09B02:H01 | MA138:H01 |
| 578 | 17675 | I:2319269:18A01:F02 | MA95:F02 |
| 579 | 17687 | I:2296344:18A01:D08 | MA95:D08 |
| 580 | 17737 | RG:155066:10006:E02 | MA155:E02 |
| 581 | 17741 | RG:180135:10006:G02 | MA155:G02 |
| 582 | 17755 | RG:178093:10006:F08 | MA155:F08 |
| 583 | 17757 | RG:184042:10006:G08 | MA155:G08 |
| 584 | 17761 | I:1741643:16A01:A02 | MA87:A02 |
| 585 | 17860 | RG:928026:10012:B02 | MA161:B02 |
| 586 | 17862 | RG:1032969:10012:C02 | MA161:C02 |
| 587 | 17872 | RG:1322660:10012:H02 | MA161:H02 |
| 588 | 17876 | RG:968474:10012:B08 | MA161:B08 |
| 589 | 17878 | RG:1047592:10012:C08 | MA161:C08 |
| 590 | 17914 | I:617750:17B01:E08 | MA93:E08 |
| 591 | 17934 | I:2808775:09B01:G02 | MA137:G02 |
| 592 | 18035 | I:966692:18A02:B08 | MA96:B08 |
| 593 | 18085 | RG:209240:10007:C02 | MA156:C02 |
| 594 | 18087 | RG:223355:10007:D02 | MA156:D02 |
| 595 | 18095 | RG:267629:10007:H02 | MA156:H02 |
| 596 | 18134 | I:2246234:16B02:C08 | MA90:C08 |
| 597 | 18212 | RG:1696513:10015:B02 | MA164:B02 |
| 598 | 18216 | RG:1733895:10015:D02 | MA164:D02 |
| 599 | 18225 | RG:1353930:10013:A08 | MA162:A08 |
| 600 | 18238 | RG:1881947:10015:G08 | MA164:G08 |

Table 2

| SEQ ID NO | Spot ID | Clone ID | MAClone ID |
|-----------|---------|----------------------|------------|
| 601 | 18443 | RG:166575:10006:F03 | MA155:F03 |
| 602 | 18465 | I:1998994:16A01:A03 | MA87:A03 |
| 603 | 18471 | I:1953051:16A01:D03 | MA87:D03 |
| 604 | 18473 | I:518826:16A01:E03 | MA87:E03 |
| 605 | 18483 | I:81490:16A01:B09 | MA87:B09 |
| 606 | 18572 | RG:1256163:10012:F03 | MA161:F03 |
| 607 | 18584 | RG:1132085:10012:D09 | MA161:D09 |
| 608 | 18614 | I:2132717:17B01:C09 | MA93:C09 |
| 609 | 18620 | I:1998428:17B01:F09 | MA93:F09 |
| 610 | 18787 | RG:206694:10007:B03 | MA156:B03 |
| 611 | 18811 | RG:261714:10007:F09 | MA156:F09 |
| 612 | 18821 | I:1461515:16A02:C03 | MA88:C03 |
| 613 | 18831 | I:338859:16A02:H03 | MA88:H03 |
| 614 | 18845 | I:1425861:16A02:G09 | MA88:G09 |
| 615 | 18848 | I:1928644:16B02:H09 | MA90:H09 |
| 616 | 18917 | RG:1404414:10013:C03 | MA162:C03 |
| 617 | 18919 | RG:1415437:10013:D03 | MA162:D03 |
| 618 | 18920 | RG:1734353:10015:D03 | MA164:D03 |
| 619 | 18926 | RG:1872251:10015:G03 | MA164:G03 |
| 620 | 18929 | RG:1354408:10013:A09 | MA162:A09 |
| 621 | 18930 | RG:1690198:10015:A09 | MA164:A09 |
| 622 | 18937 | RG:1476452:10013:E09 | MA162:E09 |
| 623 | 18988 | I:2069305:09B02:F03 | MA138:F03 |
| 624 | 19088 | I:1966067:18B01:H04 | MA97:H04 |
| 625 | 19090 | I:2128547:18B01:A10 | MA97:A10 |
| 626 | 19143 | RG:149960:10006:D04 | MA155:D04 |
| 627 | 19147 | RG:171569:10006:F04 | MA155:F04 |
| 628 | 19163 | RG:178638:10006:F10 | MA155:F10 |
| 629 | 19167 | RG:195122:10006:H10 | MA155:H10 |
| 630 | 19195 | I:814216:16A01:F10 | MA87:F10 |
| 631 | 19265 | RG:491163:10010:A04 | MA159:A04 |
| 632 | 19266 | RG:827185:10012:A04 | MA161:A04 |
| 633 | 19272 | RG:1129102:10012:D04 | MA161:D04 |
| 634 | 19279 | RG:730938:10010:H04 | MA159:H04 |
| 635 | 19282 | RG:925984:10012:A10 | MA161:A10 |
| 636 | 19283 | RG:668442:10010:B10 | MA159:B10 |
| 637 | 19284 | RG:1028911:10012:B10 | MA161:B10 |
| 638 | 19285 | RG:684866:10010:C10 | MA159:C10 |
| 639 | 19292 | RG:1283076:10012:F10 | MA161:F10 |
| 640 | 19309 | I:627654:17A01:G04 | MA91:G04 |
| 641 | 19319 | I:1833801:17A01:D10 | MA91:D10 |
| 642 | 19328 | I:961473:17B01:H10 | MA93:H10 |
| 643 | 19348 | I:2556708:09B01:B10 | MA137:B10 |
| 644 | 19511 | RG:243565:10007:D10 | MA156:D10 |
| 645 | 19517 | RG:266649:10007:G10 | MA156:G10 |
| 646 | 19524 | I:2013513:16B02:B04 | MA90:B04 |
| 647 | 19539 | I:2312442:16A02:B10 | MA88:B10 |
| 648 | 19543 | I:2060626:16A02:D10 | MA88:D10 |
| 649 | 19623 | RG:1415858:10013:D04 | MA162:D04 |
| 650 | 19627 | RG:1517435:10013:F04 | MA162:F04 |

Table 2

| SEQ ID NO | Spot ID | Clone ID | MAClone ID |
|-----------|---------|----------------------|------------|
| 651 | 19632 | RG:1914716:10015:H04 | MA164:H04 |
| 652 | 19633 | RG:1354528:10013:A10 | MA162:A10 |
| 653 | 19636 | RG:1706414:10015:B10 | MA164:B10 |
| 654 | 19653 | I:1998510:17A02:C04 | MA92:C04 |
| 655 | 19678 | I:899118:17B02:G10 | MA94:G10 |
| 656 | 19684 | I:2680168:09B02:B04 | MA138:B04 |
| 657 | 19690 | I:1354558:09B02:E04 | MA138:E04 |
| 658 | 19708 | I:1665871:09B02:F10 | MA138:F10 |
| 659 | 19782 | I:1922084:18B01:C05 | MA97:C05 |
| 660 | 19795 | I:2307946:18A01:B11 | MA95:B11 |
| 661 | 19798 | I:1923572:18B01:C11 | MA97:C11 |
| 662 | 19851 | RG:171993:10006:F05 | MA155:F05 |
| 663 | 19859 | RG:129317:10006:B11 | MA155:B11 |
| 664 | 19863 | RG:153244:10006:D11 | MA155:D11 |
| 665 | 19871 | RG:196236:10006:H11 | MA155:H11 |
| 666 | 19893 | I:557538:16A01:C11 | MA87:C11 |
| 667 | 19899 | I:782235:16A01:F11 | MA87:F11 |
| 668 | 19980 | RG:1257341:10012:F05 | MA161:F05 |
| 669 | 19981 | RG:727387:10010:G05 | MA159:G05 |
| 670 | 19992 | RG:1145235:10012:D11 | MA161:D11 |
| 671 | 19995 | RG:725145:10010:F11 | MA159:F11 |
| 672 | 19999 | RG:740079:10010:H11 | MA159:H11 |
| 673 | 20042 | I:1873176:09B01:E05 | MA137:E05 |
| 674 | 20056 | I:2081974:09B01:D11 | MA137:D11 |
| 675 | 20141 | I:2107723:18A02:G05 | MA96:G05 |
| 676 | 20211 | RG:207777:10007:B11 | MA156:B11 |
| 677 | 20213 | RG:221172:10007:C11 | MA156:C11 |
| 678 | 20230 | I:1968436:16B02:C05 | MA90:C05 |
| 679 | 20253 | I:2060973:16A02:G11 | MA88:G11 |
| 680 | 20323 | RG:1369494:10013:B05 | MA162:B05 |
| 681 | 20330 | RG:1752177:10015:E05 | MA164:E05 |
| 682 | 20331 | RG:1519327:10013:F05 | MA162:F05 |
| 683 | 20338 | RG:1694569:10015:A11 | MA164:A11 |
| 684 | 20346 | RG:1839794:10015:E11 | MA164:E11 |
| 685 | 20359 | I:514124:17A02:D05 | MA92:D05 |
| 686 | 20365 | I:997782:17A02:G05 | MA92:G05 |
| 687 | 20412 | I:1709364:09B02:F11 | MA138:F11 |
| 688 | 20485 | I:2004896:18A01:C06 | MA95:C06 |
| 689 | 20555 | RG:172982:10006:F06 | MA155:F06 |
| 690 | 20557 | RG:180978:10006:G06 | MA155:G06 |
| 691 | 20563 | RG:129528:10006:B12 | MA155:B12 |
| 692 | 20573 | RG:186511:10006:G12 | MA155:G12 |
| 693 | 20580 | I:2005910:16B01:B06 | MA89:B06 |
| 694 | 20583 | I:620871:16A01:D06 | MA87:D06 |
| 695 | 20593 | I:1920819:16A01:A12 | MA87:A12 |
| 696 | 20601 | I:990375:16A01:E12 | MA87:E12 |
| 697 | 20605 | I:690313:16A01:G12 | MA87:G12 |
| 698 | 20674 | RG:878195:10012:A06 | MA161:A06 |
| 699 | 20679 | RG:687128:10010:D06 | MA159:D06 |
| 700 | 20712 | I:884855:17B01:D06 | MA93:D06 |

Table 2

| SEQ ID NO | Spot ID | Clone ID | MAClone ID |
|-----------|---------|----------------------|------------|
| 701 | 20716 | I:1218621:17B01:F06 | MA93:F06 |
| 702 | 20719 | I:620371:17A01:H06 | MA91:H06 |
| 703 | 20744 | I:1681610:09B01:D06 | MA137:D06 |
| 704 | 20909 | RG:265206:10007:G06 | MA156:G06 |
| 705 | 20911 | RG:268073:10007:H06 | MA156:H06 |
| 706 | 20939 | I:2117221:16A02:F06 | MA88:F06 |
| 707 | 20942 | I:1760693:16B02:G06 | MA90:G06 |
| 708 | 20948 | I:776793:16B02:B12 | MA90:B12 |
| 709 | 21029 | RG:1405692:10013:C06 | MA162:C06 |
| 710 | 21044 | RG:1707747:10015:B12 | MA164:B12 |
| 711 | 21046 | RG:1722789:10015:C12 | MA164:C12 |
| 712 | 21066 | I:2112348:17B02:E06 | MA94:E06 |
| 713 | 21067 | I:630458:17A02:F06 | MA92:F06 |
| 714 | 21071 | I:901577:17A02:H06 | MA92:H06 |
| 715 | 21082 | I:2298081:17B02:E12 | MA94:E12 |
| 716 | 21120 | I:2718565:09B02:H12 | MA138:H12 |
| 717 | 21122 | M00056237C:E03 | MA181:A01 |
| 718 | 21130 | M00055261C:F04 | MA197:E01 |
| 719 | 21144 | M00055353D:A04 | MA197:D07 |
| 720 | 21152 | M00055357B:B10 | MA197:H07 |
| 721 | 21189 | M00056386D:H12 | MA173:C01 |
| 722 | 21191 | M00056394B:B04 | MA173:D01 |
| 723 | 21193 | M00056395A:B04 | MA173:E01 |
| 724 | 21195 | M00056396B:G05 | MA173:F01 |
| 725 | 21198 | M00056137A:A05 | MA180:G01 |
| 726 | 21199 | M00056401C:C03 | MA173:H01 |
| 727 | 21209 | M00056484A:F06 | MA173:E07 |
| 728 | 21212 | M00056193B:C11 | MA180:F07 |
| 729 | 21213 | M00056484B:B07 | MA173:G07 |
| 730 | 21214 | M00056193B:D06 | MA180:G07 |
| 731 | 21216 | M00056194B:G06 | MA180:H07 |
| 732 | 21217 | M00054633D:B07 | MA187:A01 |
| 733 | 21219 | M00054633D:E06 | MA187:B01 |
| 734 | 21232 | M00054848A:C03 | MA189:H01 |
| 735 | 21234 | M00054882C:C06 | MA189:A07 |
| 736 | 21237 | M00054678D:A03 | MA187:C07 |
| 737 | 21239 | M00054679B:B03 | MA187:D07 |
| 738 | 21245 | M00054680B:D06 | MA187:G07 |
| 739 | 21247 | M00054680C:A06 | MA187:H07 |
| 740 | 21252 | M00057176B:F11 | MA193:B01 |
| 741 | 21254 | M00057181A:D01 | MA193:C01 |
| 742 | 21272 | M00057219D:B04 | MA193:D07 |
| 743 | 21281 | M00042341A:D12 | MA167:A01 |
| 744 | 21284 | M00042433B:G09 | MA171:B01 |
| 745 | 21288 | M00042435A:F08 | MA171:D01 |
| 746 | 21290 | M00042437B:G03 | MA171:E01 |
| 747 | 21291 | M00042525D:E07 | MA167:F01 |
| 748 | 21292 | M00042438B:D01 | MA171:F01 |
| 749 | 21293 | M00042529C:G07 | MA167:G01 |
| 750 | 21295 | M00042529D:B12 | MA167:H01 |

Table 2

| SEQ ID NO | Spot ID | Clone ID | MAClone ID |
|-----------|---------|---------------------|------------|
| 751 | 21297 | M00042700A:E05 | MA167:A07 |
| 752 | 21300 | M00042777D:G05 | MA171:B07 |
| 753 | 21304 | M00042781C:F03 | MA171:D07 |
| 754 | 21306 | M00042783C:F10 | MA171:E07 |
| 755 | 21307 | M00042702D:B02 | MA167:F07 |
| 756 | 21312 | M00042785B:F11 | MA171:H07 |
| 757 | 21329 | M00056566C:C03 | MA174:A07 |
| 758 | 21333 | M00056567B:A09 | MA174:C07 |
| 759 | 21341 | M00056569B:D09 | MA174:G07 |
| 760 | 21343 | M00056571D:E05 | MA174:H07 |
| 761 | 21349 | RG:376801:10009:C01 | MA158:C01 |
| 762 | 21363 | RG:365436:10009:B07 | MA158:B07 |
| 763 | 21367 | RG:416839:10009:D07 | MA158:D07 |
| 764 | 21370 | RG:784224:10011:E07 | MA160:E07 |
| 765 | 21374 | RG:796852:10011:G07 | MA160:G07 |
| 766 | 21386 | M00043412A:F04 | MA184:E01 |
| 767 | 21391 | M00057273B:H10 | MA182:H01 |
| 768 | 21396 | M00054506C:B10 | MA184:B07 |
| 769 | 21404 | M00054507D:G03 | MA184:F07 |
| 770 | 21418 | M00054935B:B03 | MA198:E01 |
| 771 | 21424 | M00054935D:C11 | MA198:H01 |
| 772 | 21432 | M00054976A:E09 | MA198:D07 |
| 773 | 21461 | M00055788B:F08 | MA170:C07 |
| 774 | 21469 | M00055791A:E10 | MA170:G07 |
| 775 | 21497 | M00055224C:H11 | MA196:E07 |
| 776 | 21539 | M00055932A:C02 | MA179:B01 |
| 777 | 21542 | M00056908A:F12 | MA177:C01 |
| 778 | 21543 | M00055935D:B06 | MA179:D01 |
| 779 | 21546 | M00056908D:D08 | MA177:E01 |
| 780 | 21547 | M00055942B:F08 | MA179:F01 |
| 781 | 21550 | M00056910A:B07 | MA177:G01 |
| 782 | 21568 | M00056952B:C08 | MA177:H07 |
| 783 | 21569 | M00054728C:E03 | MA188:A01 |
| 784 | 21571 | M00054728D:E06 | MA188:B01 |
| 785 | 21583 | M00054731C:H01 | MA188:H01 |
| 786 | 21591 | M00054778B:A12 | MA188:D07 |
| 787 | 21595 | M00054778C:D08 | MA188:F07 |
| 788 | 21599 | M00054780A:G06 | MA188:H07 |
| 789 | 21633 | M00042899D:D02 | MA168:A01 |
| 790 | 21638 | M00042831B:G10 | MA172:C01 |
| 791 | 21640 | M00042833A:G07 | MA172:D01 |
| 792 | 21641 | M00042906D:F05 | MA168:E01 |
| 793 | 21645 | M00042910C:A02 | MA168:G01 |
| 794 | 21648 | M00042838C:D06 | MA172:H01 |
| 795 | 21650 | M00042867B:F03 | MA172:A07 |
| 796 | 21651 | M00055439B:G05 | MA168:B07 |
| 797 | 21659 | M00055442D:E12 | MA168:F07 |
| 798 | 21667 | M00056711D:A02 | MA175:B01 |
| 799 | 21681 | M00056771C:A12 | MA175:A07 |
| 800 | 21685 | M00056772D:G07 | MA175:C07 |

Table 2

| SEQ ID NO | Spot ID | Clone ID | MAClone ID |
|-----------|---------|----------------------|------------|
| 801 | 21691 | M00056782D:E04 | MA175:F07 |
| 802 | 21693 | M00056785D:G01 | MA175:G07 |
| 803 | 21695 | M00056788C:A01 | MA175:H07 |
| 804 | 21723 | RG:1663880:10014:F07 | MA163:F07 |
| 805 | 21733 | M00043310B:D08 | MA183:C01 |
| 806 | 21734 | M00054538C:G03 | MA185:C01 |
| 807 | 21743 | M00043315C:G05 | MA183:H01 |
| 808 | 21764 | M00055397B:E08 | MA199:B01 |
| 809 | 21765 | M00056624B:H11 | MA186:C01 |
| 810 | 21786 | M00055423C:C03 | MA199:E07 |
| 811 | 21787 | M00056668D:C06 | MA186:F07 |
| 812 | 21789 | M00056669B:A10 | MA186:G07 |
| 813 | 21790 | M00055424A:D01 | MA199:G07 |
| 814 | 21791 | M00056669B:E07 | MA186:H07 |
| 815 | 21792 | M00055424D:F01 | MA199:H07 |
| 816 | 21798 | M00056243A:H07 | MA181:C02 |
| 817 | 21800 | M00056243C:G10 | MA181:D02 |
| 818 | 21803 | M00055528D:H03 | MA169:F02 |
| 819 | 21811 | M00055607B:A11 | MA169:B08 |
| 820 | 21842 | M00055363C:E02 | MA197:A08 |
| 821 | 21852 | M00055373D:H02 | MA197:F08 |
| 822 | 21856 | M00055374D:E01 | MA197:H08 |
| 823 | 21889 | M00056401D:D09 | MA173:A02 |
| 824 | 21892 | M00056139D:A10 | MA180:B02 |
| 825 | 21896 | M00056140A:E11 | MA180:D02 |
| 826 | 21898 | M00056142D:A08 | MA180:E02 |
| 827 | 21899 | M00056412D:A09 | MA173:F02 |
| 828 | 21900 | M00056142D:H11 | MA180:F02 |
| 829 | 21901 | M00056414C:F03 | MA173:G02 |
| 830 | 21908 | M00056196A:H09 | MA180:B08 |
| 831 | 21912 | M00056200A:E11 | MA180:D08 |
| 832 | 21913 | M00056488C:G01 | MA173:E08 |
| 833 | 21914 | M00056200B:B01 | MA180:E08 |
| 834 | 21916 | M00056203B:G08 | MA180:F08 |
| 835 | 21919 | M00056493A:F09 | MA173:H08 |
| 836 | 21923 | M00054640D:D12 | MA187:B02 |
| 837 | 21927 | M00054643B:F04 | MA187:D02 |
| 838 | 21929 | M00054643C:D08 | MA187:E02 |
| 839 | 21932 | M00054854D:B06 | MA189:F02 |
| 840 | 21933 | M00054644B:F02 | MA187:G02 |
| 841 | 21934 | M00054857A:E08 | MA189:G02 |
| 842 | 21939 | M00054681D:G03 | MA187:B08 |
| 843 | 21943 | M00054682D:F11 | MA187:D08 |
| 844 | 21947 | M00054684B:C07 | MA187:F08 |
| 845 | 21960 | M00057191B:E11 | MA193:D02 |
| 846 | 21966 | M00057194B:G12 | MA193:G02 |
| 847 | 21972 | M00057222D:G09 | MA193:B08 |
| 848 | 21985 | M00042531B:H03 | MA167:A02 |
| 849 | 21986 | M00042440C:G04 | MA171:A02 |
| 850 | 21989 | M00042533C:D02 | MA167:C02 |

Table 2

| SEQ ID NO | Spot ID | Clone ID | MAClone ID |
|-----------|---------|----------------------|------------|
| 851 | 21993 | M00042536D:H05 | MA167:E02 |
| 852 | 21994 | M00042465B:E04 | MA171:E02 |
| 853 | 21995 | M00042537D:F10 | MA167:F02 |
| 854 | 21996 | M00042467B:B04 | MA171:F02 |
| 855 | 21997 | M00042538D:D12 | MA167:G02 |
| 856 | 21998 | M00042467B:B08 | MA171:G02 |
| 857 | 22003 | M00042711B:G09 | MA167:B08 |
| 858 | 22004 | M00042790B:E12 | MA171:B08 |
| 859 | 22006 | M00042791A:C10 | MA171:C08 |
| 860 | 22007 | M00042711C:H05 | MA167:D08 |
| 861 | 22016 | M00042801D:B02 | MA171:H08 |
| 862 | 22016 | M00042801D:B02 | MA171:H08 |
| 863 | 22021 | M00056532A:D09 | MA174:C02 |
| 864 | 22025 | M00056533D:H04 | MA174:E02 |
| 865 | 22035 | M00056575B:C04 | MA174:B08 |
| 866 | 22037 | M00056578C:A09 | MA174:C08 |
| 867 | 22040 | RG:1862072:20001:D08 | MA139:D08 |
| 868 | 22044 | RG:1862465:20001:F08 | MA139:F08 |
| 869 | 22049 | RG:347381:10009:A02 | MA158:A02 |
| 870 | 22071 | RG:417093:10009:D08 | MA158:D08 |
| 871 | 22082 | M00043413B:C04 | MA184:A02 |
| 872 | 22092 | M00043502D:C12 | MA184:F02 |
| 873 | 22105 | M00057341B:B11 | MA182:E08 |
| 874 | 22110 | M00054512A:F11 | MA184:G08 |
| 875 | 22111 | M00042353A:D05 | MA182:H08 |
| 876 | 22116 | M00054937B:D09 | MA198:B02 |
| 877 | 22167 | M00055797C:H09 | MA170:D08 |
| 878 | 22169 | M00055799B:C01 | MA170:E08 |
| 879 | 22183 | M00055194C:G12 | MA196:D02 |
| 880 | 22195 | M00055233B:D08 | MA196:B08 |
| 881 | 22255 | M00055966C:D06 | MA179:H02 |
| 882 | 22263 | M00056024B:B06 | MA179:D08 |
| 883 | 22265 | M00056024C:G04 | MA179:E08 |
| 884 | 22279 | M00054737D:F10 | MA188:D02 |
| 885 | 22289 | M00054780D:C09 | MA188:A08 |
| 886 | 22295 | M00054787A:E09 | MA188:D08 |
| 887 | 22297 | M00054806B:E11 | MA188:E08 |
| 888 | 22339 | M00042913B:C11 | MA168:B02 |
| 889 | 22343 | M00042915B:B10 | MA168:D02 |
| 890 | 22345 | M00054792C:E12 | MA168:E02 |
| 891 | 22350 | M00042842A:C01 | MA172:G02 |
| 892 | 22367 | M00055450A:C09 | MA168:H08 |
| 893 | 22399 | M00056804C:D01 | MA175:H08 |
| 894 | 22423 | RG:1647954:10014:D08 | MA163:D08 |
| 895 | 22427 | RG:1664311:10014:F08 | MA163:F08 |
| 896 | 22429 | RG:1671377:10014:G08 | MA163:G08 |
| 897 | 22437 | M00043316B:F10 | MA183:C02 |
| 898 | 22440 | M00054545B:A03 | MA185:D02 |
| 899 | 22442 | M00054545B:B09 | MA185:E02 |
| 900 | 22456 | M00054575A:B09 | MA185:D08 |

Table 2

| SEQ ID NO | Spot ID | Clone ID | MAClone ID |
|-----------|---------|----------------|------------|
| 901 | 22459 | M00043374B:H05 | MA183:F08 |
| 902 | 22475 | M00056641A:G11 | MA186:F02 |
| 903 | 22479 | M00056642A:D08 | MA186:H02 |
| 904 | 22480 | M00055403B:B11 | MA199:H02 |
| 905 | 22495 | M00056676B:C11 | MA186:H08 |
| 906 | 22499 | M00055530D:B02 | MA169:B03 |
| 907 | 22502 | M00056253A:D06 | MA181:C03 |
| 908 | 22504 | M00056253B:B06 | MA181:D03 |
| 909 | 22519 | M00055642D:F09 | MA169:D09 |
| 910 | 22521 | M00055643A:E09 | MA169:E09 |
| 911 | 22523 | M00055643D:E02 | MA169:F09 |
| 912 | 22548 | M00055376D:D08 | MA197:B09 |
| 913 | 22595 | M00056415C:D02 | MA173:B03 |
| 914 | 22596 | M00056146D:F05 | MA180:B03 |
| 915 | 22597 | M00056417A:F02 | MA173:C03 |
| 916 | 22598 | M00056148A:B07 | MA180:C03 |
| 917 | 22599 | M00056420C:E07 | MA173:D03 |
| 918 | 22600 | M00056150A:E04 | MA180:D03 |
| 919 | 22603 | M00056421C:H11 | MA173:F03 |
| 920 | 22604 | M00056150C:A10 | MA180:F03 |
| 921 | 22605 | M00056421D:H05 | MA173:G03 |
| 922 | 22606 | M00056150C:C04 | MA180:G03 |
| 923 | 22607 | M00056422B:D11 | MA173:H03 |
| 924 | 22608 | M00056151C:A12 | MA180:H03 |
| 925 | 22609 | M00056493C:E06 | MA173:A09 |
| 926 | 22610 | M00056205D:E03 | MA180:A09 |
| 927 | 22611 | M00056495A:G10 | MA173:B09 |
| 928 | 22618 | M00056206D:B10 | MA180:E09 |
| 929 | 22623 | M00056501D:C08 | MA173:H09 |
| 930 | 22624 | M00056209D:H10 | MA180:H09 |
| 931 | 22627 | M00054645B:C12 | MA187:B03 |
| 932 | 22629 | M00054646A:B10 | MA187:C03 |
| 933 | 22637 | M00054647D:E01 | MA187:G03 |
| 934 | 22666 | M00057202C:G06 | MA193:E03 |
| 935 | 22668 | M00057202D:C11 | MA193:F03 |
| 936 | 22693 | M00042549A:G12 | MA167:C03 |
| 937 | 22695 | M00042549D:F03 | MA167:D03 |
| 938 | 22697 | M00042551B:D12 | MA167:E03 |
| 939 | 22698 | M00042513A:D03 | MA171:E03 |
| 940 | 22700 | M00042513D:A12 | MA171:F03 |
| 941 | 22703 | M00042551D:D12 | MA167:H03 |
| 942 | 22705 | M00042717B:D05 | MA167:A09 |
| 943 | 22707 | M00042719D:C09 | MA167:B09 |
| 944 | 22710 | M00042803C:F11 | MA171:C09 |
| 945 | 22714 | M00042805D:D12 | MA171:E09 |
| 946 | 22715 | M00042731A:G04 | MA167:F09 |
| 947 | 22718 | M00042806C:E09 | MA171:G09 |
| 948 | 22720 | M00042806D:F08 | MA171:H09 |
| 949 | 22725 | M00056537A:F05 | MA174:C03 |
| 950 | 22727 | M00056537D:A07 | MA174:D03 |

Table 2

| SEQ ID NO | Spot ID | Clone ID | MAClone ID |
|-----------|---------|----------------------|------------|
| 951 | 22734 | RG:1862584:20001:G03 | MA139:G03 |
| 952 | 22737 | M00056585D:D05 | MA174:A09 |
| 953 | 22739 | M00056586C:B08 | MA174:B09 |
| 954 | 22745 | M00056592A:B08 | MA174:E09 |
| 955 | 22757 | RG:378550:10009:C03 | MA158:C03 |
| 956 | 22780 | RG:789040:10011:F09 | MA160:F09 |
| 957 | 22787 | M00057283A:D01 | MA182:B03 |
| 958 | 22792 | M00043505A:E07 | MA184:D03 |
| 959 | 22798 | M00043506B:G10 | MA184:G03 |
| 960 | 22800 | M00043507A:B02 | MA184:H03 |
| 961 | 22801 | M00042353C:F02 | MA182:A09 |
| 962 | 22812 | M00054516B:A08 | MA184:F09 |
| 963 | 22834 | M00054986D:B04 | MA198:A09 |
| 964 | 22836 | M00054987C:B10 | MA198:B09 |
| 965 | 22838 | M00054988D:B11 | MA198:C09 |
| 966 | 22857 | M00055743C:G08 | MA170:E03 |
| 967 | 22887 | M00055196B:C09 | MA196:D03 |
| 968 | 22899 | M00055238B:G05 | MA196:B09 |
| 969 | 22910 | M00056207B:H06 | MA180:G09 |
| 970 | 22945 | M00055966C:G04 | MA179:A03 |
| 971 | 22946 | M00056920D:C08 | MA177:A03 |
| 972 | 22949 | M00055969D:D01 | MA179:C03 |
| 973 | 22969 | M00056055D:F06 | MA179:E09 |
| 974 | 22970 | M00056956B:G12 | MA177:E09 |
| 975 | 22971 | M00056060D:C04 | MA179:F09 |
| 976 | 22973 | M00056061C:H04 | MA179:G09 |
| 977 | 22977 | M00054743C:E05 | MA188:A03 |
| 978 | 22979 | M00054744C:B02 | MA188:B03 |
| 979 | 22997 | M00054808A:E02 | MA188:C09 |
| 980 | 23005 | M00054811A:G01 | MA188:G09 |
| 981 | 23041 | M00054797C:G10 | MA168:A03 |
| 982 | 23042 | M00042843B:H01 | MA172:A03 |
| 983 | 23048 | M00042844D:D10 | MA172:D03 |
| 984 | 23050 | M00042845D:A12 | MA172:E03 |
| 985 | 23053 | M00054800C:H10 | MA168:G03 |
| 986 | 23055 | M00054911D:E09 | MA168:H03 |
| 987 | 23057 | M00055450A:G03 | MA168:A09 |
| 988 | 23063 | M00055456B:H05 | MA168:D09 |
| 989 | 23079 | M00056733C:D03 | MA175:D03 |
| 990 | 23087 | M00056737D:E08 | MA175:H03 |
| 991 | 23097 | M00056809B:A12 | MA175:E09 |
| 992 | 23101 | M00056809D:C07 | MA175:G09 |
| 993 | 23131 | RG:1664308:10014:F09 | MA163:F09 |
| 994 | 23139 | M00043321A:G07 | MA183:B03 |
| 995 | 23142 | M00054549A:F03 | MA185:C03 |
| 996 | 23159 | M00043381A:C08 | MA183:D09 |
| 997 | 23169 | M00056642B:G03 | MA186:A03 |
| 998 | 23199 | M00056688C:A07 | MA186:H09 |
| 999 | 23202 | M00056257C:G03 | MA181:A04 |
| 1000 | 23213 | M00055545C:F11 | MA169:G04 |

Table 2

| SEQ ID NO | Spot ID | Clone ID | MAClone ID |
|-----------|---------|---------------------|------------|
| 1001 | 23221 | M00055653C:F04 | MA169:C10 |
| 1002 | 23223 | M00055653D:F01 | MA169:D10 |
| 1003 | 23252 | M00055385A:C11 | MA197:B10 |
| 1004 | 23304 | M00056157A:F11 | MA180:D04 |
| 1005 | 23306 | M00056160A:F03 | MA180:E04 |
| 1006 | 23307 | M00056426A:H07 | MA173:F04 |
| 1007 | 23318 | M00056214C:B04 | MA180:C10 |
| 1008 | 23320 | M00056216A:F10 | MA180:D10 |
| 1009 | 23325 | M00056507A:G11 | MA173:G10 |
| 1010 | 23329 | M00054648C:C10 | MA187:A04 |
| 1011 | 23330 | M00054862A:H11 | MA189:A04 |
| 1012 | 23331 | M00054648D:F12 | MA187:B04 |
| 1013 | 23335 | M00054650C:H08 | MA187:D04 |
| 1014 | 23344 | M00054868C:C11 | MA189:H04 |
| 1015 | 23351 | M00054700C:E02 | MA187:D10 |
| 1016 | 23356 | M00054902D:G11 | MA189:F10 |
| 1017 | 23358 | M00054903B:G06 | MA189:G10 |
| 1018 | 23359 | M00054706A:D05 | MA187:H10 |
| 1019 | 23366 | M00057207A:D05 | MA193:C04 |
| 1020 | 23368 | M00057207C:F06 | MA193:D04 |
| 1021 | 23372 | M00057208B:F11 | MA193:F04 |
| 1022 | 23382 | M00057242B:B10 | MA193:C10 |
| 1023 | 23397 | M00042555A:E06 | MA167:C04 |
| 1024 | 23399 | M00042561A:H03 | MA167:D04 |
| 1025 | 23402 | M00042756C:E10 | MA171:E04 |
| 1026 | 23404 | M00042758D:F01 | MA171:F04 |
| 1027 | 23408 | M00042759B:E02 | MA171:H04 |
| 1028 | 23412 | M00042808D:D03 | MA171:B10 |
| 1029 | 23414 | M00042808D:D10 | MA171:C10 |
| 1030 | 23416 | M00042811B:A05 | MA171:D10 |
| 1031 | 23417 | M00042746B:F05 | MA167:E10 |
| 1032 | 23421 | M00042746C:D01 | MA167:G10 |
| 1033 | 23422 | M00042812D:B04 | MA171:G10 |
| 1034 | 23425 | M00056546B:F12 | MA174:A04 |
| 1035 | 23439 | M00056550A:G09 | MA174:H04 |
| 1036 | 23453 | M00056610C:B08 | MA174:G10 |
| 1037 | 23460 | RG:745556:10011:B04 | MA160:B04 |
| 1038 | 23469 | RG:446537:10009:G04 | MA158:G04 |
| 1039 | 23475 | RG:375937:10009:B10 | MA158:B10 |
| 1040 | 23476 | RG:755120:10011:B10 | MA160:B10 |
| 1041 | 23480 | RG:781108:10011:D10 | MA160:D10 |
| 1042 | 23505 | M00042450C:H10 | MA182:A10 |
| 1043 | 23507 | M00042451B:B05 | MA182:B10 |
| 1044 | 23508 | M00054517D:D12 | MA184:B10 |
| 1045 | 23544 | M00055002B:G06 | MA198:D10 |
| 1046 | 23555 | M00055749A:C09 | MA170:B04 |
| 1047 | 23559 | M00055750A:F10 | MA170:D04 |
| 1048 | 23565 | M00055757A:H06 | MA170:G04 |
| 1049 | 23591 | M00055200B:F03 | MA196:D04 |
| 1050 | 23595 | M00055203B:F05 | MA196:F04 |

Table 2

| SEQ ID NO | Spot ID | Clone ID | MAClone ID |
|-----------|---------|----------------------|------------|
| 1051 | 23657 | M00055980B:F12 | MA179:E04 |
| 1052 | 23667 | M00056066C:H10 | MA179:B10 |
| 1053 | 23669 | M00056067B:F12 | MA179:C10 |
| 1054 | 23671 | M00056075D:H10 | MA179:D10 |
| 1055 | 23672 | M00056962D:A05 | MA177:D10 |
| 1056 | 23673 | M00056081D:B09 | MA179:E10 |
| 1057 | 23674 | M00056963A:E01 | MA177:E10 |
| 1058 | 23675 | M00056081D:C02 | MA179:F10 |
| 1059 | 23678 | M00056964D:C08 | MA177:G10 |
| 1060 | 23679 | M00056084A:B08 | MA179:H10 |
| 1061 | 23683 | M00054750C:G08 | MA188:B04 |
| 1062 | 23685 | M00054750D:F04 | MA188:C04 |
| 1063 | 23693 | M00054757A:F05 | MA188:G04 |
| 1064 | 23695 | M00054760D:B10 | MA188:H04 |
| 1065 | 23746 | M00042847A:A04 | MA172:A04 |
| 1066 | 23748 | M00042847A:D10 | MA172:B04 |
| 1067 | 23755 | M00054917B:G02 | MA168:F04 |
| 1068 | 23765 | M00055468D:D05 | MA168:C10 |
| 1069 | 23767 | M00055469B:E11 | MA168:D10 |
| 1070 | 23773 | M00055492C:C01 | MA168:G10 |
| 1071 | 23775 | M00055496A:E06 | MA168:H10 |
| 1072 | 23787 | M00056742D:D01 | MA175:F04 |
| 1073 | 23805 | M00056814D:C08 | MA175:G10 |
| 1074 | 23827 | RG:1636303:10014:B10 | MA163:B10 |
| 1075 | 23829 | RG:1643142:10014:C10 | MA163:C10 |
| 1076 | 23831 | RG:1650444:10014:D10 | MA163:D10 |
| 1077 | 23840 | RG:1418984:10003:H10 | MA152:H10 |
| 1078 | 23841 | M00043339C:C12 | MA183:A04 |
| 1079 | 23843 | M00043342C:H03 | MA183:B04 |
| 1080 | 23847 | M00043350A:C04 | MA183:D04 |
| 1081 | 23875 | M00056646D:G05 | MA186:B04 |
| 1082 | 23880 | M00055406C:H08 | MA199:D04 |
| 1083 | 23887 | M00056653C:F06 | MA186:H04 |
| 1084 | 23888 | M00055408A:H06 | MA199:H04 |
| 1085 | 23905 | M00055545D:E02 | MA169:A05 |
| 1086 | 23909 | M00055548B:H07 | MA169:C05 |
| 1087 | 23912 | M00056271C:F02 | MA181:D05 |
| 1088 | 23915 | M00055550D:A05 | MA169:F05 |
| 1089 | 23929 | M00055661A:F09 | MA169:E11 |
| 1090 | 24003 | M00056427D:A09 | MA173:B05 |
| 1091 | 24004 | M00056163C:H09 | MA180:B05 |
| 1092 | 24005 | M00056428B:F07 | MA173:C05 |
| 1093 | 24006 | M00056163D:E01 | MA180:C05 |
| 1094 | 24009 | M00056428C:A12 | MA173:E05 |
| 1095 | 24011 | M00056429D:D07 | MA173:F05 |
| 1096 | 24014 | M00056175D:B05 | MA180:G05 |
| 1097 | 24017 | M00056507D:D04 | MA173:A11 |
| 1098 | 24027 | M00056511D:H07 | MA173:F11 |
| 1099 | 24033 | M00054654A:F12 | MA187:A05 |
| 1100 | 24034 | M00054868D:F12 | MA189:A05 |

Table 2

| SEQ ID NO | Spot ID | Clone ID | MAClone ID |
|-----------|---------|---------------------|------------|
| 1101 | 24039 | M00054661B:H10 | MA187:D05 |
| 1102 | 24043 | M00054666B:C07 | MA187:F05 |
| 1103 | 24044 | M00054870B:H05 | MA189:F05 |
| 1104 | 24045 | M00054669B:B03 | MA187:G05 |
| 1105 | 24049 | M00054706B:G04 | MA187:A11 |
| 1106 | 24055 | M00054720C:F01 | MA187:D11 |
| 1107 | 24057 | M00054722B:E08 | MA187:E11 |
| 1108 | 24058 | M00054908A:H08 | MA189:E11 |
| 1109 | 24061 | M00054723B:H12 | MA187:G11 |
| 1110 | 24070 | M00057210B:G10 | MA193:C05 |
| 1111 | 24084 | M00057248D:B05 | MA193:B11 |
| 1112 | 24092 | M00057252A:F06 | MA193:F11 |
| 1113 | 24099 | M00042573B:A02 | MA167:B05 |
| 1114 | 24108 | M00042766A:E10 | MA171:F05 |
| 1115 | 24113 | M00042882D:G08 | MA167:A11 |
| 1116 | 24115 | M00042885C:A12 | MA167:B11 |
| 1117 | 24116 | M00042815A:E07 | MA171:B11 |
| 1118 | 24118 | M00042817B:E11 | MA171:C11 |
| 1119 | 24121 | M00042887C:A07 | MA167:E11 |
| 1120 | 24126 | M00042818D:A08 | MA171:G11 |
| 1121 | 24133 | M00056552A:G08 | MA174:C05 |
| 1122 | 24135 | M00056552C:D08 | MA174:D05 |
| 1123 | 24137 | M00056553C:E10 | MA174:E05 |
| 1124 | 24143 | M00056555B:C11 | MA174:H05 |
| 1125 | 24151 | M00056611C:D03 | MA174:D11 |
| 1126 | 24155 | M00056611D:B03 | MA174:F11 |
| 1127 | 24157 | M00056611D:F08 | MA174:G11 |
| 1128 | 24159 | M00056614C:F06 | MA174:H11 |
| 1129 | 24161 | RG:358387:10009:A05 | MA158:A05 |
| 1130 | 24193 | M00057302A:F08 | MA182:A05 |
| 1131 | 24197 | M00057302C:H09 | MA182:C05 |
| 1132 | 24204 | M00054496A:B09 | MA184:F05 |
| 1133 | 24208 | M00054496A:H05 | MA184:H05 |
| 1134 | 24209 | M00042460B:A08 | MA182:A11 |
| 1135 | 24210 | M00054524B:B09 | MA184:A11 |
| 1136 | 24212 | M00054526C:E05 | MA184:B11 |
| 1137 | 24213 | M00042516B:A08 | MA182:C11 |
| 1138 | 24215 | M00042517D:H10 | MA182:D11 |
| 1139 | 24216 | M00054527B:H11 | MA184:D11 |
| 1140 | 24217 | M00042517D:H11 | MA182:E11 |
| 1141 | 24222 | M00054529C:G04 | MA184:G11 |
| 1142 | 24223 | M00043300D:A06 | MA182:H11 |
| 1143 | 24230 | M00054958A:G10 | MA198:C05 |
| 1144 | 24232 | M00054958B:B07 | MA198:D05 |
| 1145 | 24240 | M00054961D:E08 | MA198:H05 |
| 1146 | 24246 | M00055015C:H02 | MA198:C11 |
| 1147 | 24250 | M00055016B:D03 | MA198:E11 |
| 1148 | 24265 | M00055764D:D05 | MA170:E05 |
| 1149 | 24275 | M00055815C:E08 | MA170:B11 |
| 1150 | 24283 | M00055819B:B12 | MA170:F11 |

Table 2

| SEQ ID NO | Spot ID | Clone ID | MAClone ID |
|-----------|---------|----------------------|------------|
| 1151 | 24287 | M00055820C:H11 | MA170:H11 |
| 1152 | 24289 | M00055204B:C04 | MA196:A05 |
| 1153 | 24295 | M00055209A:C09 | MA196:D05 |
| 1154 | 24311 | M00055252C:G12 | MA196:D11 |
| 1155 | 24354 | M00056934C:D08 | MA177:A05 |
| 1156 | 24355 | M00055989C:D03 | MA179:B05 |
| 1157 | 24360 | M00056937C:G12 | MA177:D05 |
| 1158 | 24367 | M00055997B:A02 | MA179:H05 |
| 1159 | 24373 | M00056087A:G01 | MA179:C11 |
| 1160 | 24375 | M00056091A:H05 | MA179:D11 |
| 1161 | 24378 | M00056966B:A05 | MA177:E11 |
| 1162 | 24379 | M00056093A:F08 | MA179:F11 |
| 1163 | 24383 | M00056096C:H10 | MA179:H11 |
| 1164 | 24399 | M00054766B:E10 | MA188:H05 |
| 1165 | 24403 | M00054817B:H09 | MA188:B11 |
| 1166 | 24407 | M00054818D:G04 | MA188:D11 |
| 1167 | 24450 | M00042851D:H04 | MA172:A05 |
| 1168 | 24452 | M00042853A:F01 | MA172:B05 |
| 1169 | 24457 | M00055426A:G06 | MA168:E05 |
| 1170 | 24467 | M00055496A:G12 | MA168:B11 |
| 1171 | 24475 | M00055509C:C02 | MA168:F11 |
| 1172 | 24477 | M00055510B:F08 | MA168:G11 |
| 1173 | 24479 | M00055510D:A08 | MA168:H11 |
| 1174 | 24483 | M00056748C:B08 | MA175:B05 |
| 1175 | 24485 | M00056749A:F01 | MA175:C05 |
| 1176 | 24493 | M00056754B:A10 | MA175:G05 |
| 1177 | 24495 | M00056754B:H06 | MA175:H05 |
| 1178 | 24521 | RG:1653390:10014:E05 | MA163:E05 |
| 1179 | 24525 | RG:1669553:10014:G05 | MA163:G05 |
| 1180 | 24547 | M00043355A:H12 | MA183:B05 |
| 1181 | 24549 | M00043355B:F10 | MA183:C05 |
| 1182 | 24557 | M00043357B:B10 | MA183:G05 |
| 1183 | 24558 | M00054557C:D09 | MA185:G05 |
| 1184 | 24559 | M00043358B:G11 | MA183:H05 |
| 1185 | 24561 | M00043396D:B04 | MA183:A11 |
| 1186 | 24576 | M00054612D:D11 | MA185:H11 |
| 1187 | 24578 | M00055409B:D08 | MA199:A05 |
| 1188 | 24580 | M00055409D:F06 | MA199:B05 |
| 1189 | 24582 | M00055410A:A06 | MA199:C05 |
| 1190 | 24587 | M00056659A:D08 | MA186:F05 |
| 1191 | 24599 | M00056704C:H08 | MA186:D11 |
| 1192 | 24609 | M00055553C:B06 | MA169:A06 |
| 1193 | 24610 | M00056280B:D10 | MA181:A06 |
| 1194 | 24614 | M00056282D:G10 | MA181:C06 |
| 1195 | 24622 | M00056288B:A12 | MA181:G06 |
| 1196 | 24627 | M00055686D:E11 | MA169:B12 |
| 1197 | 24630 | M00042346B:F09 | MA181:C12 |
| 1198 | 24633 | M00055698C:E05 | MA169:E12 |
| 1199 | 24634 | M00042347C:D07 | MA181:E12 |
| 1200 | 24635 | M00055702C:C04 | MA169:F12 |

Table 2

| SEQ ID NO | Spot ID | Clone ID | MAClone ID |
|-----------|---------|---------------------|------------|
| 1201 | 24638 | M00042348C:F03 | MA181:G12 |
| 1202 | 24648 | M00055335D:E01 | MA197:D06 |
| 1203 | 24708 | M00056180C:E06 | MA180:B06 |
| 1204 | 24712 | M00056184B:G11 | MA180:D06 |
| 1205 | 24721 | M00056514A:F06 | MA173:A12 |
| 1206 | 24727 | M00056514C:H11 | MA173:D12 |
| 1207 | 24741 | M00054674D:C05 | MA187:C06 |
| 1208 | 24743 | M00054675A:H07 | MA187:D06 |
| 1209 | 24744 | M00054878A:G12 | MA189:D06 |
| 1210 | 24751 | M00054676B:D07 | MA187:H06 |
| 1211 | 24755 | M00054725A:E09 | MA187:B12 |
| 1212 | 24758 | M00054924C:B09 | MA189:C12 |
| 1213 | 24759 | M00054726D:B04 | MA187:D12 |
| 1214 | 24762 | M00054927A:H09 | MA189:E12 |
| 1215 | 24763 | M00054727C:F11 | MA187:F12 |
| 1216 | 24767 | M00054728A:H05 | MA187:H12 |
| 1217 | 24768 | M00054930B:G05 | MA189:H12 |
| 1218 | 24772 | M00057214C:G11 | MA193:B06 |
| 1219 | 24776 | M00057216C:G01 | MA193:D06 |
| 1220 | 24780 | M00057217C:B07 | MA193:F06 |
| 1221 | 24803 | M00042695A:H04 | MA167:B06 |
| 1222 | 24805 | M00042695D:D09 | MA167:C06 |
| 1223 | 24808 | M00042771A:D01 | MA171:D06 |
| 1224 | 24810 | M00042772D:F02 | MA171:E06 |
| 1225 | 24812 | M00042773A:A12 | MA171:F06 |
| 1226 | 24813 | M00042699B:B10 | MA167:G06 |
| 1227 | 24817 | M00042889A:H07 | MA167:A12 |
| 1228 | 24818 | M00042819A:C09 | MA171:A12 |
| 1229 | 24820 | M00042819C:B03 | MA171:B12 |
| 1230 | 24821 | M00042895B:C02 | MA167:C12 |
| 1231 | 24822 | M00042823B:A02 | MA171:C12 |
| 1232 | 24825 | M00042895D:B04 | MA167:E12 |
| 1233 | 24843 | M00056564B:F11 | MA174:F06 |
| 1234 | 24845 | M00056564C:E08 | MA174:G06 |
| 1235 | 24849 | M00056615D:A01 | MA174:A12 |
| 1236 | 24861 | M00056620D:F02 | MA174:G12 |
| 1237 | 24865 | RG:359184:10009:A06 | MA158:A06 |
| 1238 | 24887 | RG:428530:10009:D12 | MA158:D12 |
| 1239 | 24897 | M00057310A:A07 | MA182:A06 |
| 1240 | 24908 | M00054503C:H10 | MA184:F06 |
| 1241 | 24917 | M00043302C:D03 | MA182:C12 |
| 1242 | 24924 | M00054535B:F10 | MA184:F12 |
| 1243 | 24926 | M00054535C:D10 | MA184:G12 |
| 1244 | 24928 | M00054535C:H09 | MA184:H12 |
| 1245 | 24934 | M00054964B:A08 | MA198:C06 |
| 1246 | 24936 | M00054966C:H01 | MA198:D06 |
| 1247 | 24952 | M00055022D:F01 | MA198:D12 |
| 1248 | 24958 | M00055026C:C12 | MA198:G12 |
| 1249 | 24960 | M00055027B:C11 | MA198:H12 |
| 1250 | 24985 | M00055826D:C11 | MA170:E12 |

Table 2

| SEQ ID NO | Spot ID | Clone ID | MAClone ID |
|-----------|---------|----------------------|------------|
| 1251 | 24989 | M00055828C:D10 | MA170:G12 |
| 1252 | 24991 | M00055828D:F12 | MA170:H12 |
| 1253 | 24995 | M00055215C:E11 | MA196:B06 |
| 1254 | 24999 | M00055217C:E09 | MA196:D06 |
| 1255 | 25001 | M00055221B:C01 | MA196:E06 |
| 1256 | 25005 | M00055222A:E02 | MA196:G06 |
| 1257 | 25012 | M00056226D:F03 | MA180:B12 |
| 1258 | 25019 | M00055258A:G02 | MA196:F12 |
| 1259 | 25057 | M00055998A:A02 | MA179:A06 |
| 1260 | 25058 | M00056945A:B11 | MA177:A06 |
| 1261 | 25062 | M00056945D:H03 | MA177:C06 |
| 1262 | 25063 | M00056001A:F11 | MA179:D06 |
| 1263 | 25068 | M00056946D:B04 | MA177:F06 |
| 1264 | 25073 | M00056101B:B02 | MA179:A12 |
| 1265 | 25081 | M00056110C:D09 | MA179:E12 |
| 1266 | 25083 | M00056111B:H03 | MA179:F12 |
| 1267 | 25101 | M00054772B:H06 | MA188:G06 |
| 1268 | 25109 | M00054825B:B05 | MA188:C12 |
| 1269 | 25111 | M00054831A:G04 | MA188:D12 |
| 1270 | 25115 | M00054831D:B07 | MA188:F12 |
| 1271 | 25156 | M00042862D:A12 | MA172:B06 |
| 1272 | 25162 | M00042864A:E05 | MA172:E06 |
| 1273 | 25164 | M00042864D:E06 | MA172:F06 |
| 1274 | 25177 | M00055514B:A05 | MA168:E12 |
| 1275 | 25191 | M00056763B:A12 | MA175:D06 |
| 1276 | 25195 | M00056767D:F06 | MA175:F06 |
| 1277 | 25201 | M00056821A:D08 | MA175:A12 |
| 1278 | 25205 | M00056822C:G03 | MA175:C12 |
| 1279 | 25209 | M00056823D:H02 | MA175:E12 |
| 1280 | 25217 | RG:1609994:10014:A06 | MA163:A06 |
| 1281 | 25243 | RG:1667183:10014:F12 | MA163:F12 |
| 1282 | 25249 | M00043358D:C06 | MA183:A06 |
| 1283 | 25250 | M00054558B:E05 | MA185:A06 |
| 1284 | 25257 | M00043361B:G03 | MA183:E06 |
| 1285 | 25277 | M00043408C:D11 | MA183:G12 |
| 1286 | 25280 | M00054632A:E11 | MA185:H12 |
| 1287 | 25281 | M00056661A:G05 | MA186:A06 |
| 1288 | 25283 | M00056661C:C11 | MA186:B06 |
| 1289 | 25284 | M00055412D:E05 | MA199:B06 |
| 1290 | 25286 | M00055413A:G12 | MA199:C06 |
| 1291 | 25288 | M00055414D:A09 | MA199:D06 |
| 1292 | 25301 | M00056707B:C01 | MA186:C12 |
| 1293 | 25317 | M00056237D:C10 | MA181:D01 |
| 1294 | 25319 | M00056238B:D03 | MA181:E01 |
| 1295 | 25323 | M00056239B:D05 | MA181:G01 |
| 1296 | 25325 | M00056241B:H07 | MA181:H01 |
| 1297 | 25380 | I:2921194:04B02:C06 | MA118:C06 |
| 1298 | 25388 | I:1624865:04B02:G06 | MA118:G06 |
| 1299 | 25389 | I:1728607:04A02:H06 | MA116:H06 |
| 1300 | 25390 | I:2827453:04B02:H06 | MA118:H06 |

Table 2

| SEQ ID NO | Spot ID | Clone ID | MAClone ID |
|-----------|---------|---------------------|------------|
| 1301 | 25398 | I:2070593:04B02:D12 | MA118:D12 |
| 1302 | 25405 | I:2683114:04A02:H12 | MA116:H12 |
| 1303 | 25419 | I:1809336:02A02:G06 | MA108:G06 |

Table 3

| SEQ ID NO | Clone ID | MAClone ID | Mask Prent | GBHit | GBDescription | GBScore |
|-----------|----------------|------------|------------|-----------|---|----------|
| 1 | M00026919B:A10 | MA40:F01 | | Z69708 | gi 1204106 emb Z69708.1HSL241B9C Human DNA sequence from cosmid L241B9, Huntington's Disease Region, chromosome 4p16.3 contains pol | 2.2E-208 |
| 2 | M00026919B:E07 | MA40:G01 | | Y16675 | gi 3378616 emb Y16675.1HSCPRM1 Homo sapiens mRNA for aflatoxin B1-aldehyde reductase | 0 |
| 3 | M00026919D:F04 | MA40:H01 | | M62810 | gi 188563 gb M62810.1HUMMITF1 Human mitochondrial transcription factor 1 mRNA, complete cds | 1E-300 |
| 4 | M00026914D:G06 | MA40:A01 | | NM_020990 | gi 11641403 ref NM_020990.2 Homo sapiens creatine kinase, mitochondrial 1 (ubiquitous) (CKMT1), nuclear gene encoding mitochondrial | 2.3E-288 |
| 5 | M00026950A:A09 | MA40:D07 | | BC010020 | gi 14603100 gb BC010020.1BC010020 Homo sapiens, adaptor-related protein complex 3, sigma 2 subunit, clone MGC:19643 IMAGE:2959670, | 9.3E-207 |
| 6 | M00003820C:A09 | MA244:B01 | 0.83544 | AK026527 | gi 10439404 dbj AK026527.1AK026527 Homo sapiens cDNA: FLJ22874 fis, clone KAT02871 | 6.6E-24 |
| 7 | M00001673A:G03 | MA244:E01 | | BC018192 | gi 17390428 gb BC018192.1BC018192 Homo sapiens, inositol 1,3,4-triphosphate 5/6 kinase, clone MGC:21491 IMAGE:3867269, | 4.6E-274 |
| 8 | M00007939A:A12 | MA27:B07 | | | | |
| 9 | M00007939A:B11 | MA27:D07 | | AK055664 | gi 16550447 dbj AK055664.1AK055664 Homo sapiens cDNA FLJ31102 fis, clone IMR322000010 | 6.7E-186 |
| 10 | M00007939B:G03 | MA27:H07 | | BC006230 | gi 13623260 gb BC006230.1BC006230 Homo sapiens, lysophospholipase-like, clone MGC:10338 IMAGE:3945191, | 2.3E-151 |
| 11 | M00007997D:G08 | MA29:C01 | | BC012323 | gi 15147375 gb BC012323.1BC012323 Homo sapiens, Similar to cut (Drosophila)-like 1 (CCAAT displacement protein), clone IMAGE:455060 | 2.1E-198 |
| 12 | M00026894C:E11 | MA39:F07 | | AF052955 | gi 8117711 gb AF052955.1AF052955 Homo sapiens F1-ATPase epsilon-subunit (ATP5E) mRNA, complete cds; nuclear gene for mitochondrial | 9E-204 |
| 13 | M00001391A:C05 | MA15:G01 | | AK000140 | gi 7020034 dbj AK000140.1AK000140 Homo sapiens cDNA FLJ20133 fis, clone COL06539 | 2.2E-107 |

Table 3

| SEQ ID NO | Clone ID | MAClone ID | Mask Prent | GBHit | GBDescription | GBScore |
|-----------|----------------|------------|------------|----------|--|----------|
| 14 | M00006818A:A06 | MA240:C01 | 0.06554 | AL136706 | gi 12052931 cemb AL136706.1HSM801674 Homo sapiens mRNA; cDNA DKFZp566B2024 (from clone DKFZp566B2024); complete cds | 9.2E-248 |
| 15 | M00023278A:F09 | MA36:E01 | | | | |
| 16 | M00023299A:G01 | MA36:C07 | | | | |
| 17 | M00023301A:A11 | MA36:F07 | | BC007270 | gi 13938284 gb BC007270.1BC007270 Homo sapiens, clone MGC:15585 IMAGE:3160319, mRNA, complete cds | 1E-300 |
| 18 | M00008050A:D12 | MA30:C01 | | BC015839 | gi 16198382 gb BC015839.1BC015839 Homo sapiens, clone IMAGE:4296901, mRNA | 1.6E-267 |
| 19 | M00022135A:C04 | MA35:F01 | | BC007925 | gi 14043985 gb BC007925.1BC007925 Homo sapiens, retinoid X receptor, alpha, clone MGC:14451 IMAGE:4304205, mRNA, complete cds | 1.3E-124 |
| 20 | M00022137A:A05 | MA35:G01 | | AK025549 | gi 10438098 dbj AK025549.1AK025549 Homo sapiens cDNA: FLJ21896 fis, clone HEP03441 | 1.6E-267 |
| 21 | M00022176C:A07 | MA35:A07 | | BC000393 | gi 12653248 gb BC000393.1BC000393 Homo sapiens, Similar to CAAX box 1, clone MGC:8471 IMAGE:2821721, mRNA, complete cds | 2.4E-183 |
| 22 | M00008077B:A08 | MA30:D07 | | U09564 | gi 507212 gb U09564.1HSU09564 Human serine kinase mRNA, complete cds | 6.3E-211 |
| 23 | M00008077C:D09 | MA30:G07 | | U50939 | gi 1314559 gb U50939.1HSU50939 Human amyloid precursor protein-binding protein 1 mRNA, complete cds | 1.4E-258 |
| 24 | M00022081C:E09 | MA34:F01 | | AJ271408 | gi 6729589 cemb AJ271408.1HSA271408 Homo sapiens mRNA for Fas-associated factor, FAF1 (Faf1 gene) | 1E-237 |
| 25 | M00001662A:G06 | MA24:H01 | | BC006229 | gi 13623258 gb BC006229.1BC006229 Homo sapiens, cytochrome c oxidase subunit Vb, clone MGC:10622 IMAGE:3952882, mRNA, complete cds | 1.6E-264 |
| 26 | M00022102B:B11 | MA34:D07 | | AJ250229 | gi 8926686 cemb AJ250229.1HSA250229 Homo sapiens mRNA for chromosome 11 hypothetical protein (ORF1) | 0 |
| 27 | M00022102B:E08 | MA34:E07 | | | | |
| 28 | M00022569D:G06 | MA22:F01 | 0.0572 | U08839 | gi 517197 gb U08839.1HSU08839 Human urokinase-type plasminogen activator receptor mRNA, complete cds | 6.7E-233 |

Table 3

| SEQ ID NO | Clone ID | MAClone ID | Mask Prent | GBHit | GBDescription | GBScore |
|-----------|----------------|------------|------------|-----------|--|----------|
| 29 | M00001358B:B11 | MA14:A01 | | AB047848 | gi 11094286 dbj AB047848.1AB047848 Homo sapiens mRNA for zeta1-COP, complete cds | 4.3E-299 |
| 30 | M00001429A:G04 | MA16:A01 | | BC000491 | gi 12653440 gb BC000491.1BC000491 Homo sapiens, proliferating cell nuclear antigen, clone MGC:8367 IMAGE:2820036, mRNA, complete cd | 0 |
| 31 | M00001358B:F05 | MA14:B01 | | BC000706 | gi 12653834 gb BC000706.1BC000706 Homo sapiens, Similar to G8 protein, clone MGC:1225 IMAGE:3349773, mRNA, complete cds | 1.1E-299 |
| 32 | M00001429C:C03 | MA16:C01 | | X16064 | gi 37495 emb X16064.1HSTUMP Human mRNA for translationally controlled tumor protein | 0 |
| 33 | M00001359D:B04 | MA14:E01 | | AK000481 | gi 7020597 dbj AK000481.1AK000481 Homo sapiens cDNA FLJ20474 fis, clone KAT07183 | 1E-300 |
| 34 | M00001360A:E10 | MA14:F01 | | BC002899 | gi 12804092 gb BC002899.1BC002899 Homo sapiens, protein (peptidyl-prolyl cis/trans isomerase) NIMA-interacting 1, clone MGC:107171 | 6.4E-267 |
| 35 | M00001360C:B05 | MA14:G01 | | NM_001014 | gi 13904867 ref NM_001014.2 Homo sapiens ribosomal protein S10 (RPS10), mRNA | 2.1E-282 |
| 36 | M00001430B:F01 | MA16:G01 | | AL050096 | gi 4884121 emb AL050096.1HSM800178 Homo sapiens mRNA; cDNA DKFZp586A0419 (from clone DKFZp586A0419); partial cds | 6.9E-47 |
| 37 | M00001430C:A02 | MA16:H01 | | AF083248 | gi 5106790 gb AF083248.1AF083248 Homo sapiens ribosomal protein L26 homolog mRNA, complete cds | 0 |
| 38 | M00001445C:H05 | MA16:A07 | | X02152 | gi 34312 emb X02152.1HSLDHAR Human mRNA for lactate dehydrogenase-A (LDH-A, EC 1.1.1.27) | 0 |
| 39 | M00001445D:D07 | MA16:B07 | | X73458 | gi 312997 emb X73458.1HSPLK1 H.sapiens plk-1 mRNA | 2.7E-266 |
| 40 | M00001374D:D10 | MA14:G07 | | BC018620 | gi 17391359 gb BC018620.1BC018620 Homo sapiens, Similar to ADP-ribosyltransferase (NAD ⁺ ; poly (ADP-ribose) polymerase), clone IMAGE | 8.3E-254 |
| 41 | M00001375A:A08 | MA14:H07 | | AF231705 | gi 8745393 gb AF231705.1AF231705 Homo sapiens Alu co-repressor 1 (ACR1) mRNA, complete cds | 4.1E-137 |

Table 3

| SEQ ID NO | Clone ID | MAClone ID | Mask Prent | GBHit | GBDescription | GBScore |
|-----------|----------------|------------|------------|-----------|---|----------|
| 42 | M00006600A:E07 | MA241:B01 | | AK001635 | gi 7023008 dbj AK001635.1AK001635 Homo sapiens cDNA FLJ10773 fis, clone NT2RP4000246, moderately similar to NPC DERIVED PROLINE RIC | 3.2E-281 |
| 43 | M00006690A:F06 | MA241:C07 | 0.28152 | | | |
| 44 | M00023325D:A08 | MA37:B02 | | BC001901 | gi 12804898 gb BC001901.1BC001901 Homo sapiens, BCL2-antagonist of cell death, clone MGC:2100 IMAGE:3537914, mRNA, complete cds | 2.7E-294 |
| 45 | M00026921D:F12 | MA40:C02 | | AK054686 | gi 16549280 dbj AK054686.1AK054686 6 Homo sapiens cDNA FLJ30124 fis, clone BRACE1000093, highly similar to TNF RECEPTOR ASSOCIATED FA | 0 |
| 46 | M00023325D:F06 | MA37:D02 | 0.15781 | BC017660 | gi 17389200 gb BC017660.1BC017660 Homo sapiens, clone MGC:14608 IMAGE:4049404, mRNA, complete cds | 1.2E-188 |
| 47 | M00026924A:E09 | MA40:G02 | | AL359938 | gi 8977893 emb AL359938.1HSM8027 19 Homo sapiens mRNA; cDNA DKFZp547H236 (from clone DKFZp547H236) | 0 |
| 48 | M00007940C:A04 | MA27:D08 | | AF381986 | gi 17985445 gb AF381986.1AF381986 Homo sapiens haplotype X mitochondrion, complete genome | 1.6E-264 |
| 49 | M00007941C:H03 | MA27:F08 | | U97519 | gi 2213812 gb U97519.1HSU97519 Homo sapiens podocalyxin-like protein mRNA, complete cds | 4.5E-271 |
| 50 | M00021638B:F03 | MA31:F08 | | NM_004417 | gi 7108342 ref NM_004417.2 Homo sapiens dual specificity phosphatase 1 (DUSP1), mRNA | 3.2E-250 |
| 51 | M00007941D:C04 | MA27:H08 | | AL110202 | gi 5817121 emb AL110202.1HSM8008 54 Homo sapiens mRNA; cDNA DKFZp58612022 (from clone DKFZp58612022) | 2.5E-263 |
| 52 | M00004054D:D02 | | 0.19296 | | | |
| 53 | M00001507A:A10 | MA23:E08 | | AF220656 | gi 7107358 gb AF220656.1AF220656 Homo sapiens apoptosis-associated nuclear protein PHLDA1 (PHLDA1) mRNA, partial cds | 1.4E-255 |
| 54 | M00004198D:A01 | | | AY007138 | gi 9956042 gb AY007138.1 Homo sapiens clone CDABP0061 mRNA sequence | 0 |
| 55 | M00001528C:B08 | MA23:G08 | | AF106066 | gi 5353548 gb AF106066.1AF106066 Homo sapiens RAD17 pseudogene, complete sequence | 4.1E-28 |

Table 3

| SEQ ID NO | Clone ID | MAClone ID | Mask Prent | GBHit | GBDescription | GBScore |
|-----------|----------------|------------|------------|-----------|---|----------|
| 56 | M00008002C:A05 | MA29:B03 | | AB023173 | gi 4589555 dbj AB023173.1AB023173 Homo sapiens mRNA for KIAA0956 protein, partial cds | 1.6E-292 |
| 57 | M00008006C:H05 | MA29:H03 | | AF327923 | gi 13241760 gb AF327923.1AF327923 Homo sapiens transmembrane protein induced by tumor necrosis factor alpha (TMPIT) mRNA, complete | 8.2E-205 |
| 58 | M00026850C:A01 | MA39:A02 | | AK055812 | gi 16550635 dbj AK055812.1AK055812 Homo sapiens cDNA FLJ31250 fis, clone KIDNE2005336, weakly similar to Homo sapiens antigen NY-CO | 8.5E-66 |
| 59 | M00026853D:C07 | MA39:F02 | 0.27143 | AF212248 | gi 13182770 gb AF212248.1AF212248 Homo sapiens CDA09 mRNA, complete cds | 1.9E-153 |
| 60 | M00026896A:C09 | MA39:D08 | | AK018953 | gi 12858931 dbj AK018953.1AK018953 Mus musculus adult male testis cDNA, RIKEN full-length enriched library, clone:1700111D04, full | 3.9E-139 |
| 61 | M00001391B:D02 | MA15:C02 | | D86956 | gi 1503985 dbj D86956.1D86956 Human mRNA for KIAA0201 gene, complete cds | 4.7E-221 |
| 62 | M00001391B:H05 | MA15:E02 | | AL110153 | gi 5817055 emb AL110153.1HSM800798 Homo sapiens mRNA; cDNA DKFZp586E0524 (from clone DKFZp586E0524) | 1E-300 |
| 63 | M00001391D:C07 | MA15:F02 | | AL136593 | gi 7018431 emb AL136593.1HSM801567 Homo sapiens mRNA; cDNA DKFZp761K102 (from clone DKFZp761K102); complete cds | 0 |
| 64 | M00001392B:B01 | MA15:G02 | | M73791 | gi 189265 gb M73791.1HUMNOVGE NE Human novel gene mRNA, complete cds | 3.5E-94 |
| 65 | M00001407B:C03 | MA15:E08 | | BC005116 | gi 13477284 gb BC005116.1BC005116 Homo sapiens, structure specific recognition protein 1, clone MGC:1608 IMAGE:3536048, mRNA, compl | 1E-300 |
| 66 | M00005635B:E02 | MA242:B08 | 0.86798 | | | |
| 67 | M00005636B:B06 | MA242:E08 | | AK008041 | gi 12841981 dbj AK008041.1AK008041 Mus musculus adult male small intestine cDNA, RIKEN full-length enriched library, clone:2010002G | 1.5E-24 |
| 68 | M00006971A:E06 | MA240:E08 | | NM_002403 | gi 9665260 ref NM_002403.2 Homo sapiens microfibrillar-associated protein 2 (MFAP2), transcript variant 2, mRNA | 4.7E-274 |
| 69 | M00005636D:B08 | MA242:F08 | | | | |

Table 3

| SEQ ID NO | Clone ID | MAClone ID | Mask Prent | GBHit | GBDescription | GBScore |
|-----------|----------------|------------|------------|-----------|--|----------|
| 70 | M00023302C:A04 | MA36:B08 | | AF202922 | gi 13540826 gb AF202922.2AF202922 Homo sapiens LRP16 (LRP16) mRNA, complete cds | 4.6E-231 |
| 71 | M00023305A:C02 | MA36:G08 | | | | |
| 72 | M00022180A:E08 | MA35:B08 | | BC018918 | gi 17511926 gb BC018918.1BC018918 Homo sapiens, clone MGC:12603 IMAGE:4130906, mRNA, complete cds | 3.6E-203 |
| 73 | M00022181C:H11 | MA35:E08 | | AK001485 | gi 7022770 dbj AK001485.1AK001485 Homo sapiens cDNA FLJ10623 fis, clone NT2RP2005520, highly similar to Homo sapiens chromosome-ass | 1.6E-161 |
| 74 | M00001673A:C11 | | | U15128 | gi 902744 gb U15128.1HSU15128 Human beta-1,2-N-acetylglucosaminyltransferase II (MGAT2) gene, complete cds | 0 |
| 75 | M00003853B:C07 | | | BC008378 | gi 14249982 gb BC008378.1BC008378 Homo sapiens, programmed cell death 2, clone MGC:12347 IMAGE:4102043, mRNA, complete cds | 2.4E-207 |
| 76 | M00022106B:D04 | MA34:B08 | | AB055387 | gi 12862374 dbj AB055387.1AB055387 Homo sapiens mitochondrial DNA | 1.4E-86 |
| 77 | M00003858B:G01 | MA24:E08 | 0.26044 | | | |
| 78 | M00022109B:A11 | MA34:G08 | | AK023237 | gi 10435081 dbj AK023237.1AK023237 Homo sapiens cDNA FLJ13175 fis, clone NT2RP3003842 | 0 |
| 79 | M00022921A:H05 | MA22:F02 | 0.11424 | BC002976 | gi 12804234 gb BC002976.1BC002976 Homo sapiens, Similar to cytochrome b-561, clone MGC:2190 IMAGE:3535771, mRNA, complete cds | 0 |
| 80 | M00001430D:H07 | MA16:A02 | | X58965 | gi 35069 emb X58965.1HSNM23H2G H.sapiens RNA for nm23-H2 gene | 1.9E-276 |
| 81 | M00001360D:H10 | MA14:B02 | | NM_002415 | gi 4505184 ref NM_002415.1 Homo sapiens macrophage migration inhibitory factor (glycosylation-inhibiting factor) (MIF), mRNA | 6.2E-158 |
| 82 | M00001431A:E01 | MA16:B02 | | AK026534 | gi 10439413 dbj AK026534.1AK026534 Homo sapiens cDNA: FLJ22881 fis, clone KAT03571, highly similar to HUMFERL Human ferritin L chain | 1E-300 |
| 83 | M00001361A:A02 | MA14:C02 | | NM_004053 | gi 15208644 ref NM_004053.2 Homo sapiens bystin-like (BYSL), mRNA | 6.7E-270 |
| 84 | M00001362A:B03 | MA14:H02 | | L47277 | gi 986911 gb L47277.1HUMTOPATR A Homo sapiens (cell line HepG2, HeLa) alpha topoisomerase truncated-form mRNA, 3'UTR | 1E-296 |

Table 3

| SEQ ID NO | Clone ID | MAClone ID | Mask Prent | GBHit | GBDescription | GBScore |
|-----------|----------------|------------|------------|-----------|---|----------|
| 85 | M00001376C:C01 | MA14:A08 | | S73591 | gi 688296 gb S73591.1S73591 Homo sapiens brain-expressed HHCPA78 homolog VDUP1 (Gene) mRNA, complete cds | 5.8E-233 |
| 86 | M00001449A:D02 | MA16:B08 | | BC013954 | gi 5530314 gb BC013954.1BC013954 Homo sapiens, clone IMAGE:3505920, mRNA | 9.6E-291 |
| 87 | M00001378B:A02 | MA14:C08 | | BC002343 | gi 12803082 gb BC002343.1BC002343 Homo sapiens, Similar to nucleolin, clone MGC:8580 IMAGE:2960982, mRNA, complete cds | 5.2E-124 |
| 88 | M00001450A:D12 | MA16:C08 | | AF106622 | gi 4378528 gb AF106622.1AF106622 Homo sapiens mitochondrial inner membrane preprotein translocase Tim17a mRNA, nuclear gene encodin | 5E-280 |
| 89 | M00001378C:D08 | MA14:D08 | 0.06114 | BC002569 | gi 12803486 gb BC002569.1BC002569 Homo sapiens, ribosomal protein S4, X-linked, clone MGC:2328 IMAGE:3139352, mRNA, complete cds | 3E-235 |
| 90 | M00001451D:F01 | MA16:G08 | | BC001432 | gi 12655154 gb BC001432.1BC001432 Homo sapiens, heterogeneous nuclear ribonucleoprotein F, clone MGC:2197 IMAGE:3138435, mRNA, comp | 0 |
| 91 | M00006628B:A02 | MA241:C02 | | NM_005826 | gi 14141188 ref NM_005826.2 Homo sapiens heterogeneous nuclear ribonucleoprotein R (HNRPR), mRNA | 4.9E-80 |
| 92 | M00026926C:F03 | MA40:B03 | | AK027855 | gi 14042836 dbj AK027855.1AK027855 Homo sapiens cDNA FLJ14949 fis, clone PLACE2000341, highly similar to Homo sapiens sodium-depend | 1.1E-215 |
| 93 | M00026963B:H03 | MA40:A09 | | BC014557 | gi 17939595 gb BC014557.1BC014557 Homo sapiens, clone IMAGE:3837222, mRNA | 2.6E-241 |
| 94 | M00026964A:E10 | MA40:D09 | | NM_013375 | gi 17572813 ref NM_013375.2 Homo sapiens TATA-binding protein-binding protein (ABT1), mRNA | 1.5E-171 |
| 95 | M00026965C:A11 | MA40:F09 | 0.07092 | AK054883 | gi 16549505 dbj AK054883.1AK054883 Homo sapiens cDNA FLJ30321 fis, clone BRACE2006281 | 1E-176 |
| 96 | M00001398A:D11 | MA244:C09 | | BC009503 | gi 14550505 gb BC009503.1BC009503 Homo sapiens, G1 to S phase transition 1, clone MGC:1735 IMAGE:2822947, mRNA, complete cds | 1E-300 |

Table 3

| SEQ ID NO | Clone ID | MAClone ID | Mask Prent | GBHit | GBDescription | GBScore |
|-----------|----------------|------------|------------|-----------|---|----------|
| 97 | M00008095C:H08 | MA31:D03 | | BC000820 | gi 12654032 gb BC000820.1BC000820 Homo sapiens, menage a trois 1 (CAK assembly factor), clone MGC:5154 IMAGE:3453943, mRNA, complet | 5.3E-255 |
| 98 | M00007942A:F12 | MA27:B09 | | NM_001102 | gi 12025669 ref NM_001102.2 Homo sapiens actinin, alpha 1 (ACTN1), mRNA | 2.3E-257 |
| 99 | M00004212B:B12 | MA25:A09 | 0.11538 | D38112 | gi 644480 dbj D38112.1HUMMTA Homo sapiens mitochondrial DNA, complete sequence | 2.4E-48 |
| 100 | M00008014C:E11 | MA29:D05 | 0.05435 | AL080111 | gi 5262538 emb AL080111.1HSM8006 19 Homo sapiens mRNA; cDNA DKFZp586G2222 (from clone DKFZp586G2222) | 1.7E-292 |
| 101 | M00008015A:B05 | MA29:E05 | | M23161 | gi 339899 gb M23161.1HUMTRANSC Human transposon-like element mRNA | 1.3E-157 |
| 102 | M00022049A:B08 | MA33:A05 | | AK001731 | gi 7023175 dbj AK001731.1AK001731 Homo sapiens cDNA FLJ10869 fis, clone NT2RP4001677 | 5.8E-286 |
| 103 | M00026856B:F08 | MA39:A03 | | AK023351 | gi 10435249 dbj AK023351.1AK023351 Homo sapiens cDNA FLJ13289 fis, clone OVARC1001170 | 1.7E-298 |
| 104 | M00026856C:H12 | MA39:B03 | 0.55489 | | | |
| 105 | M00026900D:A03 | MA39:F09 | | NM_000995 | gi 16117786 ref NM_000995.2 Homo sapiens ribosomal protein L34 (RPL34), transcript variant 1, mRNA | 3.5E-200 |
| 106 | M00026900D:C12 | MA39:G09 | | BC014377 | gi 15680094 gb BC014377.1BC014377 Homo sapiens, clone IMAGE:4041545, mRNA, partial cds | 1.2E-274 |
| 107 | M00026901D:A03 | MA39:H09 | | AK057845 | gi 16553806 dbj AK057845.1AK057845 Homo sapiens cDNA FLJ25116 fis, clone CBR05731, highly similar to EPHRIN-A1 PRECURSOR | 3.6E-178 |
| 108 | M00001393A:G03 | MA15:E03 | | NM_001015 | gi 14277698 ref NM_001015.2 Homo sapiens ribosomal protein S11 (RPS11), mRNA | 0 |
| 109 | M00001409B:D03 | MA15:D09 | | AF104914 | gi 4206125 gb AF104914.1AF104914 Homo sapiens map 3p22; 9.65 cR from CHLC.GATA87B02 repeat region, complete sequence | 0 |
| 110 | M00001409B:G01 | MA15:E09 | | Z69043 | gi 2398656 emb Z69043.1HSTRAPRN A H.sapiens mRNA translocon-associated protein delta subunit precursor | 3.1E-278 |

Table 3

| SEQ ID NO | Clone ID | MAClone ID | Mask Prent | GBHit | GBDescription | GBScore |
|-----------|----------------|------------|------------|----------|---|----------|
| 111 | M00001410C:C09 | MA15:F09 | | BC007261 | gi 13938270 gb BC007261.1BC007261 Homo sapiens, clone MGC:15545 IMAGE:3050745, mRNA, complete cds | 5.3E-252 |
| 112 | M00001410D:A03 | MA15:G09 | | X52003 | gi 311379 emb X52003.1HSPS2MKN H.sapiens pS2 protein gene | 3.9E-265 |
| 113 | M00005504D:F06 | MA242:A03 | 0.33179 | AK026112 | gi 10438858 dbj AK026112.1AK026112 Homo sapiens cDNA: FLJ22459 fis, clone HRC10045 | 5E-144 |
| 114 | M00005510D:H10 | MA242:G03 | | | | |
| 115 | M00006990D:D06 | MA240:G09 | | M79321 | gi 187270 gb M79321.1HUMLYNTK Human Lyn B protein mRNA, complete cds | 3.8E-290 |
| 116 | SL146 | MA248:A03 | 0.09302 | AF415176 | gi 16589066 gb AF415176.1AF415176 Homo sapiens CSGEF (SGEF) mRNA, complete cds, alternatively spliced | 7.8E-92 |
| 117 | SL153 | MA248:H03 | | | | |
| 118 | SL198 | MA248:E09 | 0.45185 | BC008180 | gi 14198240 gb BC008180.1BC008180 Homo sapiens, DKFZP586A0522 protein, clone MGC:5320 IMAGE:2900478, mRNA, complete cds | 8.2E-115 |
| 119 | SL199 | MA248:F09 | | AF415176 | gi 16589066 gb AF415176.1AF415176 Homo sapiens CSGEF (SGEF) mRNA, complete cds, alternatively spliced | 6.2E-92 |
| 120 | SL200 | MA248:G09 | | BC005307 | gi 13529043 gb BC005307.1BC005307 Homo sapiens, kallikrein 3, (prostate specific antigen), clone MGC:12378 IMAGE:3950475, mRNA, com | 3.1E-191 |
| 121 | M00023283D:C03 | MA36:C03 | | AF070673 | gi 3978241 gb AF070673.1AF070673 Homo sapiens stannin mRNA, complete cds | 3.7E-181 |
| 122 | M00023283D:D03 | MA36:D03 | | Z69881 | gi 1524091 emb Z69881.1HSSERCA3 M H.sapiens mRNA for adenosine triphosphatase, calcium | 1.1E-299 |
| 123 | M00023284A:D09 | MA36:E03 | | AK024338 | gi 10436699 dbj AK024338.1AK024338 Homo sapiens cDNA FLJ14276 fis, clone PLACE1005128 | 1E-300 |
| 124 | M00023285D:C05 | MA36:H03 | | U34877 | gi 1143231 gb U34877.1HSU34877 Homo sapiens biliverdin-IX alpha reductase mRNA, complete cds | 6.5E-295 |
| 125 | M00023306C:H11 | MA36:A09 | | BC003366 | gi 13097197 gb BC003366.1BC003366 Homo sapiens, calcium-regulated heat-stable protein (24kD), clone MGC:5235 IMAGE:2900952, mRNA, c | 0 |

Table 3

| SEQ ID NO | Clone ID | MAClone ID | Mask Prent | GBHit | GBDescription | GBScore |
|-----------|----------------|------------|------------|-----------|---|----------|
| 126 | M00023308D:B06 | MA36:C09 | | M57730 | gi 179320 gb M57730.1HUMB61 Human B61 mRNA, complete cds | 2.1E-176 |
| 127 | M00023309D:H04 | MA36:E09 | | AL136720 | gi 12052958 emb AL136720.1HSM801 688 Homo sapiens mRNA; cDNA DKFZp566J2046 (from clone DKFZp566J2046); complete cds | 0 |
| 128 | M00023310A:D07 | MA36:F09 | | AL359587 | gi 8655647 emb AL359587.1HSM8026 89 Homo sapiens mRNA; cDNA DKFZp762M115 (from clone DKFZp762M115) | 0 |
| 129 | M00008079C:H04 | MA30:B09 | | AF201943 | gi 9295189 gb AF201943.1AF201943 Homo sapiens HAH-P (HAH-P) mRNA, complete cds | 5.6E-258 |
| 130 | M00008080B:B10 | MA30:F09 | | D50683 | gi 1827474 dbj D50683.1D50683 Homo sapiens mRNA for TGF-beta1IR alpha, complete cds | 1.3E-224 |
| 131 | M00022198D:C02 | MA35:F09 | | BC001546 | gi 16306729 gb BC001546.1BC001546 Homo sapiens, Similar to RIKEN cDNA 1110064N10 gene, clone MGC:4924 IMAGE:3462041, mRNA, complete | 1E-300 |
| 132 | M00022198D:G03 | MA35:G09 | | X54199 | gi 31641 emb X54199.1HSGAGMR Human mRNA for GARS-AIRS-GART | 1.1E-231 |
| 133 | M00003768B:B09 | MA24:D03 | | M32308 | gi 202453 gb M32308.1MUSZFXAA Mouse zinc finger protein (Zfx) mRNA, complete cds, clone pDP1115 | 2.4E-103 |
| 134 | M00022110C:A08 | MA34:C09 | | AK026894 | gi 10439861 dbj AK026894.1AK02689 4 Homo sapiens cDNA: FLJ23241 fis, clone COL01375 | 9.2E-288 |
| 135 | M00003886C:H08 | MA24:E09 | 0.36691 | AK056001 | gi 16550873 dbj AK056001.1AK05600 1 Homo sapiens cDNA FLJ31439 fis, clone NT2NE2000707 | 7.9E-146 |
| 136 | M00023297B:A10 | MA22:D03 | | M33376 | gi 187444 gb M33376.1HUMMCDR2 Human pseudo-chlordecone reductase mRNA, complete cds | 0 |
| 137 | M00023314C:G05 | MA22:G03 | | D87071 | gi 1510142 dbj D87071.1D87071 Human mRNA for KIAA0233 gene, complete cds | 1.7E-178 |
| 138 | M00001363B:C04 | MA14:D03 | | AY007220 | gi 9945039 gb AY007220.1 Homo sapiens S100-type calcium binding protein A14 mRNA, complete cds | 1.8E-120 |
| 139 | M00001434D:F08 | MA16:D03 | | NM_000852 | gi 6552334 ref NM_000852.2 Homo sapiens glutathione S-transferase pi (GSTP1), mRNA | 1E-300 |
| 140 | M00001435B:A04 | MA16:E03 | | X99920 | gi 1694827 emb X99920.1HSS100A13 H.sapiens mRNA for S100 calcium-binding protein A13 | 1.1E-265 |

Table 3

| SEQ ID NO | Clone ID | MAClone ID | Mask Prent | GBHit | GBDescription | GBScore |
|-----------|----------------|------------|------------|----------|---|----------|
| 141 | M00001435B:B09 | MA16:F03 | | Y00433 | gi 31917 emb Y00433.1HSGSHPX Human mRNA for glutathione peroxidase (EC 1.11.1.9.) | 8.4E-226 |
| 142 | M00001435C:F08 | MA16:H03 | | BC006498 | gi 13676331 gb BC006498.1BC006498 Homo sapiens, ribonucleotide reductase M1 polypeptide, clone MGC:2326 IMAGE:2989344, mRNA, comple | 1E-300 |
| 143 | M00001381A:F03 | MA14:A09 | | BC007590 | gi 14043203 gb BC007590.1BC007590 Homo sapiens, ribosomal protein, large, P1, clone MGC:15616 IMAGE:3343021, mRNA, complete cds | 4.8E-246 |
| 144 | M00001453B:E11 | MA16:B09 | | BC001182 | gi 12654686 gb BC001182.1BC001182 Homo sapiens, clone MGC:2616 IMAGE:3357266, mRNA, complete cds | 1E-300 |
| 145 | M00001453C:D02 | MA16:D09 | | BC007435 | gi 13938568 gb BC007435.1BC007435 Homo sapiens, RNA binding motif protein, X chromosome, clone MGC:4146 IMAGE:3010123, mRNA, comple | 1E-300 |
| 146 | M00007121D:A05 | MA243:A03 | | BC012816 | gi 15215444 gb BC012816.1BC012816 Homo sapiens, TGF β -induced factor 2 (TALE family homeobox), clone MGC:4139 IMAGE:2964507, mRNA, c | 1E-300 |
| 147 | M00007122C:F03 | MA243:B03 | | BC001866 | gi 12804840 gb BC001866.1BC001866 Homo sapiens, replication factor C (activator 1) 5 (36.5kD), clone MGC:1155 IMAGE:3544137, mRNA, | 6.4E-227 |
| 148 | M00006638A:G02 | MA241:C03 | | J05036 | gi 181193 gb J05036.1HUMCTSE Human cathepsin E mRNA, complete cds | 6.7E-153 |
| 149 | M00006639B:H09 | MA241:F03 | 0.36075 | BC014188 | gi 15559664 gb BC014188.1BC014188 Homo sapiens, Similar to golgi autoantigen, golgin subfamily a, 2, clone MGC:20672 IMAGE:4644480, | 5.6E-135 |
| 150 | M00007127C:C11 | MA243:H03 | | AB020718 | gi 4240310 dbj AB020718.1AB020718 Homo sapiens mRNA for KIAA0911 protein, complete cds | 0 |
| 151 | M00006720D:C11 | MA241:E09 | | AF242773 | gi 7638246 gb AF242773.1AF242773 Homo sapiens mesenchymal stem cell protein DSCD75 mRNA, complete cds | 1.2E-218 |
| 152 | M00006728C:E07 | MA241:F09 | | L05093 | gi 401844 gb L05093.1HUMRIBPROD Homo sapiens ribosomal protein L18a mRNA, complete cds | 0 |

Table 3

| SEQ ID NO | Clone ID | MAClone ID | Mask Prent | GBHit | GBDescription | GBScore |
|-----------|----------------|------------|------------|-----------|---|----------|
| 153 | M00026931D:E08 | MA40:F04 | | AK056187 | gi 16551522 dbj AK056187.1AK056187 Homo sapiens cDNA FLJ31625 fis, clone NT2RI2003304 | 2.9E-275 |
| 154 | M00026932D:B08 | MA40:G04 | | NM_022553 | gi 15022812 ref NM_022553.2 Homo sapiens SAC2 (suppressor of actin mutations 2, yeast, homolog)-like (SACM2L), mRNA | 1E-300 |
| 155 | M00026969D:D02 | MA40:D10 | 0.05447 | AK027681 | gi 14042541 dbj AK027681.1AK027681 Homo sapiens cDNA FLJ14775 fis, clone NT2RP4000185 | 6.5E-159 |
| 156 | M00023393B:E02 | MA37:E10 | | BC001449 | gi 12655184 gb BC001449.1BC001449 Homo sapiens, heterogeneous nuclear ribonucleoprotein R, clone MGC:2039 IMAGE:3139052, mRNA, comp | 9.4E-157 |
| 157 | M00003782D:D06 | MA244:E04 | | BC000705 | gi 12653832 gb BC000705.1BC000705 Homo sapiens, clone MGC:861 IMAGE:3349507, mRNA, complete cds | 1.6E-295 |
| 158 | M00004105D:B04 | MA244:G04 | | AK056461 | gi 16551872 dbj AK056461.1AK056461 Homo sapiens cDNA FLJ31899 fis, clone NT2RP7004173 | 1E-300 |
| 159 | M00001556D:B11 | MA244:D10 | 0.46689 | | | |
| 160 | M00021664B:G03 | MA31:E10 | 0.87158 | | | |
| 161 | M00004078A:A07 | | 0.47872 | | | |
| 162 | M00001561A:B03 | MA23:D10 | | AF090935 | gi 6690235 gb AF090935.1AF090935 Homo sapiens clone HQ0569 | 3.4E-256 |
| 163 | M00008023C:A06 | MA29:F07 | | U79296 | gi 1710278 gb U79296.1HSU79296 Human dihydrolipoamide acetyl transferase mRNA, partial cds | 2.2E-257 |
| 164 | M00008024C:F02 | MA29:G07 | 0.26504 | AF092737 | gi 4741762 gb AF092737.1AF092737 Homo sapiens ubiquitously expressed transcript (UXT) mRNA, complete cds | 3.5E-170 |
| 165 | M00008024C:G06 | MA29:H07 | | BC017335 | gi 16878274 gb BC017335.1BC017335 Homo sapiens, clone MGC:29782 IMAGE:4642600, mRNA, complete cds | 1E-300 |
| 166 | M00022057C:H10 | MA33:B07 | | AK027629 | gi 14042438 dbj AK027629.1AK027629 Homo sapiens cDNA FLJ14723 fis, clone NT2RP3001708, weakly similar to TWISTED GASTRULATION PROTE | 6.8E-79 |
| 167 | M00022059B:B06 | MA33:C07 | | BC005267 | gi 14710008 gb BC005267.1BC005267 Homo sapiens, clone IMAGE:3683864, mRNA | 1E-300 |
| 168 | M00026902B:F10 | MA39:B10 | | L15203 | gi 402482 gb L15203.1HUMPIBX Human secretory protein (P1.B) mRNA, complete cds | 4.8E-249 |

Table 3

| SEQ ID NO | Clone ID | MAClone ID | Mask Prent | GBHit | GBDescription | GBScore |
|-----------|----------------|------------|------------|----------|---|----------|
| 169 | M00001394D:B08 | MA15:C04 | | U58773 | gi 6502504 gb U58773.1HSU58773 Human calcium binding protein mRNA, complete cds | 1E-300 |
| 170 | M00001415A:G05 | MA15:A10 | | BC006337 | gi 13623468 gb BC006337.1BC006337 Homo sapiens, clone MGC:12798 IMAGE:4304127, mRNA, complete cds | 1.5E-205 |
| 171 | M00001416B:E03 | MA15:B10 | | X57198 | gi 37071 emb X57198.1HSTFIIS Human TFIIS mRNA for transcription elongation factor | 0 |
| 172 | M00001421B:B12 | MA15:H10 | | AF083246 | gi 5106786 gb AF083246.1HSPC028 Homo sapiens HSPC028 mRNA, complete cds | 0 |
| 173 | M00005528C:E02 | MA242:G04 | | AK054675 | gi 16549267 dbj AK054675.1AK054675 Homo sapiens cDNA FLJ30113 fis, clone BNGH42000474 | 1.5E-286 |
| 174 | M00023312D:F10 | MA36:A10 | 0.47266 | | | |
| 175 | M00022157A:C06 | MA35:C04 | 0.05831 | | | |
| 176 | M00022165A:A11 | MA35:H04 | | AK000084 | gi 7019941 dbj AK000084.1AK000084 Homo sapiens cDNA FLJ20077 fis, clone COL02904 | 0 |
| 177 | M00022206A:B10 | MA35:D10 | | AL137546 | gi 6808228 emb AL137546.1HSM802283 Homo sapiens mRNA; cDNA DKFZp434A1920 (from clone DKFZp434A1920); partial cds | 1E-293 |
| 178 | M00003811B:F09 | | | BC009470 | gi 14495716 gb BC009470.1BC009470 Homo sapiens, protein kinase, interferon-inducible double stranded RNA dependent activator, clone | 0 |
| 179 | M00003812D:A11 | | | AK026526 | gi 10439403 dbj AK026526.1AK026526 Homo sapiens cDNA: FLJ22873 fis, clone KAT02673, highly similar to HUML12A Human ribosomal prote | 7.6E-137 |
| 180 | M00022088D:C10 | MA34:G04 | | | | |
| 181 | M00003910B:C12 | | | AF132945 | gi 4680660 gb AF132945.1AF132945 Homo sapiens CGI-11 protein mRNA, complete cds | 0 |
| 182 | M00001366A:F06 | MA14:A04 | | U24704 | gi 2078477 gb U24704.1HSU24704 Human antiseecretory factor-1 mRNA, complete cds | 0 |
| 183 | M00001435C:F12 | MA16:B04 | | BC003576 | gi 13097755 gb BC003576.1BC003576 Homo sapiens, actinin, alpha 1, clone MGC:2358 IMAGE:3547017, mRNA, complete cds | 1E-300 |

Table 3

| SEQ ID NO | Clone ID | MAClone ID | Mask Prent | GBHit | GBDescription | GBScore |
|-----------|----------------|------------|------------|-----------|---|----------|
| 184 | M00001436B:E11 | MA16:C04 | | BC003573 | gi 13097746 gb BC003573.1BC003573 Homo sapiens, farnesyl-diphosphate farnesyltransferase 1, clone MGC:2200 IMAGE:3538137, mRNA, com | 0 |
| 185 | M00001366B:E01 | MA14:D04 | | AK000609 | gi 7020817 dbj AK000609.1AK000609 Homo sapiens cDNA FLJ20602 fis, clone KAT07189 | 1E-300 |
| 186 | M00001436C:C03 | MA16:D04 | | Z37986 | gi 780262 emb Z37986.1HSPHBIPRM H.sapiens mRNA for phenylalkylamine binding protein | 1E-300 |
| 187 | M00001437A:B01 | MA16:F04 | | NM_000994 | gi 15812220 ref NM_000994.2 Homo sapiens ribosomal protein L32 (RPL32), mRNA | 4.1E-240 |
| 188 | M00001437B:B08 | MA16:G04 | | AF095287 | gi 3766235 gb AF095287.1AF095287 Homo sapiens pituitary tumor transforming gene protein 1 (PTTG1) mRNA, complete cds | 2.5E-294 |
| 189 | M00001467B:H05 | | | J04456 | gi 187109 gb J04456.1HUMLEC Human 14 kd lectin mRNA, complete cds | 1.9E-273 |
| 190 | M00001468A:D02 | MA16:F10 | | U71213 | gi 1621431 gb U71213.1HSMIGST04 Homo sapiens microsomal glutathione S-transferase gene, exon 4, alternatively spliced transcripts, | 5.7E-127 |
| 191 | M00007131B:B11 | MA243:B04 | | BC017931 | gi 17389843 gb BC017931.1BC017931 Homo sapiens, Similar to RIKEN cDNA 1110055A02 gene, clone MGC:23962 IMAGE:4669658, mRNA, complet | 0 |
| 192 | M00006650A:A10 | MA241:E04 | | | | |
| 193 | M00006653C:B09 | MA241:G04 | 0.0956 | M17885 | gi 190231 gb M17885.1HUMPPARP0 Human acidic ribosomal phosphoprotein P0 mRNA, complete cds | 2.6E-186 |
| 194 | M00007154B:H08 | MA243:G04 | | BC016367 | gi 16741029 gb BC016367.1BC016367 Homo sapiens, retinal short-chain dehydrogenase/reductase retSDR2, clone MGC:24582 IMAGE:4133318, | 1E-300 |
| 195 | M00006740A:E02 | MA241:A10 | | | | |
| 196 | M00021621A:D04 | MA243:A10 | | NM_003137 | gi 15834623 ref NM_003137.2 Homo sapiens SFRS protein kinase 1 (SRPK1), mRNA | 2.3E-285 |
| 197 | M00006740B:F11 | MA241:B10 | | AK022929 | gi 10434601 dbj AK022929.1AK022929 9 Homo sapiens cDNA FLJ12867 fis, clone NT2RP2003702, highly similar to Homo sapiens 17 beta-hydro | 4.9E-277 |

Table 3

| SEQ ID NO | Clone ID | MAClone ID | Mask Prent | GBHit | GBDescription | GBScore |
|-----------|----------------|------------|------------|----------|---|----------|
| 198 | M00006741C:A01 | MA241:C10 | | AF201939 | gi 9295181 gb AF201939.1AF201939 Homo sapiens DC5 (DC5) mRNA, complete cds | 7.6E-183 |
| 199 | M00022171C:A04 | MA243:F10 | | BC000793 | gi 12653990 gb BC000793.1BC000793 Homo sapiens, eukaryotic translation initiation factor 1A, clone MGC:5131 IMAGE:3451631, mRNA, co | 0 |
| 200 | M00026937C:B08 | MA40:E05 | | AF151534 | gi 8099341 gb AF151534.1AF151534 Homo sapiens core histone macroH2A2.2 (MACROH2A2) mRNA, complete cds | 9.5E-177 |
| 201 | M00023367A:H06 | MA37:G05 | 0.04244 | BC015958 | gi 16358989 gb BC015958.1BC015958 Homo sapiens, clone MGC:15290 IMAGE:3940309, mRNA, complete cds | 2.6E-257 |
| 202 | M00026985C:E12 | MA40:F11 | | BC000927 | gi 12654216 gb BC000927.1BC000927 Homo sapiens, Similar to poly (A) polymerase, clone MGC:5378 IMAGE:3445706, mRNA, complete cds | 0 |
| 203 | M00008100A:A07 | MA31:B05 | | AF247820 | gi 13186200 gb AF247820.3AF247820 Homo sapiens NAG22 protein mRNA, complete cds | 4.1E-237 |
| 204 | M00007936B:H07 | MA27:E05 | | BC001929 | gi 12804952 gb BC001929.1BC001929 Homo sapiens, clone MGC:3993 IMAGE:2819500, mRNA, complete cds | 8.4E-145 |
| 205 | M00008100C:E05 | MA31:F05 | 0.05241 | AF395203 | gi 15028449 gb AF395203.1AF395203 Cercopithecus aethiops DnaJ-like protein (dj2) mRNA, complete cds | 6.5E-156 |
| 206 | M00007947B:B02 | MA27:E11 | | | | |
| 207 | M00004105A:C09 | MA25:F05 | | BC010042 | gi 14603152 gb BC010042.1BC010042 Homo sapiens, clone MGC:19606 IMAGE:3629513, mRNA, complete cds | 1.6E-202 |
| 208 | M00001433C:D09 | MA23:G05 | | U23070 | gi 1262172 gb U23070.1HSU23070 Human putative transmembrane protein (nma) mRNA, complete cds | 0 |
| 209 | M00008027B:D09 | MA29:B09 | | M33132 | gi 189423 gb M33132.1HUMP12AA Human proliferating cell nucleolar protein P120 gene, exons 1-15 | 4.8E-165 |
| 210 | M00008028D:B01 | MA29:D09 | | AB014595 | gi 3327203 dbj AB014595.1AB014595 Homo sapiens mRNA for KIAA0695 protein, complete cds | 1E-300 |
| 211 | M00008039A:C09 | MA29:F09 | 0.04 | BC013869 | gi 17105403 gb BC013869.1BC013869 Homo sapiens, clone IMAGE:3831740, mRNA | 2.6E-291 |

Table 3

| SEQ ID NO | Clone ID | MAClone ID | Mask Prent | GBHit | GBDescription | GBScore |
|-----------|----------------|------------|------------|-----------|---|----------|
| 212 | M00026905A:A10 | MA39:A11 | | AF069073 | gi 3202003 gb AF069073.1AF069073 Homo sapiens P8 protein mRNA, complete cds | 0 |
| 213 | M00026905D:C05 | MA39:C11 | | BC010631 | gi 14714946 gb BC010631.1BC010631 Homo sapiens, clone IMAGE:3867552, mRNA | 3.3E-281 |
| 214 | M00001401B:A06 | MA15:G05 | | U90313 | gi 2393721 gb U90313.1HSU90313 Human glutathione-S-transferase homolog mRNA, complete cds | 0 |
| 215 | M00001402A:A08 | MA15:H05 | 0.03584 | X74215 | gi 414045 emb X74215.1HSLON H.sapiens mRNA for Lon protease-like protein | 7E-181 |
| 216 | M00005534C:E12 | MA242:A05 | 0.55385 | | | |
| 217 | M00005542A:D09 | MA242:D05 | | NM_001428 | gi 16507965 ref NM_001428.2 Homo sapiens enolase 1, (alpha) (ENO1), mRNA | 1.1E-218 |
| 218 | M00007031D:E02 | MA240:F11 | | NM_005463 | gi 14110410 ref NM_005463.2 Homo sapiens heterogeneous nuclear ribonucleoprotein D-like (HNRPDL), transcript variant 1, mRNA | 2.8E-186 |
| 219 | M00007032A:D04 | MA240:G11 | | D89678 | gi 3218539 dbj D89678.1D89678 Homo sapiens mRNA for A+U-rich element RNA binding factor, complete cds | 5.2E-225 |
| 220 | M00005813C:F12 | MA242:H11 | | BC000659 | gi 12653746 gb BC000659.1BC000659 Homo sapiens, clone MGC:1004 IMAGE:3347423, mRNA, complete cds | 1.8E-245 |
| 221 | SL163 | MA248:B05 | 0.82548 | | | |
| 222 | SL164 | MA248:C05 | 0.43491 | AF415175 | gi 16589063 gb AF415175.1AF415175 Homo sapiens putative SH3 domain-containing guanine exchange factor SGEF (SGEF) mRNA, complete cd | 4.9E-102 |
| 223 | SL167 | MA248:F05 | 0.13452 | AK025140 | gi 10437598 dbj AK025140.1AK025140 Homo sapiens cDNA: FLJ21487 fis, clone COL05419 | 5.5E-159 |
| 224 | SL168 | MA248:G05 | 0.72115 | | | |
| 225 | SL169 | MA248:H05 | | | | |
| 226 | M00023320B:A03 | MA36:H11 | | BC006428 | gi 13623618 gb BC006428.1BC006428 Homo sapiens, hypothetical protein, clone MGC:12969 IMAGE:3343683, mRNA, complete cds | 6.8E-298 |
| 227 | M00005350B:F10 | MA246:C05 | | BC014191 | gi 15559670 gb BC014191.1BC014191 Homo sapiens, clone MGC:20633 IMAGE:4761663, mRNA, complete cds | 4.7E-218 |
| 228 | M00008069D:F01 | MA30:B05 | 0.09317 | | | |

Table 3

| SEQ ID NO | Clone ID | MAClone ID | Mask Prent | GBHit | GBDescription | GBScore |
|-----------|----------------|------------|------------|-----------|---|----------|
| 229 | M00022165B:C08 | MA35:B05 | | BC012585 | gi 15214891 gb BC012585.1BC012585 Homo sapiens, clone IMAGE:4332982, mRNA | 5.4E-199 |
| 230 | M00022165C:E12 | MA35:D05 | | NM_001024 | gi 14670385 ref NM_001024.2 Homo sapiens ribosomal protein S21 (RPS21), mRNA | 4E-184 |
| 231 | M00022166C:E07 | MA35:E05 | | D87717 | gi 1663709 dbj D87717.1D87717 Human mRNA for KIAA0013 gene, complete cds | 1.8E-139 |
| 232 | M00008072D:E12 | MA30:F05 | | BC007581 | gi 14043186 gb BC007581.1BC007581 Homo sapiens, aldehyde dehydrogenase 4 family, member A1, clone MGC:15564 IMAGE:3139944, mRNA, co | 6.5E-264 |
| 233 | M00022211B:D05 | MA35:A11 | | AK025494 | gi 10438028 dbj AK025494.1AK025494 4 Homo sapiens cDNA: FLJ21841 fis, clone HEP01831 | 2.3E-226 |
| 234 | M00008089A:E09 | MA30:G11 | | AB050577 | gi 14317901 dbj AB050577.1AB050577 7 Homo sapiens NUF2 mRNA for kinetochore protein Nuf2, complete cds | 1.1E-231 |
| 235 | M00003974D:E04 | MA24:C11 | | AF136185 | gi 6625654 gb AF136185.1AF136185 Homo sapiens collagen type XVII (COL17A1) gene, 3' UTR, long form | 3.5E-228 |
| 236 | M00003980D:F10 | MA24:F11 | | AF150100 | gi 5107187 gb AF150100.1AF150100 Homo sapiens small zinc finger-like protein (TIM9a) mRNA, complete cds | 5E-252 |
| 237 | M00003984D:C08 | MA24:H11 | | AL133560 | gi 6599130 emb AL133560.1HSM801406 Homo sapiens mRNA; cDNA DKFZp434M1414 (from clone DKFZp434M1414); partial cds | 0 |
| 238 | M00023373D:A01 | MA22:E05 | | AK023875 | gi 10435944 dbj AK023875.1AK023875 5 Homo sapiens cDNA FLJ13813 fis, clone THYRO1000358, moderately similar to SELENIUM-BINDING LIVER | 2.2E-201 |
| 239 | M00023396D:D01 | MA22:H05 | 0.48026 | | | |
| 240 | M00001437D:E12 | MA16:A05 | | M30684 | gi 177064 gb M30684.1GORMHCBAA Gorilla gorilla beta-2-microglobulin mRNA (GGOGB2M) | 2.3E-260 |
| 241 | M00001438A:B09 | MA16:B05 | | BC005230 | gi 13528857 gb BC005230.1BC005230 Homo sapiens, ubiquinol-cytochrome c reductase binding protein, clone MGC:12253 IMAGE:3961169, mR | 3.6E-259 |

Table 3

| SEQ ID NO | Clone ID | MAClone ID | Mask Prent | GBHit | GBDescription | GBScore |
|-----------|----------------|------------|------------|-----------|---|----------|
| 242 | M00001369A:C07 | MA14:E05 | | AF097514 | gi 4808600 gb AF097514.1AF097514 Homo sapiens stearoyl-CoA desaturase (SCD) mRNA, complete cds | 2.2E-229 |
| 243 | M00001439C:A07 | MA16:F05 | | BC017270 | gi 16878126 gb BC017270.1BC017270 Homo sapiens, homolog of yeast long chain polyunsaturated fatty acid elongation enzyme 2, clone M | 3.7E-106 |
| 244 | M00001369C:A05 | MA14:H05 | | AF190167 | gi 6456117 gb AF190167.1AF190167 Homo sapiens membrane associated protein SLP-2 (HUSLP2) mRNA, complete cds | 1E-300 |
| 245 | M00001468D:B11 | MA16:A11 | | BC008442 | gi 14250074 gb BC008442.1BC008442 Homo sapiens, Similar to transmembrane 4 superfamily member 1, clone MGC:14656 IMAGE:4101110, mRN | 5.3E-149 |
| 246 | M00001386B:F08 | MA14:B11 | | AF132818 | gi 6580834 gb AF132818.1AF132818 Homo sapiens colon Kruppel-like factor (CKLF) mRNA, complete cds | 3E-169 |
| 247 | M00001387A:A08 | MA14:F11 | | NM_022551 | gi 14165467 ref NM_022551.2 Homo sapiens ribosomal protein S18 (RPS18), mRNA | 7E-298 |
| 248 | M00007163A:B10 | MA243:B05 | | D29013 | gi 5171113 dbj D29013.1HUMLNCA Human mRNA for DNA polymerase beta, complete cds | 1.5E-178 |
| 249 | M00006675C:A06 | MA241:E05 | | BC009534 | gi 16306927 gb BC009534.1BC009534 Homo sapiens, clone IMAGE:3891886, mRNA, partial cds | 3.1E-250 |
| 250 | M00007191C:A06 | MA243:G05 | | BC001765 | gi 12804678 gb BC001765.1BC001765 Homo sapiens, Similar to stromal antigen 2, clone MGC:1282 IMAGE:3352347, mRNA, complete cds | 1.7E-295 |
| 251 | M00006678A:D02 | MA241:H05 | | NM_002475 | gi 17986280 ref NM_002475.2 Homo sapiens myosin light chain 1 slow a (MLC1SA), mRNA | 1E-240 |
| 252 | M00026941C:A12 | MA40:E06 | | BC018910 | gi 17511916 gb BC018910.1BC018910 Homo sapiens, clone MGC:10643 IMAGE:3959973, mRNA, complete cds | 2.6E-149 |
| 253 | M00026996A:E01 | MA40:E12 | 0.05985 | AF238079 | gi 7542489 gb AF238079.1AF238079 Homo sapiens FK506 binding protein precursor (FKBP19) mRNA, complete cds | 0 |
| 254 | M00023401B:E06 | MA37:G12 | 0.71373 | | | |

Table 3

| SEQ ID NO | Clone ID | MAClone ID | Mask Prent | GBHit | GBDescription | GBScore |
|-----------|----------------|------------|------------|----------|---|----------|
| 255 | M00027005B:D03 | MA40:H12 | | AL137626 | gi 6808422 emb AL137626.1HSM8023 90 Homo sapiens mRNA; cDNA DKFZp434O0712 (from clone DKFZp434O0712); partial cds | 5.8E-289 |
| 256 | M00007937B:A02 | MA27:C06 | | Z18948 | gi 396712 emb Z18948.1HSS100E H.sapiens mRNA for S100E calcium binding protein | 1.3E-174 |
| 257 | M00021612C:E11 | MA31:C06 | 0.60788 | AB032969 | gi 6329965 dbj AB032969.1AB032969 Homo sapiens mRNA for KIAA1143 protein, partial cds | 1.2E-92 |
| 258 | M00007938C:C12 | MA27:G06 | | BC002360 | gi 12803112 gb BC002360.1BC002360 Homo sapiens, U5 snRNP-specific protein, 116 kD, clone MGC:8581 IMAGE:2960986, mRNA, complete cds | 3.1E-122 |
| 259 | M00001623C:A06 | MA23:F12 | | BC000629 | gi 12653688 gb BC000629.1BC000629 Homo sapiens, Similar to aspartyl- tRNA synthetase, clone MGC:1562 IMAGE:3344322, mRNA, complete c | 9.9E-238 |
| 260 | M00001630D:A11 | MA23:G12 | | AF179626 | gi 6457296 gb AF179626.1AF179626 Expression vector pGP100, complete sequence | 1.7E-298 |
| 261 | M00008044B:E11 | MA29:A11 | | AF083420 | gi 5326765 gb AF083420.1AF083420 Homo sapiens brain-specific STE20- like protein kinase 3 (STK3) mRNA, complete cds | 4.5E-268 |
| 262 | M00008044C:C10 | MA29:B11 | | AF224759 | gi 12043739 gb AF224759.1AF224759 Homo sapiens adenocarcinoma antigen ART1/P17 mRNA, complete cds | 1.3E-277 |
| 263 | M00008044D:B08 | MA29:C11 | 0.82704 | BC019356 | gi 17939588 gb BC019356.1BC019356 Homo sapiens, clone IMAGE:3503646, mRNA | 5.4E-27 |
| 264 | M00008044D:C05 | MA29:D11 | | M23161 | gi 339899 gb M23161.1HUMTRANSC Human transposon-like element mRNA | 5.4E-160 |
| 265 | M00022074C:A04 | MA33:E11 | | | gi 179771 gb J03037.1HUMCAIIA Human carbonic anhydrase II mRNA, complete cds | 2.4E-263 |
| 266 | M00026910C:D12 | MA39:E12 | | J03037 | | |
| 267 | M00026913A:D06 | MA39:G12 | | AK058163 | gi 16554226 dbj AK058163.1AK05816 3 Homo sapiens cDNA FLJ25434 fis, clone TST06728, highly similar to ELONGATION FACTOR 1-ALPHA 1 | 2.9E-275 |

Table 3

| SEQ ID NO | Clone ID | MAClone ID | Mask Prent | GBHit | GBDescription | GBScore |
|-----------|----------------|------------|------------|----------|---|----------|
| 268 | M00001402C:H08 | MA15:D06 | | BC000461 | gi 12653382 gb BC000461.1BC000461 Homo sapiens, eukaryotic translation initiation factor 2, subunit 2 (beta, 38kD), clone MGC:8508 | 0 |
| 269 | M00001404C:C11 | MA15:F06 | | BC001497 | gi 16306642 gb BC001497.1BC001497 Homo sapiens, clone MGC:2068 IMAGE:2823581, mRNA, complete cds | 1.4E-286 |
| 270 | M00005587B:G05 | MA242:C06 | | BC001566 | gi 16306756 gb BC001566.1BC001566 Homo sapiens, clone IMAGE:3451980, mRNA, partial cds | 8.5E-282 |
| 271 | M00006934D:D10 | MA240:C06 | | D63861 | gi 1769811 dbj D63861.1D63861 Homo sapiens DNA for cyclophilin 40, complete cds | 7.5E-142 |
| 272 | SL176 | MA248:G06 | | | | |
| 273 | M00023295D:E05 | MA36:A06 | | M16957 | gi 188249 gb M16957.1HUMMHDR2 2D Human MHC class II HLA-DR2 (Dw2) b-associated glycoprotein beta-chain mRNA, 3' end | 5.2E-227 |
| 274 | M00023320B:C02 | MA36:A12 | | | | |
| 275 | M00005401B:F12 | MA246:B12 | | U47742 | gi 1517913 gb U47742.1HSU47742 Human monocytic leukaemia zinc finger protein (MOZ) mRNA, complete cds | 4.4E-54 |
| 276 | M00008074D:C05 | MA30:F06 | | AF035289 | gi 2661043 gb AF035289.1AF035289 Homo sapiens clone 23969 mRNA sequence | 3.3E-197 |
| 277 | M00022175B:F06 | MA35:G06 | | U81002 | gi 4580010 gb U81002.1HSU81002 Homo sapiens TRAF4 associated factor 1 mRNA, partial cds | 1.1E-212 |
| 278 | M00022230B:C10 | MA35:G12 | | BC019061 | gi 17512149 gb BC019061.1BC019061 Homo sapiens, Similar to RIKEN cDNA 1500019E20 gene, clone IMAGE:5089739, mRNA | 7.5E-149 |
| 279 | M00022093C:C08 | MA34:C06 | | AB061831 | gi 17932955 dbj AB061831.1AB061831 Homo sapiens RPL32 gene for ribosomal protein L32, complete cds and sequence | 1.1E-184 |
| 280 | M00022093C:C12 | MA34:D06 | | BC009401 | gi 14424786 gb BC009401.1BC009401 Homo sapiens, natural killer cell transcript 4, clone MGC:15353 IMAGE:4300407, mRNA, complete cds | 9.9E-294 |
| 281 | M00022132A:H07 | MA34:F12 | | BC015557 | gi 15990394 gb BC015557.1BC015557 Homo sapiens, clone MGC:1567 IMAGE:3050731, mRNA, complete cds | 1E-300 |

Table 3

| SEQ ID NO | Clone ID | MA Clone ID | Mask Prent | GBHit | GBDescription | GBScore |
|-----------|----------------|-------------|------------|----------|--|----------|
| 282 | M00023397B:D04 | MA22:A06 | | AF083441 | gi 5813822 gb AF083441.1AF083441 Homo sapiens SUI1 isolog mRNA, complete cds | 1E-300 |
| 283 | M00023399D:G04 | MA22:E06 | | BC004450 | gi 13325265 gb BC004450.1BC004450 Homo sapiens, hypothetical protein MGC2650, clone MGC:4188 IMAGE:2820830, mRNA, complete cds | 1E-300 |
| 284 | M00001439D:C09 | MA16:A06 | | BC002446 | gi 12803262 gb BC002446.1BC002446 Homo sapiens, MRJ gene for a member of the DNAJ protein family, clone MGC:1152 IMAGE:3346070, mRNA | 0 |
| 285 | M00001441A:A09 | MA16:B06 | | M57710 | gi 179530 gb M57710.1HUMBPIGE Human IgE-binding protein (epsilon-BP) mRNA, complete cds | 1.7E-295 |
| 286 | M00001369D:E02 | MA14:C06 | | AF034546 | gi 3127052 gb AF034546.1AF034546 Homo sapiens sorting nexin 3 (SNX3) mRNA, complete cds | 1.9E-195 |
| 287 | M00001371D:H10 | MA14:E06 | | | | |
| 288 | M00001372A:D01 | MA14:F06 | | AF151872 | gi 4929696 gb AF151872.1AF151872 Homo sapiens CGI-114 protein mRNA, complete cds | 0 |
| 289 | M00001444C:F03 | MA16:G06 | | AL359678 | gi 15215911 emb AL359678.15AL359678 Human DNA sequence from clone RP11-550J21 on chromosome 9, complete sequence [Homo sapiens] | 0 |
| 290 | M00001445A:B02 | | | BC003401 | gi 13097293 gb BC003401.1BC003401 Homo sapiens, ribosomal protein S14, clone MGC:5429 IMAGE:3448752, mRNA, complete cds | 9.7E-291 |
| 291 | M00001388D:F11 | MA14:D12 | | BC002609 | gi 12803554 gb BC002609.1BC002609 Homo sapiens, chromobox homolog 1 (Drosophila HP1 beta), clone MGC:1267 IMAGE:3140815, mRNA, comp | 0 |
| 292 | M00001481C:A12 | MA16:F12 | | AB033007 | gi 6330242 dbj AB033007.1AB033007 Homo sapiens mRNA for KIAA1181 protein, partial cds | 2.9E-88 |
| 293 | M00001389B:B05 | MA14:G12 | | BC013858 | gi 15426627 gb BC013858.1BC013858 Homo sapiens, clone IMAGE:3869909, mRNA | 2E-239 |
| 294 | M00001389C:G01 | MA14:H12 | 0.07529 | AY004872 | gi 9508996 gb AY004872.1 Homo sapiens thioredoxin (TXN) mRNA, complete cds | 4.6E-175 |

Table 3

| SEQ ID NO | Clone ID | MAClone ID | Mask Prent | GBHit | GBDescription | GBScore |
|-----------|---------------------|------------|------------|-----------|---|----------|
| 295 | M00001482D:D11 | MA16:H12 | 0.07738 | BC009982 | gi 14602997 gb BC009982.1BC009982 Homo sapiens, clone IMAGE:4121355, mRNA, partial cds | 5.1E-169 |
| 296 | M00006809B:F04 | MA241:D12 | 0.62333 | | | |
| 297 | I:3325119:07A01:A01 | MA127:A01 | | U21936 | gi 717118 gb U21936.1HSU21936 Human peptide transporter (HPEPT1) mRNA, complete cds | 1.4E-149 |
| 298 | I:3033345:07A01:C01 | MA127:C01 | | BC004982 | gi 13436412 gb BC004982.1BC004982 Homo sapiens, glucose phosphate isomerase, clone MGC:3935 IMAGE:2906270, mRNA, complete cds | 9E-229 |
| 299 | I:3176222:07A01:E07 | MA127:E07 | | U09413 | gi 488554 gb U09413.1HSU09413 Human zinc finger protein ZNF135 mRNA, complete cds | 1.9E-264 |
| 300 | I:2510627:07B01:G07 | MA129:G07 | | BC002803 | gi 12803912 gb BC002803.1BC002803 Homo sapiens, hypothetical protein, clone MGC:3402 IMAGE:3636703, mRNA, complete cds | 1E-300 |
| 301 | I:1705208:06B01:A01 | MA125:A01 | | X52541 | gi 31129 cemb X52541.1HSEGR1 Human mRNA for early growth response protein 1 (hEGR1) | 0 |
| 302 | I:1672781:06B01:C07 | MA125:C07 | | BC010042 | gi 14603152 gb BC010042.1BC010042 Homo sapiens, clone MGC:19606 IMAGE:3629513, mRNA, complete cds | 1E-300 |
| 303 | I:1712888:06B01:D07 | MA125:D07 | | AL137469 | gi 6808076 cemb AL137469.1HSM8021 87 Homo sapiens mRNA; cDNA DKFZp434P2422 (from clone DKFZp434P2422); partial cds | 1E-300 |
| 304 | I:1696224:06B01:E07 | MA125:E07 | | NM_005346 | gi 5579470 ref NM_005346.2 Homo sapiens heat shock 70kD protein 1B (HSPA1B), mRNA | 1E-300 |
| 305 | I:3935034:06B01:H07 | MA125:H07 | | BC007616 | gi 14043251 gb BC007616.1BC007616 Homo sapiens, clone MGC:15728 IMAGE:3354330, mRNA, complete cds | 1.2E-249 |
| 306 | I:1800114:03A01:E01 | MA111:E01 | | M24559 | gi 514365 gb M24559.1HUMIGRPOL Y Human poly-Ig receptor transmembrane secretory component mRNA, 3' end | 1.5E-205 |
| 307 | I:1976029:03A01:D07 | MA111:D07 | | BC000629 | gi 12653688 gb BC000629.1BC000629 Homo sapiens, Similar to aspartyl-tRNA synthetase, clone MGC:1562 IMAGE:3344322, mRNA, complete c | 1.1E-299 |
| 308 | I:1439934:03B01:E07 | MA113:E07 | 0.17464 | M64788 | gi 190855 gb M64788.1HUMRAP1GA P Human GTPase activating protein (rap1GAP) mRNA, complete cds | 5.9E-184 |

Table 3

| SEQ ID NO | Clone ID | MAClone ID | Mask Prent | GBHit | GBDescription | GBScore |
|-----------|---------------------|------------|------------|-----------|---|----------|
| 309 | I:2512879:01A01:C01 | MA103:C01 | | M12271 | gi 178091 gb M12271.1HUMADH1CB Homo sapiens class I alcohol dehydrogenase (ADH1) alpha subunit mRNA, complete cds | 3.7E-290 |
| 310 | I:2900277:01B01:B07 | MA105:B07 | | BC015492 | gi 15930098 gb BC015492.1BC015492 Homo sapiens, clone MGC:8967 IMAGE:3915505, mRNA, complete cds | 1E-300 |
| 311 | I:1479255:01A01:C07 | MA103:C07 | | NM_002245 | gi 15451900 ref NM_002245.2 Homo sapiens potassium channel, subfamily K, member 1 (TWIK-1) (KCNK1), mRNA | 1E-300 |
| 312 | I:2648612:04B01:A01 | MA117:A01 | | NM_006013 | gi 15718685 ref NM_006013.2 Homo sapiens ribosomal protein L10 (RPL10), mRNA | 1E-300 |
| 313 | I:1889867:04A01:C01 | MA115:C01 | | AF004563 | gi 3041874 gb AF004563.1AF004563 Homo sapiens hUNC18b alternatively-spliced mRNA, complete cds | 8.2E-148 |
| 314 | I:1858905:04A01:D01 | MA115:D01 | | BC015520 | gi 15930171 gb BC015520.1BC015520 Homo sapiens, ribonuclease, RNase A family, 4, clone MGC:9306 IMAGE:3905439, mRNA, complete cds | 1.8E-211 |
| 315 | I:2591494:04B01:H01 | MA117:H01 | | BC009084 | gi 14290606 gb BC009084.1BC009084 Homo sapiens, Similar to selenium binding protein 1, clone MGC:9270 IMAGE:3853674, mRNA, complete cds | 0 |
| 316 | I:2916261:04B01:A07 | MA117:A07 | | BC016855 | gi 16877177 gb BC016855.1BC016855 Homo sapiens, clone MGC:17066 IMAGE:3850361, mRNA, complete cds | 5.9E-289 |
| 317 | I:2397815:04B01:B07 | MA117:B07 | | BC007888 | gi 14043894 gb BC007888.1BC007888 Homo sapiens, eukaryotic translation initiation factor 2, subunit 2 (beta, 38kD), clone MGC:1417 | 3.3E-253 |
| 318 | I:2182095:04B01:D07 | MA117:D07 | | NM_002580 | gi 4505604 ref NM_002580.1 Homo sapiens pancreatitis-associated protein (PAP), mRNA | 5.8E-289 |
| 319 | I:2506194:02A01:A01 | MA107:A01 | | U36601 | gi 1036798 gb U36601.1HSU36601 Homo sapiens heparan N-deacetylase/N-sulfotransferase-2 mRNA, complete cds | 1.3E-240 |
| 320 | I:1806219:02A01:C01 | MA107:C01 | | U34279 | gi 1236798 gb U34279.1HSU34279 Human uroguanylin mRNA, complete cds | 5.4E-202 |

Table 3

| SEQ ID NO | Clone ID | MAClone ID | Mask Prent | GBHit | GBDescription | GBScore |
|-----------|---------------------|------------|------------|-----------|--|----------|
| 321 | I:1729724:02A01:G07 | MA107:G07 | | NM_002487 | gi 10800414 ref NM_002487.2 Homo sapiens ncedin homolog (mouse) (NDN), mRNA | 3.1E-169 |
| 322 | I:1886842:05A02:G01 | MA120:G01 | | BC010578 | gi 14714852 gb BC010578.1BC010578 Homo sapiens, clone MGC:9344 IMAGE:3458845, mRNA, complete cds | 1.5E-292 |
| 323 | I:1352669:05A02:B07 | MA120:B07 | 0.10093 | BC016752 | gi 16876952 gb BC016752.1BC016752 Homo sapiens, clone IMAGE:2959721, mRNA | 1.4E-169 |
| 324 | I:1755847:05B02:C07 | MA122:C07 | | U51095 | gi 1777771 gb U51095.1HSU51095 Human homeobox protein Cdx1 mRNA, complete cds | 5.9E-230 |
| 325 | I:1803418:05B02:D07 | MA122:D07 | | BC006168 | gi 13544071 gb BC006168.1BC006168 Homo sapiens, clone IMAGE:3960207, mRNA, partial cds | 0 |
| 326 | I:1568725:05B02:F07 | MA122:F07 | 0.36394 | D49410 | gi 684968 dbj D49410.1HUMIL3RA12 Homo sapiens gene for interleukin 3 receptor alpha subunit, exon 12 and partial cds | 7.7E-187 |
| 327 | I:1857708:05A02:G07 | MA120:G07 | | U43381 | gi 1155348 gb U43381.1HSU43381 Human Down Syndrome region of chromosome 21 DNA | 1.3E-283 |
| 328 | I:1687060:05B02:G07 | MA122:G07 | | U57645 | gi 1816511 gb U57645.1HSU57645 Human helix-loop-helix proteins Id-1 (ID-1) and Id-1' (ID-1) genes, complete cds | 3.3E-281 |
| 329 | I:3407289:07A02:A07 | MA128:A07 | 0.21116 | AB011135 | gi 3043649 dbj AB011135.1AB011135 Homo sapiens mRNA for KIAA0563 protein, complete cds | 1.7E-68 |
| 330 | I:1235535:07A02:B07 | MA128:B07 | | NM_001012 | gi 4506742 ref NM_001012.1 Homo sapiens ribosomal protein S8 (RPS8), mRNA | 3.8E-156 |
| 331 | I:1525795:03B02:D07 | MA114:D07 | | X05360 | gi 29838 emb X05360.1HSCDC2 Human CDC2 gene involved in cell cycle control | 1.5E-289 |
| 332 | I:3744592:03A02:H07 | MA112:H07 | | S76992 | gi 913345 gb S76992.1S76992 VAV2=VAV oncogene homolog [human, fetal brain, mRNA Partial, 2753 nt] | 1E-194 |
| 333 | I:1485817:01A02:B01 | MA104:B01 | | L14787 | gi 292930 gb L14787.1HUMZFPA Human DNA-binding protein mRNA, 3'end | 3.4E-247 |
| 334 | I:2365149:01B02:B01 | MA106:B01 | | U58917 | gi 2826475 gb U58917.1HSU58917 Homo sapiens IL-17 receptor mRNA, complete cds | 9E-208 |

Table 3

| SEQ ID NO | Clone ID | MAClone ID | Mask Prent | GBHit | GBDescription | GBScore |
|-----------|---------------------|------------|------------|----------|--|----------|
| 335 | I:1439677:01A02:D01 | MA104:D01 | | AL096780 | gi 5420184 emb AL096780.1HS384D86A Novel human gene mapping to chromosome 22p13.33 similar to mouse Choline/Ethanolamine Kinase (O55 | 1.8E-146 |
| 336 | I:2372275:01B02:G01 | MA106:G01 | | BC019252 | gi 17939418 gb BC019252.1BC019252 Homo sapiens, clone MGC:1111 IMAGE:3503549, mRNA, complete cds | 1E-300 |
| 337 | I:3211615:01B02:H01 | MA106:H01 | | BC013808 | gi 15489437 gb BC013808.1BC013808 Homo sapiens, TATA box binding protein (TBP)-associated factor, RNA polymerase I, A, 48kD, clone | 2E-230 |
| 338 | I:2368282:01B02:B07 | MA106:B07 | | AK056794 | gi 16552300 dbj AK056794.1AK056794 Homo sapiens cDNA FLJ32232 fis, clone PLACE6004578, highly similar to CYTOCHROME P450 11A1, MITO | 5.8E-209 |
| 339 | I:1737833:04A02:D01 | MA116:D01 | | D26598 | gi 565646 dbj D26598.1HUMPSH1 Human mRNA for proteasome subunit HsC10-II, complete cds | 1E-300 |
| 340 | I:2382192:04B02:F01 | MA118:F01 | | Y12653 | gi 2546963 emb Y12653.1HSDIUBIQ U H.sapiens mRNA for diubiquitin | 1.6E-264 |
| 341 | I:1958902:04A02:D07 | MA116:D07 | | D87258 | gi 1513058 dbj D87258.1D87258 Homo sapiens mRNA for serin protease with IGF-binding motif, complete cds | 0 |
| 342 | I:1704472:04B02:G07 | MA118:G07 | | U66871 | gi 1519518 gb U66871.1HSU66871 Human enhancer of rudimentary homolog mRNA, complete cds | 7E-161 |
| 343 | I:1903767:04A02:H07 | MA116:H07 | | AF025304 | gi 2739055 gb AF025304.1AF025304 Homo sapiens protein-tyrosine kinase EPHB2v (EPHB2) mRNA, complete cds | 1E-300 |
| 344 | I:1268080:02A02:C01 | MA108:C01 | | AB006631 | gi 14133200 dbj AB006631.2AB006631 Homo sapiens mRNA for KIAA0293 gene, partial cds | 0 |
| 345 | I:1347384:02A02:C07 | MA108:C07 | | U78579 | gi 1743878 gb U78579.1HSU78579 Human type I phosphatidylinositol-4-phosphate 5-kinase beta (STM7) mRNA, partial cds | 0 |
| 346 | I:2344817:08B01:H02 | MA133:H02 | | | | |
| 347 | I:3236109:08A01:B08 | MA131:B08 | 0.46441 | | | |
| 348 | I:2832506:07A01:H08 | MA127:H08 | | BC000851 | gi 12654082 gb BC000851.1BC000851 Homo sapiens, ribosomal protein L13, clone IMAGE:3458439, mRNA | 8.5E-282 |
| 349 | I:1673876:06B01:B02 | MA125:B02 | | V00568 | gi 34815 emb V00568.1HSMYC1 Human mRNA encoding the c-myc oncogene | 1E-300 |

Table 3

| SEQ ID NO | Clone ID | MAClone ID | Mask Prent | GBHit | GBDescription | GBScore |
|-----------|---------------------|------------|------------|----------|---|----------|
| 350 | I:3686211:06B01:E02 | MA125:E02 | | X59960 | gi 402620 emb X59960.1HSSPMYEL H.sapiens mRNA for sphingomyelinase | 1E-300 |
| 351 | I:2449837:06B01:H02 | MA125:H02 | | BC000070 | gi 12652644 gb BC000070.1BC000070 Homo sapiens, small nuclear ribonucleoprotein polypeptide G, clone MGC:1614 IMAGE:3503973, mRNA, | 3E-219 |
| 352 | I:1613874:06B01:C08 | MA125:C08 | | AF019952 | gi 2655036 gb AF019952.1AF019952 Homo sapiens tumor suppressing STF cDNA 1 (TSSC1) mRNA, complete cds | 0 |
| 353 | I:1813409:03A01:C02 | MA111:C02 | | BC009244 | gi 14328061 gb BC009244.1BC009244 Homo sapiens, isocitrate dehydrogenase 2 (NADP+), mitochondrial, clone MGC:3700 IMAGE:2959540, mR | 1E-300 |
| 354 | I:1975514:03A01:A08 | MA111:A08 | | S52873 | gi 263656 gb S52873.1S52873 cytidine deaminase [human, monocytoid cell line U937, mRNA Partial, 736 nt] | 5.7E-286 |
| 355 | I:1403294:01A01:B02 | MA103:B02 | 0.13199 | | gi 950198 gb U31278.1HSHU31278 Homo sapiens mitotic feedback control protein Madp2 homolog mRNA, complete cds | 0 |
| 356 | I:2414624:01B01:D02 | MA105:D02 | | U31278 | gi 15341817 gb BC013081.1BC013081 Homo sapiens, Similar to metallothionein 3 (growth inhibitory factor (neurotrophic)), clone MGC:1 | 2.6E-213 |
| 357 | I:2901811:01B01:H02 | MA105:H02 | | BC013081 | gi 32122 emb V00522.1HSHL01 Human mRNA encoding major histocompatibility complex gene HLA- DR beta-1 | 2.5E-294 |
| 358 | I:2683564:01B01:B08 | MA105:B08 | | V00522 | gi 2627330 gb AF004849.1AF004849 Homo sapiens PKY protein kinase mRNA, complete cds | 1.4E-177 |
| 359 | I:2725511:01B01:C08 | MA105:C08 | | AF004849 | gi 535474 gb M82962.1HUMPPH Human N-benzoyl-L-tyrosyl-p-amino- benzoic acid hydrolase alpha subunit (PPH alpha) mRNA, complete cds | 1E-268 |
| 360 | I:1431273:04A01:A02 | MA115:A02 | | M82962 | gi 3005731 gb AF055009.1AF055009 Homo sapiens clone 24747 mRNA sequence | 0 |
| 361 | I:1636639:04B01:A02 | MA117:A02 | | AF055009 | gi 14249818 gb BC008281.1BC008281 Homo sapiens, guanosine monophosphate reductase, clone MGC:10464 IMAGE:3635871, mRNA, complete cd | 3.2E-281 |
| 362 | I:2455617:04B01:D02 | MA117:D02 | | BC008281 | | |

Table 3

| SEQ ID NO | Clone ID | MAClone ID | Mask Prent | GBHit | GBDescription | GBScore |
|-----------|---------------------|------------|------------|----------|---|----------|
| 363 | I:2952504:04B01:F02 | MA117:F02 | | U72849 | gi 4097996 gb U72849.1HSAPEVPL7 Homo sapiens envoplakin (EVPL) gene, exon 22 and complete cds | 1E-300 |
| 364 | I:1483847:04A01:A08 | MA115:A08 | | AF026293 | gi 2559011 gb AF026293.1AF026293 Homo sapiens chaperonin containing t-complex polypeptide 1, beta subunit (Cctb) mRNA, complete cds | 4E-93 |
| 365 | I:2923150:04B01:B08 | MA117:B08 | | M18963 | gi 190978 gb M18963.1HUMREGA Human islet of Langerhans regenerating protein (reg) mRNA, complete cds | 1.2E-237 |
| 366 | I:1813133:04A01:F08 | MA115:F08 | | X12597 | gi 32326 emb X12597.1HSHMG1 Human mRNA for high mobility group-1 protein (HMG-1) | 1.3E-255 |
| 367 | I:2510171:04B01:H08 | MA117:H08 | 0.15344 | X04503 | gi 36490 emb X04503.1HSSLIPR Human SLPI mRNA fragment for secretory leucocyte protease inhibitor | 1.1E-259 |
| 368 | I:2190284:02A01:H02 | MA107:H02 | | D84107 | gi 1669546 dbj D84107.1D84107 Homo sapiens mRNA for RBP-MS/type 1, complete cds | 0 |
| 369 | I:1522716:05B02:B02 | MA122:B02 | | X56134 | gi 37849 emb X56134.1HSVIMENT Human mRNA for vimentin | 0 |
| 370 | I:1901271:05A02:G02 | MA120:G02 | | U90916 | gi 1913897 gb U90916.1HSU90916 Human clone 23815 mRNA sequence | 9E-288 |
| 371 | I:1820522:05B02:H02 | MA122:H02 | | BC002806 | gi 12803918 gb BC002806.1BC002806 Homo sapiens, phosphatidic acid phosphatase type 2C, clone MGC:3813 IMAGE:3659728, mRNA, complete | 1.1E-299 |
| 372 | I:2365295:05A02:A08 | MA120:A08 | | BC015460 | gi 15930032 gb BC015460.1BC015460 Homo sapiens, Similar to glutaminyl-peptide cyclotransferase (glutaminyl cyclase), clone IMAGE:39 | 3.8E-26 |
| 373 | I:1335140:05A02:C08 | MA120:C08 | | X02152 | gi 34312 emb X02152.1HSLDHAR Human mRNA for lactate dehydrogenase-A (LDH-A, EC 1.1.1.27) | 0 |
| 374 | I:1822577:05B02:D08 | MA122:D08 | | BC001941 | gi 12804976 gb BC001941.1BC001941 Homo sapiens, tissue specific transplantation antigen P35B, clone MGC:4302 IMAGE:2819332, mRNA, c | 1.7E-270 |
| 375 | I:1306814:06B02:A08 | MA126:A08 | | AK026649 | gi 10439547 dbj AK026649.1AK026649 Homo sapiens cDNA: FLJ22996 fis, clone KAT11938 | 9.8E-135 |

Table 3

| SEQ ID NO | Clone ID | MAClone ID | Mask Prent | GBHit | GBDescription | GBScore |
|-----------|---------------------|------------|------------|----------|---|----------|
| 376 | I:3034694:06B02:D08 | MA126:D08 | | BC008935 | gi 14286273 gb BC008935.1BC008935 Homo sapiens, Similar to solute carrier family 25 (mitochondrial carrier; adenine nucleotide tran | 4.6E-299 |
| 377 | I:1453049:03B02:A02 | MA114:A02 | | X76180 | gi 452649 emb X76180.1HSLASNA H.sapiens mRNA for lung amiloride sensitive Na ⁺ channel protein | 2.7E-269 |
| 378 | I:1453748:03B02:D02 | MA114:D02 | | BC013579 | gi 15488897 gb BC013579.1BC013579 Homo sapiens, Similar to calpastatin, clone MGC:9402 IMAGE:3878564, mRNA, complete cds | 2.6E-135 |
| 379 | I:3001492:03A02:G02 | MA112:G02 | | X75042 | gi 402648 emb X75042.1HSRNAREL H.sapiens rel proto-oncogene mRNA | 1.6E-295 |
| 380 | I:3876715:03A02:C08 | MA112:C08 | | BC000373 | gi 12653210 gb BC000373.1BC000373 Homo sapiens, Similar to amyloid beta (A4) precursor-like protein 2, clone MGC:8371 IMAGE:2820109 | 6.4E-161 |
| 381 | I:2992851:03A02:D08 | MA112:D08 | | AF190637 | gi 10441643 gb AF190637.1AF190637 Homo sapiens nephrin mRNA, complete cds | 1.5E-286 |
| 382 | I:1500649:03B02:G08 | MA114:G08 | | AB008430 | gi 2766164 dbj AB008430.1AB008430 Homo sapiens mRNA for CDEP, complete cds | 1E-234 |
| 383 | I:1512943:01A02:B02 | MA104:B02 | | AJ005036 | gi 3059108 emb AJ005036.1HSAJ5036 Homo sapiens mRNA for phosphodiesterase 3A (from corpus cavernosum) | 9.1E-288 |
| 384 | I:1467565:01A02:D02 | MA104:D02 | | BC014991 | gi 15929072 gb BC014991.1BC014991 Homo sapiens, clone MGC:23226 IMAGE:4909112, mRNA, complete cds | 3.7E-262 |
| 385 | I:2455118:01B02:D08 | MA106:D08 | | X16396 | gi 35070 emb X16396.1HSNMTDC Human mRNA for NAD-dependent methylene tetrahydrofolate dehydrogenase cyclohydrolase (EC 1.5.1.15) | 0 |
| 386 | I:2840251:01B02:E08 | MA106:E08 | | U52513 | gi 1777781 gb U52513.1HSU52513 Human RIG-G mRNA, complete cds | 0 |
| 387 | I:2911347:10B02:E02 | MA67:E02 | 0.28302 | | | |
| 388 | I:1812030:10B02:G08 | MA67:G08 | | AB049758 | gi 10800085 dbj AB049758.1AB049758 Homo sapiens mawbp mRNA for MAWD binding protein, complete cds | 3.6E-200 |
| 389 | I:2663606:04B02:F08 | MA118:F08 | | U37690 | gi 1017824 gb U37690.1HSU37690 Human RNA polymerase II subunit (hsRPB10) mRNA, complete cds | 5.2E-196 |

Table 3

| SEQ ID NO | Clone ID | MAClone ID | Mask Prent | GBHit | GBDescription | GBScore |
|-----------|---------------------|------------|------------|-----------|---|----------|
| 390 | I:1308333:02A02:E02 | MA108:E02 | | BC017338 | gi 16878283 gb BC017338.1BC017338 Homo sapiens, fucosidase, alpha-L- 1, tissue, clone MGC:29579 IMAGE:4871788, mRNA, complete cds | 1.4E-286 |
| 391 | I:1578941:02B02:E02 | MA110:E02 | | AK058013 | gi 16554011 dbj AK058013.1AK058013 Homo sapiens cDNA FLJ25284 fis, clone STM06787, highly similar to 15-HYDROXYPROSTAGLANDIN DEHYDR | 1.2E-246 |
| 392 | I:1535439:02A02:D08 | MA108:D08 | | M83363 | gi 190096 gb M83363.1HUMPMCA Human plasma membrane calcium-pumping ATPase (PMCA4) mRNA, complete cds | 3.1E-250 |
| 393 | I:1857475:02B02:H08 | MA110:H08 | | AF009203 | gi 2454508 gb AF009203.1AF009203 Homo sapiens YAC clone 377A1 unknown mRNA, 3'untranslated region | 1.5E-292 |
| 394 | I:2908878:08B01:F09 | MA133:F09 | 0.46085 | | | |
| 395 | I:2830575:07A01:C03 | MA127:C03 | 0.06365 | D16431 | gi 598955 dbj D16431.1HUMHDGF Human mRNA for hepatoma-derived growth factor, complete cds | 1.7E-289 |
| 396 | I:1557906:07B01:G03 | MA129:G03 | | AK057477 | gi 16553199 dbj AK057477.1AK057477 Homo sapiens cDNA FLJ32915 fis, clone TEST12006425 | 5.8E-230 |
| 397 | I:2200604:06B01:F03 | MA125:F03 | | U47105 | gi 4457236 gb U47105.2HSU47105 Homo sapiens H105c3 (H105c3) mRNA, complete cds | 0 |
| 398 | I:1653326:06A01:C09 | MA123:C09 | | BC018881 | gi 17403014 gb BC018881.1BC018881 Homo sapiens, clone IMAGE:3617364, mRNA | 1E-296 |
| 399 | I:1720149:06A01:G09 | MA123:G09 | | U48959 | gi 7239695 gb U48959.2HSU48959 Homo sapiens myosin light chain kinase (MLCK) mRNA, complete cds | 2.4E-291 |
| 400 | I:1560987:03B01:G03 | MA113:G03 | | U17077 | gi 1000711 gb U17077.1HSU17077 Human BENE mRNA, partial cds | 2.3E-92 |
| 401 | I:1510714:03B01:G09 | MA113:G09 | | NM_000240 | gi 4557734 ref NM_000240.1 Homo sapiens monoamine oxidase A (MAOA), nuclear gene encoding mitochondrial protein, mRNA | 6.3E-264 |
| 402 | I:2501484:01B01:A03 | MA105:A03 | | AB002438 | gi 2943813 dbj AB002438.1AB002438 Homo sapiens mRNA from chromosome 5q21-22, clone:FBR89 | 1.1E-268 |
| 403 | I:1379063:01A01:B03 | MA103:B03 | | U28055 | gi 1141776 gb U28055.1HSU28055 Homo sapiens hepatocyte growth factor-like protein homolog mRNA, partial cds | 0 |

Table 3

| SEQ ID NO | Clone ID | MAClone ID | Mask Prent | GBHit | GBDescription | GBScore |
|-----------|---------------------|------------|------------|-----------|---|----------|
| 404 | I:2797902:01B01:C03 | MA105:C03 | 0.07692 | BC019038 | gi 17512114 gb BC019038.1BC019038 Homo sapiens, small nuclear RNA activating complex, polypeptide 1, 43kD, clone MGC:20773 IMAGE:45 | 6.6E-289 |
| 405 | I:1805613:01B01:G03 | MA105:G03 | | U79725 | gi 1814276 gb U79725.1HSU79725 Human A33 antigen precursor mRNA, complete cds | 5.4E-202 |
| 406 | I:1524885:01A01:H03 | MA103:H03 | | Y12065 | gi 2230877 emb Y12065.1HSNOP56 Homo sapiens mRNA for nucleolar protein hNop56 | 0 |
| 407 | I:2888464:01B01:H03 | MA105:H03 | | S73591 | gi 688296 gb S73591.1S73591 Homo sapiens brain-expressed HHCPA78 homolog VDUP1 (Gene) mRNA, complete cds | 1.7E-267 |
| 408 | I:1992788:04B01:B03 | MA117:B03 | | AL161985 | gi 7328121 emb AL161985.1HSM8026 09 Homo sapiens mRNA; cDNA DKFZp761J1810 (from clone DKFZp761J1810) | 0 |
| 409 | I:1413451:04A01:F03 | MA115:F03 | | D88648 | gi 2653566 dbj D88648.1D88648 Homo sapiens mRNA for B-FABP, complete cds | 4.1E-184 |
| 410 | I:2779515:04B01:C09 | MA117:C09 | | AL136543 | gi 6807646 emb AL136543.1HSM8015 17 Homo sapiens mRNA; cDNA DKFZp761K0511 (from clone DKFZp761K0511); partial cds | 2.2E-285 |
| 411 | I:1583076:02B01:G09 | MA109:G09 | | NM_000669 | gi 1496888 ref NM_000669.2 Homo sapiens alcohol dehydrogenase 1C (class I), gamma polypeptide (ADH1C), mRNA | 6E-261 |
| 412 | I:3070110:05A02:B03 | MA120:B03 | | AF061016 | gi 3127126 gb AF061016.1AF061016 Homo sapiens UDP-glucose dehydrogenase (UGDH) mRNA, complete cds | 6.4E-295 |
| 413 | I:1904493:05A02:H03 | MA120:H03 | | Z22555 | gi 397606 emb Z22555.1HSCLA1GNA H.sapiens encoding CLA-1 mRNA | 9.7E-229 |
| 414 | I:2860815:05A02:A09 | MA120:A09 | | AF067420 | gi 3201899 gb AF067420.1AF067420 Homo sapiens SNC73 protein (SNC73) mRNA, complete cds | 1.7E-100 |
| 415 | I:1930135:07A02:G03 | MA128:G03 | | | | |
| 416 | I:3747901:06B02:G03 | MA126:G03 | | BC004979 | gi 13436403 gb BC004979.1BC004979 Homo sapiens, clone MGC:3855 IMAGE:2905681, mRNA, complete cds | 1.6E-289 |
| 417 | I:1720946:06A02:A09 | MA124:A09 | | BC010733 | gi 14789594 gb BC010733.1BC010733 Homo sapiens, clone IMAGE:3897044, mRNA, partial cds | 1.1E-296 |

Table 3

| SEQ ID NO | Clone ID | MAClone ID | Mask Prent | GBHit | GBDescription | GBScore |
|-----------|---------------------|------------|------------|-----------|---|----------|
| 418 | I:2877413:06B02:D09 | MA126:D09 | | BC000700 | gi 12653822 gb BC000700.1BC000700 Homo sapiens, clone MGC:3101 IMAGE:3350198, mRNA, complete cds | 5.5E-255 |
| 419 | I:3035279:06B02:E09 | MA126:E09 | | BC001125 | gi 12654578 gb BC001125.1BC001125 Homo sapiens, peptidylprolyl isomerase B (cyclophilin B), clone MGC:2224 IMAGE:2966791, mRNA, com | 2E-276 |
| 420 | I:2503913:03A02:E09 | MA112:E09 | | BC010952 | gi 15012094 gb BC010952.1BC010952 Homo sapiens, Similar to protease inhibitor 3, skin-derived (SKALP), clone MGC:13613 IMAGE:408315 | 1.5E-261 |
| 421 | I:1517380:01A02:B03 | MA104:B03 | | AB033032 | gi 6330486 dbj AB033032.1AB033032 Homo sapiens mRNA for KIAA1206 protein, partial cds | 1.2E-277 |
| 422 | I:3138128:01B02:C03 | MA106:C03 | | D31887 | gi 505101 dbj D31887.1HUMORFKG1 P Human mRNA for KIAA0062 gene, partial cds | 1E-300 |
| 423 | I:2453722:01A02:E03 | MA104:E03 | | BC003582 | gi 13097770 gb BC003582.1BC003582 Homo sapiens, polymerase (RNA) II (DNA directed) polypeptide F, clone MGC:2669 IMAGE:3546712, mRN | 1E-300 |
| 424 | I:1414260:01A02:A09 | MA104:A09 | | AB002318 | gi 2224580 dbj AB002318.1AB002318 Human mRNA for KIAA0320 gene, partial cds | 3.4E-284 |
| 425 | I:2891247:01B02:A09 | MA106:A09 | | D43638 | gi 940399 dbj D43638.1HUMMTG8AP Human mRNA for MTG8a protein, complete cds | 8.4E-151 |
| 426 | I:1682176:01A02:F09 | MA104:F09 | | U78556 | gi 1688306 gb U78556.1HSU78556 Human cisplatin resistance associated alpha protein (hCRA alpha) mRNA, complete cds | 1E-293 |
| 427 | I:2739076:04A02:D03 | MA116:D03 | | NM_001023 | gi 14591915 ref NM_001023.2 Homo sapiens ribosomal protein S20 (RPS20), mRNA | 2.1E-248 |
| 428 | I:1900378:04B02:F03 | MA118:F03 | | AB002363 | gi 2224670 dbj AB002363.1AB002363 Human mRNA for KIAA0365 gene, partial cds | 3.1E-275 |
| 429 | I:1603391:04A02:G03 | MA116:G03 | | AF036874 | gi 9738910 gb AF036874.1AF036874 Homo sapiens multiple endocrine neoplasia type 1 candidate protein number 18 (HSPF2) mRNA, complet | 3.7E-275 |
| 430 | I:2018222:04A02:C09 | MA116:C09 | | BC008795 | gi 14250659 gb BC008795.1BC008795 Homo sapiens, proteasome (prosome, macropain) subunit, beta type, 9 (large multifunctional protea | 2E-192 |

Table 3

| SEQ ID NO | Clone ID | MAClone ID | Mask Prent | GBHit | GBDescription | GBScore |
|-----------|---------------------|------------|------------|----------|---|----------|
| 431 | I:1327263:04A02:F09 | MA116:F09 | | M25629 | gi 186652 gb M25629.1HUMKALX Human kallikrein mRNA, complete cds, clone clone pHKK25 | 1.4E-283 |
| 432 | I:1734393:02A02:B09 | MA108:B09 | | X73502 | gi 406853 emb X73502.1HSENCY20 H. Sapiens mRNA for cytokeratin 20 | 0 |
| 433 | I:2190607:02A02:E09 | MA108:E09 | | BC008012 | gi 14124971 gb BC008012.1BC008012 Homo sapiens, eukaryotic translation elongation factor 1 delta (guanine nucleotide exchange prote | 3.5E-244 |
| 434 | I:2447969:08A01:E04 | MA131:E04 | 0.16896 | | | |
| 435 | I:1753033:08B01:H10 | MA133:H10 | | AL359055 | gi 8518180 emb AL359055.1IR234443 6 Homo sapiens mRNA full length insert cDNA clone EUROIMAGE 2344436 | 9.6E-24 |
| 436 | I:2456393:07B01:E10 | MA129:E10 | | BC005029 | gi 13477142 gb BC005029.1BC005029 Homo sapiens, hypothetical protein FLJ10718, clone MGC:12594 IMAGE:4040181, mRNA, complete cds | 3.6E-259 |
| 437 | I:1719920:06B01:A04 | MA125:A04 | 0.13978 | BC001903 | gi 12804902 gb BC001903.1BC001903 Homo sapiens, Similar to interleukin 10 receptor, beta, clone MGC:2210 IMAGE:3544611, mRNA, compl | 1.4E-274 |
| 438 | I:2927362:06B01:H04 | MA125:H04 | | BC019336 | gi 17939560 gb BC019336.1BC019336 Homo sapiens, clone IMAGE:3617778, mRNA, partial cds | 0 |
| 439 | I:4082816:06B01:F10 | MA125:F10 | | BC001365 | gi 12655034 gb BC001365.1BC001365 Homo sapiens, ribosomal protein L4, clone MGC:2201 IMAGE:3051487, mRNA, complete cds | 6.1E-230 |
| 440 | I:1803446:03A01:A04 | MA111:A04 | | BC000062 | gi 12652632 gb BC000062.1BC000062 Homo sapiens, solute carrier family 1 (neutral amino acid transporter), member 5, clone MGC:1387 | 1E-300 |
| 441 | I:1557490:03A01:C04 | MA111:C04 | | BC003560 | gi 13097707 gb BC003560.1BC003560 Homo sapiens, ribophorin II, clone MGC:1817 IMAGE:3546673, mRNA, complete cds | 0 |
| 442 | I:1445895:03B01:E10 | MA113:E10 | | BC009196 | gi 14327943 gb BC009196.1BC009196 Homo sapiens, phosphatidic acid phosphatase type 2B, clone MGC:15306 IMAGE:3960223, mRNA, complet | 3.6E-131 |
| 443 | I:1336836:01A01:H04 | MA103:H04 | | M32215 | gi 307524 gb M32215.1HUMTSHRX Human thyroid stimulatory hormone receptor (TSHR) mRNA, complete cds | 1E-300 |

Table 3

| SEQ ID NO | Clone ID | MAClone ID | Mask Prent | GBHit | GBDescription | GBScore |
|-----------|---------------------|------------|------------|-----------|---|----------|
| 444 | I:1802745:01B01:E10 | MA105:E10 | | D42087 | gi 576555 dbj D42087.1HUMHA0793 A Human mRNA for KIAA0118 gene, partial cds | 8.4E-279 |
| 445 | I:2503003:01B01:H10 | MA105:H10 | | AF020352 | gi 2655054 gb AF020352.1AF020352 Homo sapiens NADH:ubiquinone oxidoreductase 15 kDa IP subunit mRNA, nuclear gene encoding mitochon | 1.4E-255 |
| 446 | I:1655377:10A01:F04 | MA64:F04 | | AK000706 | gi 7020960 dbj AK000706.1AK000706 Homo sapiens cDNA FLJ20699 fis, clone KAIA2372 | 2.7E-210 |
| 447 | I:1430662:04A01:A04 | MA115:A04 | | AF078035 | gi 4322303 gb AF078035.1AF078035 Homo sapiens translation initiation factor IF2 mRNA, complete cds | 3.9E-262 |
| 448 | I:3335055:04A01:G04 | MA115:G04 | | BC004390 | gi 13325149 gb BC004390.1BC004390 Homo sapiens, phosphatidylserine synthase 1, clone MGC:10968 IMAGE:3634879, mRNA, complete cds | 3.7E-181 |
| 449 | I:2457671:04B01:B10 | MA117:B10 | | BC000469 | gi 12653398 gb BC000469.1BC000469 Homo sapiens, eukaryotic translation initiation factor 3, subunit 7 (zeta, 66/67kD), clone MGC:85 | 4.3E-299 |
| 450 | I:1641421:02A01:C10 | MA107:C10 | | S69369 | gi 545844 gb S69369.1S69369 PAX3A=transcription factor [human, adult cerebellum, mRNA, 1248 nt] | 1.5E-180 |
| 451 | I:1655225:02B01:E10 | MA109:E10 | | AB002331 | gi 2224606 dbj AB002331.1AB002331 Human mRNA for KIAA0333 gene, partial cds | 7.1E-273 |
| 452 | I:1313325:05A02:B04 | MA120:B04 | | U09550 | gi 1184036 gb U09550.1HSU09550 Human oviductal glycoprotein mRNA, complete cds | 5.2E-283 |
| 453 | I:1558081:05B02:A10 | MA122:A10 | | NM_004530 | gi 11342665 ref NM_004530.1 Homo sapiens matrix metalloproteinase 2 (gelatinase A, 72kD gelatinase, 72kD type IV collagenase) (MMP2 | 0 |
| 454 | I:1889191:05A02:H10 | MA120:H10 | | BC001619 | gi 12804426 gb BC001619.1BC001619 Homo sapiens, Similar to aldehyde dehydrogenase 5, clone MGC:2230 IMAGE:3356389, mRNA, complete c | 1.1E-299 |
| 455 | I:3495906:07A02:C10 | MA128:C10 | | U19251 | gi 2642132 gb U19251.1HSU19251 Homo sapiens neuronal apoptosis inhibitory protein mRNA, complete cds | 0 |
| 456 | I:3704132:03A02:D10 | MA112:D10 | | Z49194 | gi 974830 emb Z49194.1HSOBF1 H.sapiens mRNA for oct-binding factor | 1.3E-102 |

Table 3

| SEQ ID NO | Clone ID | MAClone ID | Mask Prent | GBHit | GBDescription | GBScore |
|-----------|---------------------|------------|------------|----------|---|----------|
| 457 | I:1636553:03B02:F10 | MA114:F10 | | AB001895 | gi 2588990 dbj AB001895.1AB001895 Homo sapiens mRNA for B120, complete cds | 2.8E-130 |
| 458 | I:1402228:03B02:H10 | MA114:H10 | | BC008588 | gi 14250316 gb BC008588.1BC008588 Homo sapiens, Similar to plastin 3 (T isoform), clone IMAGE:3447893, mRNA, partial cds | 7.8E-170 |
| 459 | I:1361963:01A02:B04 | MA104:B04 | | L13616 | gi 439874 gb L13616.1HUMFAKX Human focal adhesion kinase (FAK) mRNA, complete cds | 2.4E-291 |
| 460 | I:1510424:01A02:D04 | MA104:D04 | | X04481 | gi 34627 cemb X04481.1HSMH3C2R Human mRNA for complement component C2 | 1E-300 |
| 461 | I:2918558:01B02:D04 | MA106:D04 | | AF000994 | gi 2580573 gb AF000994.1HSAF000994 Homo sapiens ubiquitous TPR motif, Y isoform (UTY) mRNA, alternative transcript 3, complete cds | 8.8E-285 |
| 462 | I:1731061:01A02:D10 | MA104:D10 | | BC000418 | gi 12653298 gb BC000418.1BC000418 Homo sapiens, ectodermal-neural cortex (with BTB-like domain), clone MGC:8659 IMAGE:2964376, mRNA | 1E-300 |
| 463 | I:2579602:04A02:A04 | MA116:A04 | | BC005128 | gi 13477308 gb BC005128.1BC005128 Homo sapiens, ribosomal protein L7a, clone MGC:10607 IMAGE:3938260, mRNA, complete cds | 1E-300 |
| 464 | I:2824181:04B02:A04 | MA118:A04 | | BC004900 | gi 13436172 gb BC004900.1BC004900 Homo sapiens, ribosomal protein L13a, clone IMAGE:3545758, mRNA, partial cds | 1E-300 |
| 465 | I:2123183:04A02:B04 | MA116:B04 | | BC001164 | gi 12654652 gb BC001164.1BC001164 Homo sapiens, proteasome (prosome, macropain) 26S subunit, non-ATPase, 8, clone MGC:1660 IMAGE:35 | 2.1E-198 |
| 466 | I:1958560:04A02:C10 | MA116:C10 | 0.0522 | BC016147 | gi 16359382 gb BC016147.1BC016147 Homo sapiens, clone MGC:9485 IMAGE:3921259, mRNA, complete cds | 1.5E-277 |
| 467 | I:1447903:04A02:G10 | MA116:G10 | | AK056274 | gi 16551627 dbj AK056274.1AK056274 Homo sapiens cDNA FLJ31712 fis, clone NT2RI2006445, moderately similar to INSULIN-LIKE GROWTH FA | 2.2E-48 |
| 468 | I:1875576:02A02:E10 | MA108:E10 | | U04897 | gi 451563 gb U04897.1HSU04897 Human orphan hormone nuclear receptor RORalpha1 mRNA, complete cds | 1.1E-140 |

Table 3

| SEQ ID NO | Clone ID | MAClone ID | Mask Prent | GBHit | GBDescription | GBScore |
|-----------|---------------------|------------|------------|-----------|--|----------|
| 469 | I:1709457:02B02:G10 | MA110:G10 | | X65873 | gi 34082 emb X65873.1HSKHCMR H.sapiens mRNA for kinesin (heavy chain) | 0 |
| 470 | I:2155675:08B01:G05 | MA133:G05 | 0.83871 | | | |
| 471 | I:1635069:07A01:A05 | MA127:A05 | | D15049 | gi 475003 dbj D15049.1HUMSAP1C Homo sapiens mRNA for protein tyrosine phosphatase precursor, complete cds | 3.5E-197 |
| 472 | I:1453445:07A01:G05 | MA127:G05 | 0.07788 | BC001784 | gi 13937607 gb BC001784.1BC001784 Homo sapiens, Similar to acidic 82 kDa protein mRNA, clone IMAGE:3542384, mRNA | 1.2E-265 |
| 473 | I:3002566:07A01:D11 | MA127:D11 | | D26350 | gi 450468 dbj D26350.1HUMHT21 Human mRNA for type 2 inositol 1,4,5-trisphosphate receptor, complete cds | 0 |
| 474 | I:1631511:06A01:C05 | MA123:C05 | | BC001454 | gi 12655192 gb BC001454.1BC001454 Homo sapiens, phosphoenolpyruvate carboxykinase 2 (mitochondrial), clone MGC:1492 IMAGE:3138368, | 0 |
| 475 | I:1610523:06A01:H05 | MA123:H05 | | L19183 | gi 307154 gb L19183.1HUMMAC30X Human MAC30 mRNA, 3' end | 0 |
| 476 | I:3297656:06B01:E11 | MA125:E11 | | D14530 | gi 414348 dbj D14530.1HUMRSPT Human homolog of yeast ribosomal protein S28, complete cds | 5E-277 |
| 477 | I:2509730:06B01:H11 | MA125:H11 | | X91788 | gi 1001874 emb X91788.1HSICLNGE N H.sapiens mRNA for Icln protein | 0 |
| 478 | I:2121863:03B01:D05 | MA113:D05 | | BC002738 | gi 12803796 gb BC002738.1BC002738 Homo sapiens, cysteine-rich protein 1 (intestinal), clone MGC:3888 IMAGE:3631097, mRNA, complete | 6.9E-47 |
| 479 | I:1413704:03B01:E05 | MA113:E05 | | NM_003903 | gi 14110370 ref NM_003903.2 Homo sapiens CDC16 cell division cycle 16 homolog (S. cerevisiae) (CDC16), mRNA | 8.5E-254 |
| 480 | I:1626232:03A01:A11 | MA111:A11 | | AF048700 | gi 2935439 gb AF048700.1AF048700 Homo sapiens gastrointestinal peptide (PEC-60) mRNA, complete cds | 3.5E-203 |
| 481 | I:2354446:01B01:B05 | MA105:B05 | | AF131913 | gi 4928275 gb AF131913.1AF131913 Homo sapiens alpha-(1,3/1,4)-fucosyltransferase (FT3B) mRNA, complete cds | 1.2E-218 |
| 482 | I:2916753:01B01:E05 | MA105:E05 | | X62534 | gi 32332 emb X62534.1HSHMG2 H.sapiens HMG-2 mRNA | 3.9E-179 |

Table 3

| SEQ ID NO | Clone ID | MAClone ID | Mask Prent | GBHit | GBDescription | GBScore |
|-----------|---------------------|------------|------------|----------|---|----------|
| 483 | I:2555034:01A01:A11 | MA103:A11 | 0.09272 | U39196 | gi 1055027 gb U39196.1HSU39196 Human clone hGIRK1 G-protein coupled inwardly rectifying potassium channel mRNA, complete cds | 9.4E-151 |
| 484 | I:2804190:01B01:D11 | MA105:D11 | | BC004300 | gi 13279166 gb BC004300.1BC004300 Homo sapiens, Similar to villin-like, clone MGC:10896 IMAGE:3622951, mRNA, complete cds | 2.8E-166 |
| 485 | I:1814488:01A01:E11 | MA103:E11 | | AF044773 | gi 3002950 gb AF044773.1AF044773 Homo sapiens breakpoint cluster region protein 1 (BCRG1) mRNA, complete cds | 8.8E-208 |
| 486 | I:2474163:01B01:E11 | MA105:E11 | | J03037 | gi 179771 gb J03037.1HUMCAIIA Human carbonic anhydrase II mRNA, complete cds | 1.2E-143 |
| 487 | I:1402967:01A01:G11 | MA103:G11 | | Y00651 | gi 34504 emb Y00651.1HSMCP Human mRNA for membrane cofactor protein | 1.5E-227 |
| 488 | I:2821541:10A01:D11 | MA64:D11 | 0.356 | | | |
| 489 | I:2888814:04B01:A05 | MA117:A05 | | Y10806 | gi 1808645 emb Y10806.1HSY10806 H.sapiens mRNA for arginine methyltransferase, splice variant, 1316 bp | 1E-300 |
| 490 | I:1451005:04A01:C05 | MA115:C05 | | BC001771 | gi 12804688 gb BC001771.1BC001771 Homo sapiens, general transcription factor IIF, polypeptide 2 (30kD subunit), clone MGC:1502 IMAG | 3.3E-200 |
| 491 | I:1457726:04A01:H05 | MA115:H05 | | AK001686 | gi 7023098 dbj AK001686.1AK001686 Homo sapiens cDNA FLJ10824 fis, clone NT2RP4001086 | 3.9E-209 |
| 492 | I:2883195:04B01:H05 | MA117:H05 | | BC000672 | gi 12653772 gb BC000672.1BC000672 Homo sapiens, guanine nucleotide binding protein (G protein), beta polypeptide 2-like 1, clone MG | 1E-290 |
| 493 | I:1603605:04A01:G11 | MA115:G11 | 0.04363 | D38305 | gi 1580723 dbj D38305.1HUMTOB Human mRNA for Tob, complete cds | 1.3E-268 |
| 494 | I:2832224:04A01:H11 | MA115:H11 | | L09604 | gi 177899 gb L09604.1HUMA4 Homo sapiens differentiation-dependent A4 protein mRNA, complete cds | 0 |
| 495 | I:2231364:02A01:A05 | MA107:A05 | | D87469 | gi 1665820 dbj D87469.1D87469 Human mRNA for KIAA0279 gene, partial cds | 0 |
| 496 | I:1595081:02B01:F11 | MA109:F11 | | S36219 | gi 249623 gb S36219.1S36219 prostaglandin G/H synthase {alternative splicing product} [human, lung fibroblast, clone HCO-T9, mRNA, | 1E-300 |

Table 3

| SEQ ID NO | Clone ID | MA Clone ID | Mask Prent | GBHit | GBDescription | GBScore |
|-----------|---------------------|-------------|------------|-----------|---|----------|
| 497 | I:1877913:05B02:C05 | MA122:C05 | | U51903 | gi 1262925 gb U51903.1HSU51903 Human RasGAP-related protein (IQGAP2) mRNA, complete cds | 1E-300 |
| 498 | I:1666130:05B02:F05 | MA122:F05 | | X05790 | gi 28535 emb X05790.1HSAGALAR Human mRNA for alpha-galactosidase A (EC 3.2.1-22) | 0 |
| 499 | I:1709995:05B02:H05 | MA122:H05 | | U78525 | gi 2558667 gb U78525.1HSU78525 Homo sapiens eukaryotic translation initiation factor (eIF3) mRNA, complete cds | 8.3E-279 |
| 500 | I:3872557:07A02:B05 | MA128:B05 | | NM_000518 | gi 13788565 ref NM_000518.3 Homo sapiens hemoglobin, beta (HBB), mRNA | 0 |
| 501 | I:2734906:07A02:E11 | MA128:E11 | | NM_001997 | gi 17981709 ref NM_001997.2 Homo sapiens Finkel-Biskis-Reilly murine sarcoma virus (FBR-MuSV) ubiquitously expressed (fox derived); | 1.3E-277 |
| 502 | I:1798585:06A02:B05 | MA124:B05 | | BC008767 | gi 14250615 gb BC008767.1BC008767 Homo sapiens, Similar to acyl-Coenzyme A oxidase 1, palmitoyl, clone MGC:1198 IMAGE:3051501, mRNA | 0 |
| 503 | I:1683389:06A02:F05 | MA124:F05 | | BC015335 | gi 15929831 gb BC015335.1BC015335 Homo sapiens, immature colon carcinoma transcript 1, clone MGC:21251 IMAGE:4418983, mRNA, complet | 0 |
| 504 | I:1704517:06A02:G05 | MA124:G05 | | BC005820 | gi 14710649 gb BC005820.1BC005820 Homo sapiens, clone IMAGE:3937549, mRNA | 0 |
| 505 | I:2792982:06B02:H05 | MA126:H05 | | X71345 | gi 405755 emb X71345.1HSTRYIVB H.sapiens mRNA for trypsinogen IV b-form | 0 |
| 506 | I:3511355:06B02:D11 | MA126:D11 | | NM_001002 | gi 16933547 ref NM_001002.2 Homo sapiens ribosomal protein, large, P0 (RPLP0), transcript variant 1, mRNA | 1E-300 |
| 507 | I:1738060:03A02:A05 | MA112:A05 | | BC000508 | gi 12653472 gb BC000508.1BC000508 Homo sapiens, proteasome (prosome, macropain) subunit, beta type, 1, clone MGC:8505 IMAGE:2822268 | 1.1E-243 |
| 508 | I:1810821:03B02:B05 | MA114:B05 | | BC016956 | gi 16877417 gb BC016956.1BC016956 Homo sapiens, clone MGC:21520 IMAGE:3900854, mRNA, complete cds | 7E-217 |

Table 3

| SEQ ID NO | Clone ID | MAClone ID | Mask Prent | GBHit | GBDescription | GBScore |
|-----------|---------------------|------------|------------|-----------|--|----------|
| 509 | I:2451279:03A02:E05 | MA112:E05 | | BC009868 | gi 14602690 gb BC009868.1BC009868 Homo sapiens, replication protein A3 (14kD), clone MGC:16404 IMAGE:3940438, mRNA, complete cds | 1.8E-167 |
| 510 | I:1431166:03B02:E05 | MA114:E05 | | BC010444 | gi 14714612 gb BC010444.1BC010444 Homo sapiens, matrilin 2, clone MGC:17281 IMAGE:4215380, mRNA, complete cds | 5.5E-230 |
| 511 | I:2949427:03B02:A11 | MA114:A11 | | BC006794 | gi 13905021 gb BC006794.1BC006794 Homo sapiens, Similar to interferon induced transmembrane protein 3 (1-8U), clone MGC:5225 IMAGE: | 3.2E-225 |
| 512 | I:1458366:03B02:E11 | MA114:E11 | | AF009202 | gi 2454507 gb AF009202.1AF009202 Homo sapiens YAC clone 136A2 unknown mRNA, 3'untranslated region | 3.7E-290 |
| 513 | I:1525881:03B02:G11 | MA114:G11 | | AF368463 | gi 14583005 gb AF368463.1AF368463 Homo sapiens carboxypeptidase M mRNA, complete cds | 8.5E-176 |
| 514 | I:2071473:01A02:E05 | MA104:E05 | | X17567 | gi 36512 emb X17567.1HSSNRNPB H.sapiens RNA for snRNP protein B | 0 |
| 515 | I:2481012:01A02:C11 | MA104:C11 | | BC001625 | gi 12804436 gb BC001625.1BC001625 Homo sapiens, Similar to for protein disulfide isomerase-related, clone MGC:1259 IMAGE:3537659, m | 1.6E-236 |
| 516 | I:2816931:01B02:C11 | MA106:C11 | | D88827 | gi 2342505 dbj D88827.1D88827 Homo sapiens mRNA for zinc finger protein FPM315, complete cds | 4.2E-159 |
| 517 | I:1806769:01B02:F11 | MA106:F11 | | NM_005971 | gi 11612675 ref NM_005971.2 Homo sapiens FXYD domain-containing ion transport regulator 3 (FXYD3), transcript variant 1, mRNA | 8.8E-242 |
| 518 | I:2636634:04B02:A11 | MA118:A11 | | L32137 | gi 602449 gb L32137.1HUMCOMP Human germline oligomeric matrix protein (COMP) mRNA, complete cds | 2.5E-210 |
| 519 | I:1649959:02B02:E11 | MA110:E11 | | BC002700 | gi 12803726 gb BC002700.1BC002700 Homo sapiens, Similar to keratin 7, clone MGC:3625 IMAGE:3610347, mRNA, complete cds | 2.5E-254 |
| 520 | I:1633719:02B02:F11 | MA110:F11 | | J05428 | gi 340079 gb J05428.1HUMUDPGTA Human 3,4-catechol estrogen UDP-glucuronosyltransferase mRNA, complete cds | 3.8E-290 |
| 521 | I:1901035:02B02:G11 | MA110:G11 | | AF081513 | gi 5725637 gb AF081513.1AF081513 Homo sapiens TGF-beta type secreted signaling protein LEFTYA mRNA, complete cds | 1.2E-143 |

Table 3

| SEQ ID NO | Clone ID | MAClone ID | Mask Prent | GBHit | GBDescription | GBScore |
|-----------|---------------------|------------|------------|----------|---|----------|
| 522 | I:2503879:08B01:C12 | MA133:C12 | | AF150733 | gi 7688664 gb AF150733.1AF150733 Homo sapiens AD-014 protein mRNA, complete cds | 3.9E-237 |
| 523 | I:2383065:07B01:B06 | MA129:B06 | | AJ335311 | gi 15879729 emb AJ335311.1HSA335311 Homo sapiens genomic sequence surrounding NotI site, clone NR1-WB8C | 3.7E-50 |
| 524 | I:3357245:07A01:F06 | MA127:F06 | | X95073 | gi 2879814 emb X95073.1HSTRAXGEN H.sapiens mRNA for translin associated protein X | 0 |
| 525 | I:2832314:07A01:G06 | MA127:G06 | | M26252 | gi 338826 gb M26252.1HUMTCBA Human TCB gene encoding cytosolic thyroid hormone-binding protein, complete cds | 7.8E-279 |
| 526 | I:3667096:07A01:D12 | MA127:D12 | | BC003412 | gi 13097323 gb BC003412.1BC003412 Homo sapiens, cyclophilin, clone MGC:5016 IMAGE:3451034, mRNA, complete cds | 1E-300 |
| 527 | I:1798283:06A01:D06 | MA123:D06 | | BC016835 | gi 16877126 gb BC016835.1BC016835 Homo sapiens, Similar to synaptophysin-like protein, clone MGC:10011 IMAGE:3883697, mRNA, complet | 1E-300 |
| 528 | I:1648206:03A01:B06 | MA111:B06 | | AJ420535 | gi 17066399 emb AJ420535.1HSA420535 Homo sapiens mRNA full length insert cDNA clone EUROIMAGE 993611 | 6.2E-264 |
| 529 | I:3360476:03B01:B12 | MA113:B12 | | Y08768 | gi 1877211 emb Y08768.1HSIL13 H.sapiens mRNA for IL-13 receptor | 1.4E-177 |
| 530 | I:2500511:03B01:C12 | MA113:C12 | | AJ001531 | gi 2661423 emb AJ001531.1HSNEUR OTR Homo sapiens mRNA for neurotrypsin | 3.9E-265 |
| 531 | I:1730806:03B01:D12 | MA113:D12 | | AL049705 | gi 4678821 emb AL049705.1HS262D122 Human gene from PAC 262D12, chromosome 1 | 7.8E-220 |
| 532 | I:2479074:01B01:C06 | MA105:C06 | | AF096304 | gi 4191395 gb AF096304.1AF096304 Homo sapiens putative sterol reductase SR-1 (TM7SF2) mRNA, complete cds | 0 |
| 533 | I:1635004:01B01:E06 | MA105:E06 | | BC003661 | gi 13177786 gb BC003661.1BC003661 Homo sapiens, lectin, galactoside-binding, soluble, 4 (galectin 4), clone MGC:698 IMAGE:2967411, | 4.6E-231 |
| 534 | I:2378569:01B01:G06 | MA105:G06 | | BC000341 | gi 12653146 gb BC000341.1BC000341 Homo sapiens, signal sequence receptor, beta (translocon-associated protein beta), clone MGC:8566 | 8.7E-236 |

Table 3

| SEQ ID NO | Clone ID | MA Clone ID | Mask Prent | GBHit | GBDescription | GBScore |
|-----------|---------------------|-------------|------------|-----------|---|----------|
| 535 | I:2207849:01A01:D12 | MA103:D12 | | X65019 | gi 33792 emb X65019.1HSIL1BRNA H.sapiens mRNA for interleukin-1B converting enzyme | 0 |
| 536 | I:1504554:01A01:F12 | MA103:F12 | 0.1646 | U43843 | gi 1532120 gb U43843.1HSU43843 Human h-neuro-d4 protein mRNA, complete cds | 4.6E-151 |
| 537 | I:2989991:04B01:A06 | MA117:A06 | | AF400442 | gi 15217078 gb AF400442.1AF400442 Homo sapiens pigment epithelium-derived factor (SERPINF1) mRNA, complete cds | 1E-300 |
| 538 | I:2852561:04B01:B06 | MA117:B06 | | J02769 | gi 177206 gb J02769.1HUM4F2A Human 4F2 antigen heavy chain mRNA, complete cds | 1.4E-255 |
| 539 | I:2832839:04A01:C12 | MA115:C12 | | NM_006399 | gi 5453562 ref NM_006399.1 Homo sapiens basic leucine zipper transcription factor, ATF-like (BATF), mRNA | 2.6E-138 |
| 540 | I:2845548:04B01:E12 | MA117:E12 | | AY034482 | gi 15809587 gb AY034482.1 Homo sapiens hnRNP Q2 mRNA, complete cds | 3.1E-278 |
| 541 | I:1251819:02B01:B06 | MA109:B06 | | X78669 | gi 469884 emb X78669.1HSERC55R H.sapiens ERC-55 mRNA | 9.1E-288 |
| 542 | I:1672930:02B01:D06 | MA109:D06 | | X83617 | gi 620082 emb X83617.1HSRANBP1 H.sapiens mRNA for RanBP1 | 4.7E-274 |
| 543 | I:2122820:02B01:E06 | MA109:E06 | | BC001738 | gi 12804628 gb BC001738.1BC001738 Homo sapiens, Similar to ubiquitin-conjugating enzyme E2G 2 (homologous to yeast UBC7), clone MGC | 3.9E-234 |
| 544 | I:2174920:02A01:H06 | MA107:H06 | | BC006230 | gi 13623260 gb BC006230.1BC006230 Homo sapiens, lysophospholipase-like, clone MGC:10338 IMAGE:3945191, mRNA, complete cds | 9.5E-260 |
| 545 | I:1875994:05B02:E06 | MA122:E06 | | BC002638 | gi 12803606 gb BC002638.1BC002638 Homo sapiens, hypothetical protein, clone MGC:3365 IMAGE:3608062, mRNA, complete cds | 2.2E-217 |
| 546 | I:1858644:05A02:G06 | MA120:G06 | | M55268 | gi 177837 gb M55268.1HUMA1CKII Human casein kinase II alpha' subunit mRNA, complete cds | 3.4E-284 |
| 547 | I:1700047:06A02:E06 | MA124:E06 | | BC000405 | gi 12653272 gb BC000405.1BC000405 Homo sapiens, small nuclear ribonucleoprotein polypeptide A, clone MGC:8567 IMAGE:2822987, mRNA, | 1.4E-224 |
| 548 | I:1718257:06B02:E06 | MA126:E06 | | AF020760 | gi 5870864 gb AF020760.2AF020760 Homo sapiens serine protease (OMI) mRNA, complete cds | 0 |

Table 3

| SEQ ID NO | Clone ID | MAClone ID | Mask Prent | GBHit | GBDescription | GBScore |
|-----------|----------------------|------------|------------|-----------|---|----------|
| 549 | I:1612306:06A02:F06 | MA124:F06 | | BC002594 | gi 12803530 gb BC002594.1BC002594 Homo sapiens, dolichyl-diphosphooligosaccharide-protein glycosyltransferase, clone MGC:2191 IMAGE | 4.5E-271 |
| 550 | I:1637427:06A02:F12 | MA124:F12 | | U31659 | gi 1136305 gb U31659.1HSU31659 Human TBP-associated factor TAFII80 mRNA, complete cds | 7.5E-217 |
| 551 | I:2513883:03A02:B12 | MA112:B12 | | X76717 | gi 435674 emb X76717.1HSMT1L H.sapiens MT-11 mRNA | 2.1E-142 |
| 552 | I:2645840:01A02:G06 | MA104:G06 | | X97795 | gi 1495482 emb X97795.1HSRAD54 H.sapiens mRNA homologous to S. cerevisiae RAD54 | 1.7E-295 |
| 553 | I:1737403:01A02:A12 | MA104:A12 | | Z29067 | gi 479172 emb Z29067.1HSNEK3R H.sapiens nek3 mRNA for protein kinase | 0 |
| 554 | I:1733522:01B02:H12 | MA106:H12 | | BC017880 | gi 17389723 gb BC017880.1BC017880 Homo sapiens, clone MGC:22754 IMAGE:4277855, mRNA, complete cds | 7.7E-95 |
| 555 | RG:160664:10006:E07 | MA155:E07 | | NM_020975 | gi 10862702 ref NM_020975.1 Homo sapiens ret proto-oncogene (multiple endocrine neoplasia and medullary thyroid carcinoma 1, Hirsch | 1.7E-298 |
| 556 | I:747335:16A01:E01 | MA87:E01 | | NM_000985 | gi 14591906 ref NM_000985.2 Homo sapiens ribosomal protein L17 (RPL17), mRNA | 3.1E-272 |
| 557 | I:2085191:16A01:H01 | MA87:H01 | | M22612 | gi 521215 gb M22612.1HUMTRPSGN A Human pancreatic trypsin 1 (TRY1) mRNA, complete cds | 1E-287 |
| 558 | I:1211126:16A01:E07 | MA87:E07 | | Y13901 | gi 2832349 emb Y13901.1HSFGFR4G Homo sapiens FGFR-4 gene | 1E-300 |
| 559 | RG:669310:10010:C01 | MA159:C01 | | BC000833 | gi 12654054 gb BC000833.1BC000833 Homo sapiens, clone IMAGE:3455871, mRNA, partial cds | 0 |
| 560 | RG:730402:10010:H01 | MA159:H01 | 0.225 | BC000633 | gi 12653696 gb BC000633.1BC000633 Homo sapiens, TTK protein kinase, clone MGC:865 IMAGE:3343925, mRNA, complete cds | 2.1E-38 |
| 561 | RG:1047541:10012:C07 | MA161:C07 | | AF156965 | gi 5731112 gb AF156965.1AF156965 Homo sapiens translocon-associated protein alpha subunit mRNA, complete cds | 0 |
| 562 | RG:1161753:10012:E07 | MA161:E07 | | X12883 | gi 30310 emb X12883.1HSCYKT18 Human mRNA for cytokeratin 18 | 0 |
| 563 | I:1218464:17B01:E01 | MA93:E01 | 0.47248 | | | |

Table 3

| SEQ ID NO | Clone ID | MAClone ID | Mask Prent | GBHit | GBDescription | GBScore |
|-----------|----------------------|------------|------------|-----------|---|----------|
| 564 | I:958633:17B01:G07 | MA93:G07 | | AF267862 | gi 12006050 gb AF267862.1AF267862 Homo sapiens DC44 mRNA, complete cds | 1.8E-180 |
| 565 | I:1602726:09B01:B07 | MA137:B07 | 0.45675 | | | |
| 566 | RG:205212:10007:B01 | MA156:B01 | | AF069747 | gi 4106379 gb AF069747.1AF069747 Homo sapiens MTG8-like protein MTGR1a mRNA, complete cds | 6.1E-227 |
| 567 | RG:207395:10007:B07 | MA156:B07 | | Z74616 | gi 1418929 cemb Z74616.1HSPPA2ICO H.sapiens mRNA for prepro-alpha2(I) collagen | 0 |
| 568 | I:349535:16B02:G01 | MA90:G01 | 0.19957 | | | |
| 569 | I:2323525:16A02:H01 | MA88:H01 | 0.30114 | | | |
| 570 | I:1965049:16B02:D07 | MA90:D07 | | AF113007 | gi 6642737 gb AF113007.1AF113007 Homo sapiens PRO0066 mRNA, complete cds | 4.1E-162 |
| 571 | I:2054436:16A02:G07 | MA88:G07 | 0.15978 | | | |
| 572 | RG:1506197:10013:F01 | MA162:F01 | | NM_052841 | gi 17017992 ref NM_052841.2 Homo sapiens serine/threonine kinase 22C (spermiogenesis associated) (STK22C), mRNA | 2E-137 |
| 573 | RG:1871436:10015:G01 | MA164:G01 | | X60489 | gi 31099 cemb X60489.1HSEF1B Human mRNA for elongation factor-1-beta | 0 |
| 574 | RG:1705470:10015:B07 | MA164:B07 | | L38734 | gi 769675 gb L38734.1HUMHTK Homo sapiens hepatoma transmembrane kinase ligand (HTK ligand) mRNA, complete cds | 2.1E-282 |
| 575 | I:546910:17B02:B07 | MA94:B07 | | AK002212 | gi 7023953 dbj AK002212.1AK002212 Homo sapiens cDNA FLJ11350 fis, clone Y79AA1001647 | 3.3E-97 |
| 576 | I:1799023:09B02:F01 | MA138:F01 | | AK023003 | gi 10434717 dbj AK023003.1AK023003 Homo sapiens cDNA FLJ12941 fis, clone NT2RP2005116, moderately similar to PUTATIVE EUKARYOTIC TR | 2.5E-164 |
| 577 | I:2380380:09B02:H01 | MA138:H01 | | AF268037 | gi 8745546 gb AF268037.1AF268037 Homo sapiens C8ORF4 protein (C8ORF4) mRNA, complete cds | 0 |
| 578 | I:2319269:18A01:F02 | MA95:F02 | | AK022882 | gi 10434533 dbj AK022882.1AK022882 Homo sapiens cDNA FLJ12820 fis, clone NT2RP2002736 | 1.1E-206 |
| 579 | I:2296344:18A01:D08 | MA95:D08 | | AJ387747 | gi 6562532 cemb AJ387747.1HSA387747 Homo sapiens mRNA for sialin | 3.6E-225 |
| 580 | RG:155066:10006:E02 | MA155:E02 | | BC018851 | gi 17402989 gb BC018851.1BC018851 Homo sapiens, clone IMAGE:3141444, mRNA | 2.2E-279 |
| 581 | RG:180135:10006:G02 | MA155:G02 | | L37043 | gi 852056 gb L37043.1HUMCSNK1E Homo sapiens casein kinase I epsilon mRNA, complete cds | 0 |

Table 3

| SEQ ID NO | Clone ID | MAClone ID | Mask Prent | GBHit | GBDescription | GBScore |
|-----------|----------------------|------------|------------|----------|---|----------|
| 582 | RG:178093:10006:F08 | MA155:F08 | | AL117430 | gi 5911865 emb AL117430.1HSM800939 Homo sapiens mRNA; cDNA DKFZp434D156 (from clone DKFZp434D156); partial cds | 0 |
| 583 | RG:184042:10006:G08 | MA155:G08 | | BC017459 | gi 16907188 gb BC017459.1BC017459 Homo sapiens, clone IMAGE:4645230, mRNA | 5.3E-240 |
| 584 | I:1741643:16A01:A02 | MA87:A02 | | D38551 | gi 1531549 dbj D38551.1HUMORF005 Human mRNA for KIAA0078 gene, complete cds | 1.1E-209 |
| 585 | RG:928026:10012:B02 | MA161:B02 | | AL050147 | gi 4884153 emb AL050147.1HSM800223 Homo sapiens mRNA; cDNA DKFZp586E0820 (from clone DKFZp586E0820); partial cds | 1.3E-218 |
| 586 | RG:1032969:10012:C02 | MA161:C02 | | AF261717 | gi 8926204 gb AF261717.1AF261717 Homo sapiens SAR1 (SAR1) mRNA, complete cds | 0 |
| 587 | RG:1322660:10012:H02 | MA161:H02 | | L05144 | gi 189944 gb L05144.1HUMPHOCAR Homo sapiens (clone lamda-hPEC-3) phosphoenolpyruvate carboxykinase (PCK1) mRNA, complete cds | 5.3E-283 |
| 588 | RG:968474:10012:B08 | MA161:B08 | | Y11339 | gi 7576275 emb Y11339.2HSY11339 Homo sapiens mRNA for GalNAc alpha-2, 6-sialyltransferase I, long form | 1.7E-227 |
| 589 | RG:1047592:10012:C08 | MA161:C08 | | X05803 | gi 34080 emb X05803.1HSKERUV Human radiated keratinocyte mRNA 266 (keratin-related protein) | 1E-300 |
| 590 | I:617750:17B01:E08 | MA93:E08 | 0.19395 | | | |
| 591 | I:2808775:09B01:G02 | MA137:G02 | 0.40171 | | | |
| 592 | I:966692:18A02:B08 | MA96:B08 | 0.32029 | AK055949 | gi 16550804 dbj AK055949.1AK055949 Homo sapiens cDNA FLJ31387 fis, clone NT2NE1000018, weakly similar to SUPPRESSOR PROTEIN SRP40 | 3.7E-123 |
| 593 | RG:209240:10007:C02 | MA156:C02 | | BC001737 | gi 12804626 gb BC001737.1BC001737 Homo sapiens, clone IMAGE:3354010, mRNA, partial cds | 3E-192 |
| 594 | RG:223355:10007:D02 | MA156:D02 | | Z11696 | gi 23882 emb Z11696.1HS44KDAP H.sapiens 44kDa protein kinase related to rat ERK1 | 5.4E-252 |
| 595 | RG:267629:10007:H02 | MA156:H02 | | U73824 | gi 1857236 gb U73824.1HSU73824 Human p97 mRNA, complete cds | 3.2E-269 |
| 596 | I:2246234:16B02:C08 | MA90:C08 | | | | |
| 597 | RG:1696513:10015:B02 | MA164:B02 | 0.07275 | AF377330 | gi 14278713 gb AF377330.2AF377330 Homo sapiens urokinase-type plasminogen activator (PLAU) gene, complete cds | 0 |

Table 3

| SEQ ID NO | Clone ID | MAClone ID | Mask Prent | GBHit | GBDescription | GBScore |
|-----------|--------------------------|------------|------------|----------|---|----------|
| 598 | RG:1733895:10015:D0 2 | MA164:D02 | | BC009470 | gi 14495716 gb BC009470.1BC009470 Homo sapiens, protein kinase, interferon-inducible double stranded RNA dependent activator, clone | 0 |
| 599 | RG:1353930:10013:A08 | MA162:A08 | | U86453 | gi 2317893 gb U86453.1HSU86453 Human phosphatidylinositol 3-kinase catalytic subunit p110delta mRNA, complete cds | 6.4E-295 |
| 600 | RG:1881947:10015:G0 8 | MA164:G08 | | BC005858 | gi 13543399 gb BC005858.1BC005858 Homo sapiens, clone MGC:3255 IMAGE:3506187, mRNA, complete cds | 0 |
| 601 | RG:166575:10006:F03 | MA155:F03 | | AK057849 | gi 16553810 dbj AK057849.1AK05784 9 Homo sapiens cDNA FLJ25120 fis, clone CBR06020 | 1E-300 |
| 602 | I:1998994:16A01:A03 | MA87:A03 | | J04205 | gi 178686 gb J04205.1HUMANTLAA Human La protein mRNA, complete cds | 1.6E-258 |
| 603 | I:1953051:16A01:D03 | MA87:D03 | | BC004138 | gi 13278716 gb BC004138.1BC004138 Homo sapiens, ribosomal protein L6, clone MGC:1635 IMAGE:2823733, mRNA, complete cds | 2E-276 |
| 604 | I:518826:16A01:E03 | MA87:E03 | | BC007771 | gi 14043585 gb BC007771.1BC007771 Homo sapiens, dual specificity phosphatase 2, clone MGC:12703 IMAGE:4297852, mRNA, complete cds | 2.8E-266 |
| 605 | I:81490:16A01:B09 | MA87:B09 | | BC007942 | gi 14044027 gb BC007942.1BC007942 Homo sapiens, nucleolar autoantigen (55kD) similar to rat synaptonemal complex protein, clone MGC | 1.9E-270 |
| 606 | RG:1256163:10012:F03 | MA161:F03 | | M36501 | gi 177871 gb M36501.1HUMA2MGL Human alpha-2-macroglobulin mRNA, 3' end | 1E-300 |
| 607 | RG:1132085:10012:D0 9 | MA161:D09 | | BC006510 | gi 13676353 gb BC006510.1BC006510 Homo sapiens, Similar to cyclin B1, related sequence 1, clone MGC:2548 IMAGE:2963100, mRNA, compl | 0 |
| 608 | I:2132717:17B01:C09 | MA93:C09 | | AB058749 | gi 14017908 dbj AB058749.1AB05874 9 Homo sapiens mRNA for KIAA1846 protein, partial cds | 3.8E-256 |
| 609 | I:1998428:17B01:F09 | MA93:F09 | | AF115926 | gi 17998664 gb AF115926.1AF115926 Homo sapiens XAG-2 homolog long protein (HPC8) mRNA, complete cds | 6.9E-208 |
| 610 | RG:206694:10007:B03 | MA156:B03 | | X00588 | gi 31113 emb X00588.1HSEGFPRE Human mRNA for precursor of epidermal growth factor receptor | 1E-300 |

Table 3

| SEQ ID NO | Clone ID | MAClone ID | Mask Prent | GBHit | GBDescription | GBScore |
|-----------|----------------------|------------|------------|----------|---|----------|
| 611 | RG:261714:10007:F09 | MA156:F09 | | AF116618 | gi 7959738 gb AF116618.1AF116618 Homo sapiens PRO1038 mRNA, complete cds | 0 |
| 612 | I:1461515:16A02:C03 | MA88:C03 | 0.3525 | | | |
| 613 | I:338859:16A02:H03 | MA88:H03 | 0.27273 | | | |
| 614 | I:1425861:16A02:G09 | MA88:G09 | 0.4929 | | | |
| 615 | I:1928644:16B02:H09 | MA90:H09 | 0.34967 | AK055711 | gi 16550506 dbj AK055711.1AK055711 Homo sapiens cDNA FLJ31149 fis, clone IMR322001491, moderately similar to Rattus norvegicus tric | 7.1E-131 |
| 616 | RG:1404414:10013:C03 | MA162:C03 | | U01038 | gi 393016 gb U01038.1HSU01038 Human pLK mRNA, complete cds | 6.5E-277 |
| 617 | RG:1415437:10013:D03 | MA162:D03 | | BC001190 | gi 12654700 gb BC001190.1BC001190 Homo sapiens, Similar to creatine kinase, brain, clone MGC:3160 IMAGE:3354679, mRNA, complete cds | 0 |
| 618 | RG:1734353:10015:D03 | MA164:D03 | | BC002555 | gi 12803460 gb BC002555.1BC002555 Homo sapiens, CDC-like kinase 3, clone MGC:1777 IMAGE:3138580, mRNA, complete cds | 0 |
| 619 | RG:1872251:10015:G03 | MA164:G03 | | Y17151 | gi 4826562 emb Y17151.2HSY17151 Homo sapiens mRNA for multidrug resistance protein 3 (ABCC3) | 1.7E-31 |
| 620 | RG:1354408:10013:A09 | MA162:A09 | | AF257466 | gi 8453155 gb AF257466.1AF257466 Homo sapiens N-acetylneuraminic acid phosphate synthase mRNA, complete cds | 3.7E-290 |
| 621 | RG:1690198:10015:A09 | MA164:A09 | | X90563 | gi 1480099 emb X90563.1HSPARGA M H.sapiens mRNA for peroxisome proliferator activated receptor gamma | 0 |
| 622 | RG:1476452:10013:E09 | MA162:E09 | | BC007276 | gi 13938296 gb BC007276.1BC007276 Homo sapiens, Similar to heat shock cognate 71-kd protein, clone MGC:15597 IMAGE:3162067, mRNA, c | 1E-300 |
| 623 | I:2069305:09B02:F03 | MA138:F03 | | BC015139 | gi 15929410 gb BC015139.1BC015139 Homo sapiens, clone IMAGE:4040789, mRNA, partial cds | 0 |
| 624 | I:1966067:18B01:H04 | MA97:H04 | | AF062916 | gi 3941523 gb AF062916.1AF062916 Arabidopsis thaliana putative transcription factor (MYB92) mRNA, complete cds | 3.6E-22 |
| 625 | I:2128547:18B01:A10 | MA97:A10 | | AF151839 | gi 4929630 gb AF151839.1AF151839 Homo sapiens CGI-81 protein mRNA, complete cds | 4.6E-268 |

Table 3

| SEQ ID NO | Clone ID | MAClone ID | Mask Prent | GBHit | GBDescription | GBScore |
|-----------|----------------------|------------|------------|-----------|---|----------|
| 626 | RG:149960:10006:D04 | MA155:D04 | | BC017483 | gi 17028354 gb BC017483.1BC017483 Homo sapiens, clone IMAGE:3506553, mRNA | 3.9E-237 |
| 627 | RG:171569:10006:F04 | MA155:F04 | | M64174 | gi 190734 gb M64174.1HUMPTKJAK 1 Human protein-tyrosine kinase (JAK1) mRNA, complete cds | 1E-300 |
| 628 | RG:178638:10006:F10 | MA155:F10 | | BC004408 | gi 13325179 gb BC004408.1BC004408 Homo sapiens, Similar to high-mobility group 20B, clone MGC:11001 IMAGE:3638942, mRNA, complete c | 1.1E-225 |
| 629 | RG:195122:10006:H10 | MA155:H10 | | Z11695 | gi 23878 emb Z11695.1HS40KDAP H.sapiens 40 kDa protein kinase related to rat ERK2 | 4.3E-271 |
| 630 | I:814216:16A01:F10 | MA87:F10 | | BC006395 | gi 13623564 gb BC006395.1BC006395 Homo sapiens, cell division cycle 25B, clone MGC:12797 IMAGE:4135465, mRNA, complete cds | 9.3E-254 |
| 631 | RG:491163:10010:A04 | MA159:A04 | | BC008767 | gi 14250615 gb BC008767.1BC008767 Homo sapiens, Similar to acyl-Coenzyme A oxidase 1, palmitoyl, clone MGC:1198 IMAGE:3051501, mRNA | 9.3E-232 |
| 632 | RG:827185:10012:A04 | MA161:A04 | | AK055642 | gi 16550422 dbj AK055642.1AK055642 2 Homo sapiens cDNA FLJ31080 fis, clone HSYRA2001615, highly similar to Sus scrofa calcium/calmodu | 2.5E-251 |
| 633 | RG:1129102:10012:D04 | MA161:D04 | | NM_000975 | gi 15431289 ref NM_000975.2 Homo sapiens ribosomal protein L11 (RPL11), mRNA | 1E-300 |
| 634 | RG:730938:10010:H04 | MA159:H04 | | BC000580 | gi 12653606 gb BC000580.1BC000580 Homo sapiens, clone IMAGE:3162218, mRNA, partial cds | 2.1E-254 |
| 635 | RG:925984:10012:A10 | MA161:A10 | | J03358 | gi 339714 gb J03358.1HUMTKFER Human tyrosine kinase (FER) mRNA, complete cds | 1.2E-246 |
| 636 | RG:668442:10010:B10 | MA159:B10 | | X74764 | gi 433337 emb X74764.1HSRPTK H.sapiens mRNA for receptor protein tyrosine kinase | 0 |
| 637 | RG:1028911:10012:B10 | MA161:B10 | | U88666 | gi 1857943 gb U88666.1HSU88666 Homo sapiens serine kinase SRPK2 mRNA, complete cds | 1E-300 |
| 638 | RG:684866:10010:C10 | MA159:C10 | | X51521 | gi 31282 emb X51521.1HSEZRIN Human mRNA for ezrin | 1E-293 |

Table 3

| SEQ ID NO | Clone ID | MAClone ID | Mask Prent | GBHit | GBDescription | GBScore |
|-----------|----------------------|------------|------------|----------|---|----------|
| 639 | RG:1283076:10012:F10 | MA161:F10 | | BC007888 | gi 14043894 gb BC007888.1BC007888 Homo sapiens, eukaryotic translation initiation factor 2, subunit 2 (beta, 38kD), clone MGC:1417 | 0 |
| 640 | I:627654:17A01:G04 | MA91:G04 | | AF081192 | gi 3420798 gb AF081192.1AF081192 Homo sapiens histone H2A.F/Z variant (H2AV) mRNA, complete cds | 0 |
| 641 | I:1833801:17A01:D10 | MA91:D10 | | BC009836 | gi 14602636 gb BC009836.1BC009836 Homo sapiens, clone MGC:15133 IMAGE:4098463, mRNA, complete cds | 1.9E-270 |
| 642 | I:961473:17B01:H10 | MA93:H10 | 0.20615 | AK024678 | gi 10437017 dbj AK024678.1AK024678 Homo sapiens cDNA: FLJ21025 fis, clone CAE06758 | 2.7E-117 |
| 643 | I:2556708:09B01:B10 | MA137:B10 | | BC018807 | gi 17402954 gb BC018807.1BC018807 Homo sapiens, clone IMAGE:4861487, mRNA | 1.6E-55 |
| 644 | RG:243565:10007:D10 | MA156:D10 | | AF015254 | gi 4090840 gb AF015254.1AF015254 Homo sapiens serine/threonine kinase (STK-1) mRNA, complete cds | 8.4E-186 |
| 645 | RG:266649:10007:G10 | MA156:G10 | | AB034951 | gi 11526572 dbj AB034951.1AB034951 Homo sapiens HSC54 mRNA for heat shock cognate protein 54, complete cds | 1E-300 |
| 646 | I:2013513:16B02:B04 | MA90:B04 | | AF155913 | gi 6435129 gb AF155913.1AF155913 Mus musculus putative E1-E2 ATPase mRNA, complete cds | 3.7E-51 |
| 647 | I:2312442:16A02:B10 | MA88:B10 | 0.38737 | AK021945 | gi 10433249 dbj AK021945.1AK021945 Homo sapiens cDNA FLJ11883 fis, clone HEMBA1007178 | 1.9E-131 |
| 648 | I:2060626:16A02:D10 | MA88:D10 | | AK055800 | gi 16550622 dbj AK055800.1AK055800 Homo sapiens cDNA FLJ31238 fis, clone KIDNE2004864 | 1.1E-191 |
| 649 | RG:1415858:10013:D04 | MA162:D04 | | D85759 | gi 1526445 dbj D85759.1D85759 Homo sapiens mRNA for MNB protein kinase, complete cds | 4.8E-271 |
| 650 | RG:1517435:10013:F04 | MA162:F04 | | X13546 | gi 32328 emb X13546.1HSHMG17G Human HMG-17 gene for non-histone chromosomal protein HMG-17 | 6.7E-292 |
| 651 | RG:1914716:10015:H04 | MA164:H04 | | X13697 | gi 36414 emb X13697.1HSSBLA Human mRNA for ribonucleoprotein SS-B/La | 1E-300 |
| 652 | RG:1354528:10013:A10 | MA162:A10 | | AF197898 | gi 6166494 gb AF197898.1AF197898 Homo sapiens nemo-like kinase mRNA, complete cds | 6.7E-298 |

Table 3

| SEQ ID NO | Clone ID | MAClone ID | Mask Prent | GBHit | GBDescription | GBScore |
|-----------|----------------------|------------|------------|----------|--|----------|
| 653 | RG:1706414:10015:B10 | MA164:B10 | | M36501 | gi 177871 gb M36501.1HUMA2MGL Human alpha-2-macroglobulin mRNA, 3' end | 0 |
| 654 | I:1998510:17A02:C04 | MA92:C04 | | BC004872 | gi 13436100 gb BC004872.1BC004872 Homo sapiens, clone MGC:11034 IMAGE:3677618, mRNA, complete cds | 1.4E-252 |
| 655 | I:899118:17B02:G10 | MA94:G10 | | AK055564 | gi 16550323 dbj AK055564.1AK055564 Homo sapiens cDNA FLJ31002 fis, clone HLUNG2000004 | 4E-159 |
| 656 | I:2680168:09B02:B04 | MA138:B04 | | AL050071 | gi 4884302 emb AL050071.1HSM8003 96 Homo sapiens mRNA; cDNA DKFZp566B0846 (from clone DKFZp566B0846); partial cds | 0 |
| 657 | I:1354558:09B02:E04 | MA138:E04 | | AK054675 | gi 16549267 dbj AK054675.1AK054675 Homo sapiens cDNA FLJ30113 fis, clone BNGH42000474 | 1E-156 |
| 658 | I:1665871:09B02:F10 | MA138:F10 | | AF288394 | gi 12620197 gb AF288394.1AF288394 Homo sapiens Clorf19 mRNA, partial cds | 0 |
| 659 | I:1922084:18B01:C05 | MA97:C05 | | AK000057 | gi 7019894 dbj AK000057.1AK000057 Homo sapiens cDNA FLJ20050 fis, clone COL00688 | 1.3E-246 |
| 660 | I:2307946:18A01:B11 | MA95:B11 | | BC016150 | gi 16740553 gb BC016150.1BC016150 Homo sapiens, Similar to CAP-binding protein complex interacting protein 2, clone IMAGE:3637027, | 8.9E-226 |
| 661 | I:1923572:18B01:C11 | MA97:C11 | | AL049959 | gi 4884211 emb AL049959.1HSM8003 04 Homo sapiens mRNA; cDNA DKFZp564K1023 (from clone DKFZp564K1023) | 2.3E-154 |
| 662 | RG:171993:10006:F05 | MA155:F05 | 0.31835 | AK057735 | gi 16553657 dbj AK057735.1AK057735 5 Homo sapiens cDNA FLJ25006 fis, clone CBL00989 | 3.9E-142 |
| 663 | RG:129317:10006:B11 | MA155:B11 | | AF103796 | gi 4185795 gb AF103796.1AF103796 Homo sapiens placenta-specific ATP-binding cassette transporter (ABCP) mRNA, complete cds | 1E-300 |
| 664 | RG:153244:10006:D11 | MA155:D11 | | L06139 | gi 292823 gb L06139.1HUMTEKRPT K Homo sapiens receptor protein-tyrosine kinase (TEK) mRNA, complete cds | 1.1E-299 |
| 665 | RG:196236:10006:H11 | MA155:H11 | | AF359246 | gi 13991617 gb AF359246.1AF359246 Homo sapiens fibroblast growth factor receptor 4 variant mRNA, complete cds | 5E-249 |

Table 3

| SEQ ID NO | Clone ID | MAClone ID | Mask Prent | GBHit | GBDescription | GBScore |
|-----------|----------------------|------------|------------|----------|---|----------|
| 666 | I:557538:16A01:C11 | MA87:C11 | | BC013142 | gi 15341912 gb BC013142.1BC013142 Homo sapiens, interleukin 1, alpha, clone MGC:9225 IMAGE:3875617, mRNA, complete cds | 1.1E-240 |
| 667 | I:782235:16A01:F11 | MA87:F11 | | K01228 | gi 180391 gb K01228.1HUMCG1PA1 Human proalpha 1 (I) chain of type I procollagen mRNA (partial) | 9E-251 |
| 668 | RG:1257341:10012:F05 | MA161:F05 | | BC007952 | gi 14044057 gb BC007952.1BC007952 Homo sapiens, pyruvate kinase, muscle, clone MGC:14360 IMAGE:4299213, mRNA, complete cds | 1E-300 |
| 669 | RG:727387:10010:G05 | MA159:G05 | | BC001413 | gi 13937593 gb BC001413.1BC001413 Homo sapiens, clone IMAGE:3140866, mRNA | 0 |
| 670 | RG:1145235:10012:D11 | MA161:D11 | | BC007540 | gi 14043108 gb BC007540.1BC007540 Homo sapiens, clone IMAGE:3609337, mRNA, partial cds | 3.4E-71 |
| 671 | RG:725145:10010:F11 | MA159:F11 | | AJ000512 | gi 2463200 emb AJ000512.1HSSGK Homo sapiens sgk gene | 8.4E-264 |
| 672 | RG:740079:10010:H11 | MA159:H11 | | M14505 | gi 456426 gb M14505.1HUMCDPK Human (clone PSK-J3) cyclin-dependent protein kinase mRNA, complete cds., | 0 |
| 673 | I:1873176:09B01:E05 | MA137:E05 | | BC001909 | gi 12804912 gb BC001909.1BC001909 Homo sapiens, clone IMAGE:3537447, mRNA, partial cds | 0 |
| 674 | I:2081974:09B01:D11 | MA137:D11 | | AK057078 | gi 16552660 dbj AK057078.1AK057078 Homo sapiens cDNA FLJ32516 fis, clone SMINT1000103, highly similar to Homo sapiens ankyrin repea | 0 |
| 675 | I:2107723:18A02:G05 | MA96:G05 | | AK000193 | gi 7020116 dbj AK000193.1AK000193 Homo sapiens cDNA FLJ20186 fis, clone COLF0428 | 1.2E-265 |
| 676 | RG:207777:10007:B11 | MA156:B11 | | X04714 | gi 28779 emb X04714.1HSAPOB10 Human mRNA for apolipoprotein B-100 (apoB-100) | 1E-300 |
| 677 | RG:221172:10007:C11 | MA156:C11 | | M14333 | gi 181171 gb M14333.1HUMCSYNA Homo sapiens c-syn protooncogene mRNA, complete cds | 2.2E-97 |
| 678 | I:1968436:16B02:C05 | MA90:C05 | 0.33281 | | | |
| 679 | I:2060973:16A02:G11 | MA88:G11 | | AB035384 | gi 7619897 dbj AB035384.1AB035384 Homo sapiens mRNA for SRp25 nuclear protein, complete cds | 2.6E-291 |
| 680 | RG:1369494:10013:B05 | MA162:B05 | | AF008552 | gi 2979629 gb AF008552.1AF008552 Homo sapiens aurora-related kinase 2 (ARK2) mRNA, complete cds | 1E-300 |
| 681 | RG:1752177:10015:E05 | MA164:E05 | | | | |

Table 3

| SEQ ID NO | Clone ID | MAClone ID | Mask Prent | GBHit | GBDescription | GBScore |
|-----------|----------------------|------------|------------|-----------|---|----------|
| 682 | RG:1519327:10013:F05 | MA162:F05 | | X66364 | gi 36620 cmb X66364.1HSSSTHPKE H.sapiens mRNA PSSALRE for serine/threonine protein kinase | 0 |
| 683 | RG:1694569:10015:A11 | MA164:A11 | | X06323 | gi 34753 cmb X06323.1HSMRL3R Human MRL3 mRNA for ribosomal protein L3 homologue (MRL3 = mammalian ribosome L3) | 0 |
| 684 | RG:1839794:10015:E11 | MA164:E11 | | U28387 | gi 881950 gb U28387.1HISU28387 Human hexokinase II pseudogene, complete cds | 5.2E-175 |
| 685 | I:514124:17A02:D05 | MA92:D05 | | AJ420434 | gi 17066298 cmb AJ420434.1HSA420434 Homo sapiens mRNA full length insert cDNA clone EUROIMAGE 1499812 | 6.5E-114 |
| 686 | I:997782:17A02:G05 | MA92:G05 | | AB018346 | gi 3882326 dbj AB018346.1AB018346 Homo sapiens mRNA for KIAA0803 protein, partial cds | 2.8E-185 |
| 687 | I:1709364:09B02:F11 | MA138:F11 | | NM_018440 | gi 16753228 ref NM_018440.2 Homo sapiens phosphoprotein associated with glycosphingolipid-enriched microdomains (PAG), mRNA | 6.4E-180 |
| 688 | I:2004896:18A01:C06 | MA95:C06 | | AK023512 | gi 10435467 dbj AK023512.1AK023512 Homo sapiens cDNA FLJ13450 fis, clone PLACE1003027, highly similar to Homo sapiens mRNA for KIAA | 2E-117 |
| 689 | RG:172982:10006:F06 | MA155:F06 | | D83492 | gi 2281007 dbj D83492.1D83492 Homo sapiens mRNA for Eph-family protein, complete cds | 0 |
| 690 | RG:180978:10006:G06 | MA155:G06 | | D83492 | gi 2281007 dbj D83492.1D83492 Homo sapiens mRNA for Eph-family protein, complete cds | 0 |
| 691 | RG:129528:10006:B12 | MA155:B12 | | U00238 | gi 404860 gb U00238.1U00238 Homo sapiens glutamine PRPP amidotransferase (GPAT) mRNA, complete cds | 1.6E-286 |
| 692 | RG:186511:10006:G12 | MA155:G12 | | AK000250 | gi 7020204 dbj AK000250.1AK000250 Homo sapiens cDNA FLJ20243 fis, clone COLF6418, highly similar to NUCL_HUMAN NUCLEOLIN | 3.4E-204 |
| 693 | I:2005910:16B01:B06 | MA89:B06 | | AJ340058 | gi 15884476 cmb AJ340058.1HSA340058 Homo sapiens genomic sequence surrounding NotI site, clone NR5-ID23C | 2.8E-110 |
| 694 | I:620871:16A01:D06 | MA87:D06 | | BC007422 | gi 13938544 gb BC007422.1BC007422 Homo sapiens, acid phosphatase 1, soluble, clone MGC:3499 IMAGE:3027769, mRNA, complete cds | 3.5E-250 |

Table 3

| SEQ ID NO | Clone ID | MAClone ID | Mask Prent | GBHit | GBDescription | GBScore |
|-----------|---------------------|------------|------------|----------|---|----------|
| 695 | I:1920819:16A01:A12 | MA87:A12 | | BC015123 | gi 15929378 gb BC015123.1BC015123 Homo sapiens, Similar to retinoblastoma-binding protein 4, clone IMAGE:3686783, mRNA, partial cds | 8.2E-276 |
| 696 | I:990375:16A01:E12 | MA87:E12 | | M10050 | gi 182355 gb M10050.1HUMFABPL Human liver fatty acid binding protein (FABP) mRNA, complete cds | 1.8E-267 |
| 697 | I:690313:16A01:G12 | MA87:G12 | | BC017201 | gi 16877960 gb BC017201.1BC017201 Homo sapiens, insulin-like growth factor binding protein 7, clone MGC:3699 IMAGE:3632247, mRNA, c | 3.8E-200 |
| 698 | RG:878195:10012:A06 | MA161:A06 | | M83653 | gi 179635 gb M83653.1HUMC1PHTY R Homo sapiens cytoplasmic phosphotyrosyl protein phosphatase (clone type 1) complete cds | 0 |
| 699 | RG:687128:10010:D06 | MA159:D06 | | S75546 | gi 914097 gb S75546.1S75546 protein kinase PRK1 [human, fetal brain, mRNA, 3001 nt] | 1.7E-38 |
| 700 | I:884855:17B01:D06 | MA93:D06 | | AK055393 | gi 16550110 dbj AK055393.1AK055393 Homo sapiens cDNA FLJ30831 fis, clone FEBRA2001989 | 4E-228 |
| 701 | I:1218621:17B01:F06 | MA93:F06 | | | | |
| 702 | I:620371:17A01:H06 | MA91:H06 | | BC016472 | gi 16741273 gb BC016472.1BC016472 Homo sapiens, clone MGC:17244 IMAGE:4178911, mRNA, complete cds | 1E-203 |
| 703 | I:1681610:09B01:D06 | MA137:D06 | | AK055827 | gi 16550653 dbj AK055827.1AK055827 Homo sapiens cDNA FLJ31265 fis, clone KIDNE2006030, moderately similar to Gallus gallus syndesmo | 1.3E-124 |
| 704 | RG:265206:10007:G06 | MA156:G06 | | U25975 | gi 984304 gb U25975.1HSU25975 Human serine kinase (hPAK65) mRNA, partial cds | 1E-231 |
| 705 | RG:268073:10007:H06 | MA156:H06 | | AF226044 | gi 9295326 gb AF226044.1AF226044 Homo sapiens HSNFRK (HSNFRK) mRNA, complete cds | 9.8E-118 |
| 706 | I:2117221:16A02:F06 | MA88:F06 | 0.22151 | AF130089 | gi 11493482 gb AF130089.1AF130089 Homo sapiens clone FLB9440 PRO2550 mRNA, complete cds | 9.5E-152 |
| 707 | I:1760693:16B02:G06 | MA90:G06 | | | | |
| 708 | I:776793:16B02:B12 | MA90:B12 | | AF086524 | gi 3483869 gb AF086524.1HUMZE04F10 Homo sapiens full length insert cDNA clone ZE04F10 | 1.5E-283 |

Table 3

| SEQ ID NO | Clone ID | MA Clone ID | Mask Prent | GBHit | GBDescription | GBScore |
|-----------|----------------------|-------------|------------|-----------|---|----------|
| 709 | RG:1405692:10013:C06 | MA162:C06 | | X60489 | gi 31099 emb X60489.1HSEF1B Human mRNA for elongation factor-1-beta | 0 |
| 710 | RG:1707747:10015:B12 | MA164:B12 | | M29536 | gi 182066 gb M29536.1HUMELF2 Human translational initiation factor 2 beta subunit (eIF-2-beta) mRNA, complete cds | 0 |
| 711 | RG:1722789:10015:C12 | MA164:C12 | | AF183421 | gi 9963780 gb AF183421.1AF183421 Homo sapiens small GTP-binding protein rab22b mRNA, complete cds | 0 |
| 712 | I:2112348:17B02:E06 | MA94:E06 | | AK026529 | gi 10439407 dbj AK026529.1AK026529 Homo sapiens cDNA: FLJ22876 fis, clone KAT02954, highly similar to AF056183 Homo sapiens WS beta | 1.7E-196 |
| 713 | I:630458:17A02:F06 | MA92:F06 | | AK025537 | gi 10438082 dbj AK025537.1AK025537 Homo sapiens cDNA: FLJ21884 fis, clone HEP02863 | 7.2E-211 |
| 714 | I:901577:17A02:H06 | MA92:H06 | | AK000771 | gi 7021067 dbj AK000771.1AK000771 Homo sapiens cDNA FLJ20764 fis, clone COL08503 | 2.3E-195 |
| 715 | I:2298081:17B02:E12 | MA94:E12 | | AL080169 | gi 5262637 emb AL080169.1HSM800688 Homo sapiens mRNA; cDNA DKFZp434C171 (from clone DKFZp434C171); partial cds | 0 |
| 716 | I:2718565:09B02:H12 | MA138:H12 | | AF207600 | gi 9998951 gb AF207600.2AF207600 Homo sapiens ethanolamine kinase (EK11) mRNA, complete cds | 3.2E-253 |
| 717 | M00056237C:E03 | MA181:A01 | 0.8773 | U27317 | gi 9989705 gb U27317.2HSHSD11K1 Homo sapiens 11 beta-hydroxysteroid dehydrogenase 2 (HSD11B2) gene, complete cds | 7.9E-23 |
| 718 | M00055261C:F04 | MA197:E01 | | NM_033643 | gi 16117795 ref NM_033643.1 Homo sapiens ribosomal protein L36 (RPL36), transcript variant 1, mRNA | 8.3E-223 |
| 719 | M00055353D:A04 | MA197:D07 | | BC006794 | gi 13905021 gb BC006794.1BC006794 Homo sapiens, Similar to interferon induced transmembrane protein 3 (1-8U), clone MGC:5225 IMAGE: | 1.1E-156 |
| 720 | M00055357B:B10 | MA197:H07 | | BC006794 | gi 13905021 gb BC006794.1BC006794 Homo sapiens, Similar to interferon induced transmembrane protein 3 (1-8U), clone MGC:5225 IMAGE: | 3E-275 |
| 721 | M00056386D:H12 | MA173:C01 | | BC007700 | gi 14712760 gb BC007700.1BC007700 Homo sapiens, clone IMAGE:3954272, mRNA | 6.1E-180 |

Table 3

| SEQ ID NO | Clone ID | MAClone ID | Mask Prent | GBHit | GBDescription | GBScore |
|-----------|----------------|------------|------------|-----------|---|----------|
| 722 | M00056394B:B04 | MA173:D01 | | BC006791 | gi 13905015 gb BC006791.1BC006791 Homo sapiens, ribosomal protein L10a, clone MGC:5203 IMAGE:2901249, mRNA, complete cds | 1E-175 |
| 723 | M00056395A:B04 | MA173:E01 | | BC016835 | gi 16877126 gb BC016835.1BC016835 Homo sapiens, Similar to synaptophysin-like protein, clone MGC:10011 IMAGE:3883697, mRNA, complet | 4.2E-55 |
| 724 | M00056396B:G05 | MA173:F01 | | AK026171 | gi 10438934 dbj AK026171.1AK026171 Homo sapiens cDNA: FLJ22518 fis, clone HRC12216, highly similar to AF151069 Homo sapiens HSPC235 | 2.9E-94 |
| 725 | M00056137A:A05 | MA180:G01 | | | | |
| 726 | M00056401C:C03 | MA173:H01 | | L20688 | gi 404044 gb L20688.1HUMLYGDI Human GDP-dissociation inhibitor protein (Ly-GDI) mRNA, complete cds | 6.4E-267 |
| 727 | M00056484A:F06 | MA173:E07 | | NM_003145 | gi 6552341 ref NM_003145.2 Homo sapiens signal sequence receptor, beta (translocon-associated protein beta) (SSR2), mRNA | 1.3E-252 |
| 728 | M00056193B:C11 | MA180:F07 | | AF119905 | gi 7770246 gb AF119905.1AF119905 Homo sapiens PRO2853 mRNA, complete cds | 4.6E-193 |
| 729 | M00056484B:B07 | MA173:G07 | | AF203815 | gi 6979641 gb AF203815.1AF203815 Homo sapiens alpha gene sequence | 6.6E-214 |
| 730 | M00056193B:D06 | MA180:G07 | | AF004162 | gi 3046385 gb AF004162.1AF004162 Homo sapiens nickel-specific induction protein (Cap43) mRNA, complete cds | 8.3E-201 |
| 731 | M00056194B:G06 | MA180:H07 | | BC016834 | gi 16877123 gb BC016834.1BC016834 Homo sapiens, clone IMAGE:3883264, mRNA, partial cds | 2.5E-294 |
| 732 | M00054633D:B07 | MA187:A01 | | BC018210 | gi 17390469 gb BC018210.1BC018210 Homo sapiens, tubulin-specific chaperone a, clone MGC:9129 IMAGE:3861138, mRNA, complete cds | 7.9E-279 |
| 733 | M00054633D:E06 | MA187:B01 | | X52003 | gi 311379 emb X52003.1HSPS2MKN H.sapiens pS2 protein gene | 3E-275 |
| 734 | M00054848A:C03 | MA189:H01 | | NM_001010 | gi 17158043 ref NM_001010.2 Homo sapiens ribosomal protein S6 (RPS6), mRNA | 3.6E-287 |

Table 3

| SEQ ID NO | Clone ID | MAClone ID | Mask Prent | GBHit | GBDescription | GBScore |
|-----------|----------------|------------|------------|-----------|--|----------|
| 735 | M00054882C:C06 | MA189:A07 | | BC000915 | gi 14705283 gb BC000915.2BC000915 Homo sapiens, PDZ and LIM domain 1 (clfin), clone MGC:5344 IMAGE:2985229, mRNA, complete cds | 5.3E-283 |
| 736 | M00054678D:A03 | MA187:C07 | | BC015564 | gi 15990405 gb BC015564.1BC015564 Homo sapiens, cold shock domain protein A, clone MGC:12695 IMAGE:4137643, mRNA, complete cds | 7.8E-279 |
| 737 | M00054679B:B03 | MA187:D07 | | BC015642 | gi 15990506 gb BC015642.1BC015642 Homo sapiens, Similar to serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antiproteina | 4.8E-277 |
| 738 | M00054680B:D06 | MA187:G07 | | BC009623 | gi 16307089 gb BC009623.1BC009623 Homo sapiens, Similar to nucleophosmin (nucleolar phosphoprotein B23, numatrin), clone MGC:17308 | 8.4E-279 |
| 739 | M00054680C:A06 | MA187:H07 | | U28387 | gi 881950 gb U28387.1HSU28387 Human hexokinase II pseudogene, complete cds | 9E-83 |
| 740 | M00057176B:F11 | MA193:B01 | | BC000419 | gi 12653300 gb BC000419.1BC000419 Homo sapiens, catechol-O-methyltransferase, clone MGC:8663 IMAGE:2964400, mRNA, complete cds | 1.1E-296 |
| 741 | M00057181A:D01 | MA193:C01 | | AY008283 | gi 15192138 gb AY008283.1 Homo sapiens porimin mRNA, complete cds | 4.9E-196 |
| 742 | M00057219D:B04 | MA193:D07 | | NM_001015 | gi 14277698 ref NM_001015.2 Homo sapiens ribosomal protein S11 (RPS11), mRNA | 3.4E-175 |
| 743 | M00042341A:D12 | MA167:A01 | | NM_002153 | gi 4504502 ref NM_002153.1 Homo sapiens hydroxysteroid (17-beta) dehydrogenase 2 (HSD17B2), mRNA | 8.3E-123 |
| 744 | M00042433B:G09 | MA171:B01 | | AJ295637 | gi 9581767 emb AJ295637.1HSA295637 7 Homo sapiens mRNA for URIM protein | 1.2E-221 |
| 745 | M00042435A:F08 | MA171:D01 | | BC014048 | gi 15559357 gb BC014048.1BC014048 Homo sapiens, clone IMAGE:3348134, mRNA, partial cds | 4.6E-122 |
| 746 | M00042437B:G03 | MA171:E01 | | X59315 | gi 33247 emb X59315.1HSIGKL012 H.sapiens gene for Ig kappa light chain variable region "012" | 1.5E-119 |

Table 3

| SEQ ID NO | Clone ID | MAClone ID | Mask Prent | GBHit | GBDescription | GBScore |
|-----------|----------------|------------|------------|-----------|---|----------|
| 747 | M00042525D:E07 | MA167:F01 | | BC005982 | gi 13543665 gb BC005982.1BC005982 Homo sapiens, peptidylprolyl isomerase A (cyclophilin A), clone MGC:14681 IMAGE:4109260, mRNA, co | 1.4E-105 |
| 748 | M00042438B:D01 | MA171:F01 | | NM_004063 | gi 16507959 ref NM_004063.2 Homo sapiens cadherin 17, LI cadherin (liver-intestine) (CDH17), mRNA | 6.1E-264 |
| 749 | M00042529C:G07 | MA167:G01 | | L02785 | gi 291963 gb L02785.1HUMDRA Homo sapiens colon mucosa-associated (DRA) mRNA, complete cds | 5.8E-261 |
| 750 | M00042529D:B12 | MA167:H01 | 0.07368 | BC007011 | gi 13937818 gb BC007011.1BC007011 Homo sapiens, clone MGC:12335 IMAGE:3686576, mRNA, complete cds | 2.1E-145 |
| 751 | M00042700A:E05 | MA167:A07 | | U07550 | gi 469170 gb U07550.1HSU07550 Human chaperonin 10 mRNA, complete cds | 4.1E-212 |
| 752 | M00042777D:G05 | MA171:B07 | | AY007243 | gi 12621025 gb AY007243.1 Homo sapiens regenerating gene type IV mRNA, complete cds | 6.1E-264 |
| 753 | M00042781C:F03 | MA171:D07 | | BC016753 | gi 16876954 gb BC016753.1BC016753 Homo sapiens, clone MGC:1138 IMAGE:2987963, mRNA, complete cds | 3.7E-259 |
| 754 | M00042783C:F10 | MA171:E07 | 0.80366 | | | |
| 755 | M00042702D:B02 | MA167:F07 | | AJ010446 | gi 3954892 emb AJ010446.1HSA010446 Homo sapiens mRNA for immunoglobulin kappa light chain,anti-RhD, therad 24 | 2.8E-154 |
| 756 | M00042785B:F11 | MA171:H07 | | AF254415 | gi 13897565 gb AF254415.1AF254415 Homo sapiens gastrointestinal secretory protein GISP mRNA, complete cds | 3.9E-209 |
| 757 | M00056566C:C03 | MA174:A07 | | NM_031901 | gi 16950594 ref NM_031901.2 Homo sapiens mitochondrial ribosomal protein S21 (MRPS21), transcript variant 1, nuclear gene encoding | 1.4E-255 |
| 758 | M00056567B:A09 | MA174:C07 | | BC000396 | gi 12653254 gb BC000396.1BC000396 Homo sapiens, ubiquitin-conjugating enzyme E2N (homologous to yeast UBC13), clone MGC:8489 IMAGE: | 1E-293 |
| 759 | M00056569B:D09 | MA174:G07 | | U61267 | gi 1418285 gb U61267.1HSU61267 Homo sapiens putative splice factor transformer2-beta mRNA, complete cds | 4.4E-243 |

Table 3

| SEQ ID NO | Clone ID | MAClone ID | Mask Prent | GBHit | GBDescription | GBScore |
|-----------|---------------------|------------|------------|-----------|---|----------|
| 760 | M00056571D:E05 | MA174:H07 | | BC017696 | gi 17389285 gb BC017696.1BC017696 Homo sapiens, Similar to RIKEN cDNA 2410075D05 gene, clone MGC:21057 IMAGE:4393374, mRNA, complct | 6.6E-239 |
| 761 | RG:376801:10009:C01 | MA158:C01 | | AB017642 | gi 4519628 dbj AB017642.1AB017642 Homo sapiens mRNA for oxidative-stress responsive 1, complete cds | 8.9E-282 |
| 762 | RG:365436:10009:B07 | MA158:B07 | | AK022055 | gi 10433374 dbj AK022055.1AK022055 Homo sapiens cDNA FLJ11993 fis, clone HEMBB1001429, highly similar to Homo sapiens leucine amino | 1.1E-290 |
| 763 | RG:416839:10009:D07 | MA158:D07 | | AK026432 | gi 10439295 dbj AK026432.1AK026432 Homo sapiens cDNA: FLJ22779 fis, clone KAIA1741 | 0 |
| 764 | RG:784224:10011:E07 | MA160:E07 | | L03840 | gi 182570 gb L03840.1HUMFGFR4X Human fibroblast growth factor receptor 4 (FGFR4) mRNA, complete cds | 7.3E-258 |
| 765 | RG:796852:10011:G07 | MA160:G07 | | AF087909 | gi 10121889 gb AF087909.1AF087909 Homo sapiens NIMA-related kinase 6 (NEK6) mRNA, complete cds | 4.4E-271 |
| 766 | M00043412A:F04 | MA184:E01 | | NM_000993 | gi 15812219 ref NM_000993.2 Homo sapiens ribosomal protein L31 (RPL31), mRNA | 8.3E-158 |
| 767 | M00057273B:H10 | MA182:H01 | | AB042820 | gi 11041627 dbj AB042820.1AB042820 Homo sapiens RPL6 gene for ribosomal protein L6, complete cds | 5.6E-41 |
| 768 | M00054506C:B10 | MA184:B07 | | NM_001012 | gi 4506742 ref NM_001012.1 Homo sapiens ribosomal protein S8 (RPS8), mRNA | 2.6E-185 |
| 769 | M00054507D:G03 | MA184:F07 | | U19765 | gi 790570 gb U19765.1HSU19765 Human nucleic acid binding protein gene, complete cds | 1.5E-221 |
| 770 | M00054935B:B03 | MA198:E01 | 0.06563 | NM_001644 | gi 5921993 ref NM_001644.2 Homo sapiens apolipoprotein B mRNA editing enzyme, catalytic polypeptide 1 (APOBEC1), transcript variant | 1.2E-128 |
| 771 | M00054935D:C11 | MA198:H01 | | NM_002026 | gi 16933541 ref NM_002026.1 Homo sapiens fibronectin 1 (FN1), transcript variant 1, mRNA | 1.1E-190 |
| 772 | M00054976A:E09 | MA198:D07 | | BC017189 | gi 16877928 gb BC017189.1BC017189 Homo sapiens, myo-inositol 1-phosphate synthase A1, clone MGC:726 IMAGE:3140452, mRNA, complete c | 2.7E-188 |
| 773 | M00055788B:F08 | MA170:C07 | | V00662 | gi 13003 emb V00662.1MIHSXX H.sapiens mitochondrial genome | 1.3E-165 |

Table 3

| SEQ ID NO | Clone ID | MAClone ID | Mask Prent | GBHit | GBDescription | GBScore |
|-----------|----------------|------------|------------|-----------|---|----------|
| 774 | M00055791A:E10 | MA170:G07 | | X01117 | gi 57149 emb X01117.1RNRRA06 Rat 18S rRNA sequence | 7E-92 |
| 775 | M00055224C:H11 | MA196:E07 | | BC008952 | gi 14286301 gb BC008952.1BC008952 Homo sapiens, lactate dehydrogenase B, clone MGC:3600 IMAGE:3028947, mRNA, complete cds | 5E-171 |
| 776 | M00055932A:C02 | MA179:B01 | | BC019362 | gi 17939458 gb BC019362.1BC019362 Homo sapiens, guanine nucleotide binding protein (G protein), beta polypeptide 2-like 1, clone MG | 2.1E-226 |
| 777 | M00056908A:F12 | MA177:C01 | 0.86486 | | | |
| 778 | M00055935D:B06 | MA179:D01 | | D17041 | gi 598766 dbj D17041.1HUMD3F06M 5 Human HepG2 partial cDNA, clone hmd3f06m5 | 3.3E-182 |
| 779 | M00056908D:D08 | MA177:E01 | | AK026649 | gi 10439547 dbj AK026649.1AK026649 Homo sapiens cDNA: FLJ22996 fis, clone KAT11938 | 2.3E-154 |
| 780 | M00055942B:F08 | MA179:F01 | | X98311 | gi 1524059 emb X98311.1HSCGM2A NT H.sapiens mRNA for carcinoembryonic antigen family member 2, CGM2 | 5.9E-196 |
| 781 | M00056910A:B07 | MA177:G01 | | BC009599 | gi 16307042 gb BC009599.1BC009599 Homo sapiens, clone MGC:14690 IMAGE:4134557, mRNA, complete cds | 8.3E-254 |
| 782 | M00056952B:C08 | MA177:H07 | | Z85181 | gi 1834892 emb Z85181.1HSZ85181 H.sapiens Ig lambda light chain variable region gene (6-09OIIA61) rearranged; Ig-Light-Lambda; VLam | 8E-186 |
| 783 | M00054728C:E03 | MA188:A01 | | M34664 | gi 184411 gb M34664.1HUMHSP60A Human chaperonin (HSP60) mRNA, complete cds | 1.3E-283 |
| 784 | M00054728D:E06 | MA188:B01 | | X16064 | gi 37495 emb X16064.1HSTUMP Human mRNA for translationally controlled tumor protein | 1E-300 |
| 785 | M00054731C:H01 | MA188:H01 | | X73502 | gi 406853 emb X73502.1HSENCY20 H. Sapiens mRNA for cytokeratin 20 | 1.9E-267 |
| 786 | M00054778B:A12 | MA188:D07 | | AJ276249 | gi 7362984 emb AJ276249.1HSA276249 Homo sapiens partial mRNA, clone c1-10c16 | 2E-91 |
| 787 | M00054778C:D08 | MA188:F07 | | NM_002137 | gi 14043073 ref NM_002137.2 Homo sapiens heterogeneous nuclear ribonucleoprotein A2/B1 (HNRPA2B1), transcript variant A2, mRNA | 1.8E-34 |

Table 3

| SEQ ID NO | Clone ID | MAClone ID | Mask Prent | GBHit | GBDescription | GBScore |
|-----------|----------------|------------|------------|-----------|---|----------|
| 788 | M00054780A:G06 | MA188:H07 | | BC000035 | gi 12652584 gb BC000035.1BC000035 Homo sapiens, CGI-89 protein, clone MGC:845 IMAGE:3506601, mRNA, complete cds | 3.6E-287 |
| 789 | M00042899D:D02 | MA168:A01 | | Y00339 | gi 29586 emb Y00339.1HSCA2 Human mRNA for carbonic anhydrase II (EC 4.2.1.1) | 1.5E-233 |
| 790 | M00042831B:G10 | MA172:C01 | | AK024740 | gi 10437104 dbj AK024740.1AK024740 Homo sapiens cDNA: FLJ21087 fis, clone CAS03323 | 6.2E-264 |
| 791 | M00042833A:G07 | MA172:D01 | | AF047470 | gi 2906145 gb AF047470.1AF047470 Homo sapiens malate dehydrogenase precursor (MDH) mRNA, nuclear gene encoding mitochondrial protei | 3E-166 |
| 792 | M00042906D:F05 | MA168:E01 | | L31792 | gi 471076 gb L31792.1HUMCGM2A Homo sapiens carcinoembryonic antigen (CGM2) mRNA, complete cds | 1.1E-200 |
| 793 | M00042910C:A02 | MA168:G01 | | AF113700 | gi 6855634 gb AF113700.1AF113700 Homo sapiens clone FLB9737 | 7.6E-245 |
| 794 | M00042838C:D06 | MA172:H01 | | AK026558 | gi 10439440 dbj AK026558.1AK026558 Homo sapiens cDNA: FLJ22905 fis, clone KAT05654, highly similar to HUMRPL18A Homo sapiens riboso | 1.7E-214 |
| 795 | M00042867B:F03 | MA172:A07 | 0.30983 | D87666 | gi 1620016 dbj D87666.1D87666 Human heart mRNA for heat shock protein 90, partial cds | 1.3E-101 |
| 796 | M00055439B:G05 | MA168:B07 | | AY029066 | gi 14017398 gb AY029066.1 Homo sapiens Humanin (HN1) mRNA, complete cds | 9.6E-263 |
| 797 | M00055442D:E12 | MA168:F07 | | BC005354 | gi 13529169 gb BC005354.1BC005354 Homo sapiens, ribosomal protein, large P2, clone MGC:12453 IMAGE:4052568, mRNA, complete cds | 6.6E-239 |
| 798 | M00056711D:A02 | MA175:B01 | | Z11566 | gi 1066270 emb Z11566.1HSPR22MR H.sapiens mRNA for Pr22 protein | 6.7E-133 |
| 799 | M00056771C:A12 | MA175:A07 | | X02152 | gi 34312 emb X02152.1HSLDHAR Human mRNA for lactate dehydrogenase-A (LDH-A, EC 1.1.1.27) | 6E-130 |
| 800 | M00056772D:G07 | MA175:C07 | | NM_001016 | gi 14277699 ref NM_001016.2 Homo sapiens ribosomal protein S12 (RPS12), mRNA | 1.2E-218 |
| 801 | M00056782D:E04 | MA175:F07 | | AF346968 | gi 13272626 gb AF346968.1AF346968 Homo sapiens mitochondrion, complete genome | 3.6E-172 |

Table 3

| SEQ ID NO | Clone ID | MAClone ID | Mask Prent | GBHit | GBDescription | GBScore |
|-----------|----------------------|------------|------------|-----------|---|----------|
| 802 | M00056785D:G01 | MA175:G07 | | NM_001019 | gi 14165468 ref NM_001019.2 Homo sapiens ribosomal protein S15a (RPS15A), mRNA | 1.5E-230 |
| 803 | M00056788C:A01 | MA175:H07 | | AY029066 | gi 14017398 gb AY029066.1 Homo sapiens Humanin (HN1) mRNA, complete cds | 3.5E-287 |
| 804 | RG:1663880:10014:F07 | MA163:F07 | | BC019315 | gi 17939511 gb BC019315.1BC019315 Homo sapiens, N-acetylneuraminic acid phosphate synthase; sialic acid synthase, clone MGC:4339 IM | 1E-300 |
| 805 | M00043310B:D08 | MA183:C01 | | NM_000969 | gi 14591908 ref NM_000969.2 Homo sapiens ribosomal protein L5 (RPL5), mRNA | 1.5E-261 |
| 806 | M00054538C:G03 | MA185:C01 | | BC000734 | gi 12653884 gb BC000734.1BC000734 Homo sapiens, eukaryotic translation initiation factor 3, subunit 6 (48kD), clone MGC:2060 IMAGE: | 4E-234 |
| 807 | M00043315C:G05 | MA183:H01 | | AK023362 | gi 10435266 dbj AK023362.1AK023362 Homo sapiens cDNA FLJ13300 fis, clone OVARC1001342, highly similar to 40S RIBOSOMAL PROTEIN S8 | 2.7E-241 |
| 808 | M00055397B:E08 | MA199:B01 | | X06747 | gi 36101 emb X06747.1HSRNP A1 Human hnRNP core protein A1 | 9.7E-132 |
| 809 | M00056624B:H11 | MA186:C01 | | X56597 | gi 31394 emb X56597.1HSFIB Human humFib mRNA for fibrillarin | 7.7E-192 |
| 810 | M00055423C:C03 | MA199:E07 | | L01124 | gi 307390 gb L01124.1HUMRPS13A Human ribosomal protein S13 (RPS13) mRNA, complete cds | 9.1E-154 |
| 811 | M00056668D:C06 | MA186:F07 | | BC013231 | gi 15301504 gb BC013231.1BC013231 Homo sapiens, clone IMAGE:3462987, mRNA | 9.8E-263 |
| 812 | M00056669B:A10 | MA186:G07 | | NM_001025 | gi 14790142 ref NM_001025.2 Homo sapiens ribosomal protein S23 (RPS23), mRNA | 3.7E-290 |
| 813 | M00055424A:D01 | MA199:G07 | | BC002362 | gi 12803116 gb BC002362.1BC002362 Homo sapiens, lactate dehydrogenase B, clone MGC:8627 IMAGE:2961445, mRNA, complete cds | 6.4E-183 |
| 814 | M00056669B:E07 | MA186:H07 | | NM_002295 | gi 9845501 ref NM_002295.2 Homo sapiens laminin receptor 1 (67kD, ribosomal protein SA) (LAMR1), mRNA | 9.1E-232 |
| 815 | M00055424D:F01 | MA199:H07 | | NM_001012 | gi 4506742 ref NM_001012.1 Homo sapiens ribosomal protein S8 (RPS8), mRNA | 4.4E-190 |
| 816 | M00056243A:H07 | MA181:C02 | 0.86405 | | | |
| 817 | M00056243C:G10 | MA181:D02 | 0.46512 | | | |

Table 3

| SEQ ID NO | Clone ID | MA Clone ID | Mask Prent | GBHit | GBDescription | GBScore |
|-----------|----------------|-------------|------------|-----------|--|----------|
| 818 | M00055528D:H03 | MA169:F02 | 0.6783 | | gi 6841243 gb AF161415.1AF161415 Homo sapiens HSPC297 mRNA, partial cds | 3.5E-253 |
| 819 | M00055607B:A11 | MA169:B08 | | AF161415 | | |
| 820 | M00055363C:E02 | MA197:A08 | 0.62737 | | gi 15278200 gb BC013016.1BC013016 Homo sapiens, Similar to ribosomal protein L19, clone MGC:4526 IMAGE:3010178, mRNA, complete cds | 3.3E-125 |
| 821 | M00055373D:H02 | MA197:F08 | | BC013016 | | |
| 822 | M00055374D:E01 | MA197:H08 | | NM_000979 | gi 15431298 ref NM_000979.2 Homo sapiens ribosomal protein L18 (RPL18), mRNA | 1.5E-261 |
| 823 | M00056401D:D09 | MA173:A02 | | BC008492 | gi 14250147 gb BC008492.1BC008492 Homo sapiens, ribosomal protein L3, clone MGC:14821 IMAGE:4251511, mRNA, complete cds | 1.6E-105 |
| 824 | M00056139D:A10 | MA180:B02 | | X16356 | gi 37203 emb X16356.1HSTM3CEA Human mRNA for transmembrane carcinoembryonic antigen BGPC (part.) (formerly TM3-CEA) | 3.9E-237 |
| 825 | M00056140A:E11 | MA180:D02 | | U96628 | gi 2343084 gb U96628.1HSU96628 Homo sapiens nuclear antigen H731-like protein mRNA, complete cds | 2.4E-182 |
| 826 | M00056142D:A08 | MA180:E02 | | BC015958 | gi 16358989 gb BC015958.1BC015958 Homo sapiens, clone MGC:15290 IMAGE:3940309, mRNA, complete cds | 4.2E-268 |
| 827 | M00056412D:A09 | MA173:F02 | 0.85039 | | | |
| 828 | M00056142D:H11 | MA180:F02 | | AK025078 | gi 10437520 dbj AK025078.1AK025078 Homo sapiens cDNA: FLJ21425 fis, clone COL04162 | 3.8E-120 |
| 829 | M00056414C:F03 | MA173:G02 | | M29548 | gi 181966 gb M29548.1HUMEFIAB Human elongation factor 1-alpha (EF1A) mRNA, partial cds | 1.7E-114 |
| 830 | M00056196A:H09 | MA180:B08 | | D84239 | gi 1944351 dbj D84239.1D84239 Homo sapiens mRNA for IgG Fc binding protein, complete cds | 2E-251 |
| 831 | M00056200A:E11 | MA180:D08 | | U14528 | gi 549987 gb U14528.1HSU14528 Human sulfate transporter (DTD) mRNA, complete cds | 4.3E-299 |
| 832 | M00056488C:G01 | MA173:E08 | | L08048 | gi 184250 gb L08048.1HUMHMG1C Human non-histone chromosomal protein (HMG-1) retropseudogene | 3.3E-281 |
| 833 | M00056200B:B01 | MA180:E08 | | D84239 | gi 1944351 dbj D84239.1D84239 Homo sapiens mRNA for IgG Fc binding protein, complete cds | 1.5E-233 |
| 834 | M00056203B:G08 | MA180:F08 | 0.89391 | | | |

Table 3

| SEQ ID NO | Clone ID | MAClone ID | Mask Prent | GBHit | GBDescription | GBScore |
|-----------|----------------|------------|------------|----------|--|----------|
| 835 | M00056493A:F09 | MA173:H08 | | X14831 | gi 37199 emb X14831.1HSTM2CEA Human mRNA for transmembrane carcinoembryonic antigen BGPb (formerly TM2-CEA) | 4.2E-115 |
| 836 | M00054640D:D12 | MA187:B02 | 0.89884 | | | |
| 837 | M00054643B:F04 | MA187:D02 | 0.66848 | | | |
| 838 | M00054643C:D08 | MA187:E02 | | BC000491 | gi 12653440 gb BC000491.1BC000491 Homo sapiens, proliferating cell nuclear antigen, clone MGC:8367 IMAGE:2820036, mRNA, complete cds | 1.6E-236 |
| 839 | M00054854D:B06 | MA189:F02 | | M16660 | gi 184420 gb M16660.1HUMHSP90 Human 90-kDa heat-shock protein gene, cDNA, complete cds | 2.4E-263 |
| 840 | M00054644B:F02 | MA187:G02 | | BC017414 | gi 16924273 gb BC017414.1BC017414 Homo sapiens, Similar to signal recognition particle 9kD, clone IMAGE:4655251, mRNA, partial cds | 1.2E-246 |
| 841 | M00054857A:E08 | MA189:G02 | | BC016753 | gi 16876954 gb BC016753.1BC016753 Homo sapiens, clone MGC:1138 IMAGE:2987963, mRNA, complete cds | 8.6E-229 |
| 842 | M00054681D:G03 | MA187:B08 | | BC019360 | gi 17939583 gb BC019360.1BC019360 Homo sapiens, clone IMAGE:4025624, mRNA | 1E-300 |
| 843 | M00054682D:F11 | MA187:D08 | 0.13542 | AF116637 | gi 7959775 gb AF116637.1AF116637 Homo sapiens PRO1489 mRNA, complete cds | 3.2E-210 |
| 844 | M00054684B:C07 | MA187:F08 | | BC001781 | gi 12804704 gb BC001781.1BC001781 Homo sapiens, ribosomal protein L44, clone MGC:2064 IMAGE:3353669, mRNA, complete cds | 8.6E-176 |
| 845 | M00057191B:E11 | MA193:D02 | | AK026528 | gi 10439405 dbj AK026528.1AK026528 Homo sapiens cDNA: FLJ22875 fis, clone KAT02879 | 4.6E-274 |
| 846 | M00057194B:G12 | MA193:G02 | | AF228422 | gi 12656020 gb AF228422.1AF228422 Homo sapiens normal mucosa of esophagus specific 1 (NMES1) mRNA, complete cds | 1.9E-117 |
| 847 | M00057222D:G09 | MA193:B08 | | D49400 | gi 1395161 dbj D49400.1HUMVATPA SE Homo sapiens mRNA for vacuolar ATPase, complete cds | 3.9E-262 |
| 848 | M00042531B:H03 | MA167:A02 | | M15042 | gi 180198 gb M15042.1HUMCEA Human carcinoembryonic antigen mRNA | 6.3E-211 |
| 849 | M00042440C:G04 | MA171:A02 | 0.89441 | | | |

Table 3

| SEQ ID NO | Clone ID | MAClone ID | Mask Prent | GBHit | GBDescription | GBScore |
|-----------|----------------|------------|------------|-----------|---|----------|
| 850 | M00042533C:D02 | MA167:C02 | | X56999 | gi 37568 emb X56999.1HSUBA52P Human UbA52 placental mRNA for ubiquitin-52 amino acid fusion protein | 3.7E-29 |
| 851 | M00042536D:H05 | MA167:E02 | | AF146019 | gi 10197599 gb AF146019.1AF146019 Homo sapiens hepatocellular carcinoma antigen gene 520 mRNA, complete cds | 3E-26 |
| 852 | M00042465B:E04 | MA171:E02 | | BC016732 | gi 16876903 gb BC016732.1BC016732 Homo sapiens, thymosin, beta 4, X chromosome, clone MGC:24503 IMAGE:4096207, mRNA, complete cds | 5.7E-202 |
| 853 | M00042537D:F10 | MA167:F02 | | BC000889 | gi 12654142 gb BC000889.1BC000889 Homo sapiens, RNA polymerase I 16 kDa subunit, clone MGC:4881 IMAGE:3462906, mRNA, complete cds | 1.6E-236 |
| 854 | M00042467B:B04 | MA171:F02 | | V00572 | gi 35434 emb V00572.1HSPGK1 Human mRNA encoding phosphoglycerate kinase | 1E-240 |
| 855 | M00042538D:D12 | MA167:G02 | | X68195 | gi 36165 emb X68195.1HSRSPAC H.sapiens genomic DNA of ribosomal RNA intergenic spacer sequence | 6.6E-24 |
| 856 | M00042467B:B08 | MA171:G02 | | U11861 | gi 515482 gb U11861.1HSU11861 Human G10 homolog (cdg-2) mRNA, complete cds | 1.7E-165 |
| 857 | M00042711B:G09 | MA167:B08 | | AF130094 | gi 11493492 gb AF130094.1AF130094 Homo sapiens clone FLC0165 mRNA sequence | 3E-207 |
| 858 | M00042790B:E12 | MA171:B08 | | AF039400 | gi 4009457 gb AF039400.1AF039400 Homo sapiens calcium-dependent chloride channel-1 (hCLCA1) mRNA, complete cds | 5.9E-261 |
| 859 | M00042791A:C10 | MA171:C08 | | NM_000147 | gi 4503802 ref NM_000147.1 Homo sapiens fucosidase, alpha-L- 1, tissue (FUCA1), mRNA | 1.3E-252 |
| 860 | M00042711C:H05 | MA167:D08 | | X16354 | gi 37197 emb X16354.1HSTM1CEA Human mRNA for transmembrane carcinoembryonic antigen BGPα (formerly TM1-CEA) | 2.7E-163 |
| 861 | M00042801D:B02 | MA171:H08 | | BC002348 | gi 12803088 gb BC002348.1BC002348 Homo sapiens, nuclear transport factor 2 (placental protein 15), clone MGC:8327 IMAGE:2819267, mR | 4.9E-196 |

Table 3

| SEQ ID NO | Clone ID | MAClone ID | Mask Prent | GBHit | GBDescription | GBScore |
|-----------|----------------------|------------|------------|-----------|---|----------|
| 862 | M00042801D:B02 | MA171:H08 | | BC002348 | gi 12803088 gb BC002348.1BC002348 Homo sapiens, nuclear transport factor 2 (placental protein 15), clone MGC:8327 IMAGE:2819267, mR | 4.9E-196 |
| 863 | M00056532A:D09 | MA174:C02 | 0.78082 | | | |
| 864 | M00056533D:H04 | MA174:E02 | | AK000070 | gi 7019918 dbj AK000070.1AK000070 Homo sapiens cDNA FLJ20063 fis, clone COL01524 | 3.6E-287 |
| 865 | M00056575B:C04 | MA174:B08 | | AK000113 | gi 7019989 dbj AK000113.1AK000113 Homo sapiens cDNA FLJ20106 fis, clone COL04830 | 2.4E-263 |
| 866 | M00056578C:A09 | MA174:C08 | | NM_000988 | gi 17017972 ref NM_000988.2 Homo sapiens ribosomal protein L27 (RPL27), mRNA | 2.1E-198 |
| 867 | RG:1862072:20001:D08 | MA139:D08 | | X61633 | gi 37957 emb X61633.1HSWIGEEEX4 H.sapiens Wilms tumor gene 1, exon 4 | 9.2E-25 |
| 868 | RG:1862465:20001:F08 | MA139:F08 | 0.81221 | | | |
| 869 | RG:347381:10009:A02 | MA158:A02 | | U38846 | gi 1200183 gb U38846.1HSU38846 Human stimulator of TAR RNA binding (SRB) mRNA, complete cds | 0 |
| 870 | RG:417093:10009:D08 | MA158:D08 | 0.08361 | M17885 | gi 190231 gb M17885.1HUMPPARP0 Human acidic ribosomal phosphoprotein P0 mRNA, complete cds | 4.4E-216 |
| 871 | M00043413B:C04 | MA184:A02 | | AK027437 | gi 14042109 dbj AK027437.1AK027437 Homo sapiens cDNA FLJ14531 fis, clone NT2RM2000371, weakly similar to POLYRIBONUCLEOTIDE NUCLEOT | 5.2E-174 |
| 872 | M00043502D:C12 | MA184:F02 | | BC000820 | gi 12654032 gb BC000820.1BC000820 Homo sapiens, menage a trois 1 (CAK assembly factor), clone MGC:5154 IMAGE:3453943, mRNA, complet | 5.2E-252 |
| 873 | M00057341B:B11 | MA182:E08 | | BC001955 | gi 12805002 gb BC001955.1BC001955 Homo sapiens, ribosomal protein S10, clone MGC:4389 IMAGE:2905318, mRNA, complete cds | 1.1E-243 |
| 874 | M00054512A:F11 | MA184:G08 | 0.19488 | | | |
| 875 | M00042353A:D05 | MA182:H08 | | BC016352 | gi 16741002 gb BC016352.1BC016352 Homo sapiens, small acidic protein, clone MGC:24468 IMAGE:4082845, mRNA, complete cds | 2E-123 |
| 876 | M00054937B:D09 | MA198:B02 | | S79979 | gi 1839333 gb S79979.1S79979 ribosomal protein L37 [human, HeLa cells, Genomic/mRNA, 754 nt] | 2.8E-75 |

Table 3

| SEQ ID NO | Clone ID | MAClone ID | Mask Prent | GBHit | GBDescription | GBScore |
|-----------|----------------|------------|------------|-----------|---|----------|
| 877 | M00055797C:H09 | MA170:D08 | | BC009699 | gi 16307220 gb BC009699.1BC009699 Homo sapiens, Similar to RNA helicase-related protein, clone MGC:9246 IMAGE:3892441, mRNA, complete cds | 8.2E-226 |
| 878 | M00055799B:C01 | MA170:E08 | | X01117 | gi 57149 emb X01117.1RNRRNA06 Rat 18S rRNA sequence | 1.5E-51 |
| 879 | M00055194C:G12 | MA196:D02 | | BC008062 | gi 14165518 gb BC008062.1BC008062 Homo sapiens, basic transcription factor 3, clone MGC:2209 IMAGE:2966788, mRNA, complete cds | 7.7E-27 |
| 880 | M00055233B:D08 | MA196:B08 | 0.55474 | | | |
| 881 | M00055966C:D06 | MA179:H02 | | | | |
| 882 | M00056024B:B06 | MA179:D08 | | BC011949 | gi 15080385 gb BC011949.1BC011949 Homo sapiens, Similar to carbonic anhydrase II, clone MGC:9006 IMAGE:3863603, mRNA, complete cds | 6E-261 |
| 883 | M00056024C:G04 | MA179:E08 | | | | |
| 884 | M00054737D:F10 | MA188:D02 | | BC018828 | gi 17402971 gb BC018828.1BC018828 Homo sapiens, clone IMAGE:3343539, mRNA | 3.5E-284 |
| 885 | M00054780D:C09 | MA188:A08 | | BC007967 | gi 14044092 gb BC007967.1BC007967 Homo sapiens, clone MGC:14460 IMAGE:4304670, mRNA, complete cds | 2.2E-151 |
| 886 | M00054787A:E09 | MA188:D08 | | NM_006013 | gi 15718685 ref NM_006013.2 Homo sapiens ribosomal protein L10 (RPL10), mRNA | 8E-279 |
| 887 | M00054806B:E11 | MA188:E08 | | AK026650 | gi 10439548 dbj AK026650.1AK026650 Homo sapiens cDNA: FLJ22997 fis, clone KAT11962, highly similar to HSEF1AC Human mRNA for elonga | 1.3E-252 |
| 888 | M00042913B:C11 | MA168:B02 | | NM_000999 | gi 16306562 ref NM_000999.2 Homo sapiens ribosomal protein L38 (RPL38), mRNA | 2.4E-182 |
| 889 | M00042915B:B10 | MA168:D02 | | AK058013 | gi 16554011 dbj AK058013.1AK058013 Homo sapiens cDNA FLJ25284 fis, clone STM06787, highly similar to 15-HYDROXYPROSTAGLANDIN DEHYDR | 2.2E-201 |
| 890 | M00054792C:E12 | MA168:E02 | | D14530 | gi 414348 dbj D14530.1HUMRSPT Human homolog of yeast ribosomal protein S28, complete cds | 4.1E-268 |
| 891 | M00042842A:C01 | MA172:G02 | 0.66829 | | | |
| 892 | M00055450A:C09 | MA168:H08 | 0.8 | | | |

Table 3

| SEQ ID NO | Clone ID | MAClone ID | Mask Prent | GBHit | GBDescription | GBScore |
|-----------|----------------------|------------|------------|-----------|---|----------|
| 893 | M00056804C:D01 | MA175:H08 | | AF126743 | gi 5052332 gb AF126743.1AF126743 Homo sapiens DNAJ domain-containing protein MCJ (MCJ) mRNA, complete cds | 3.1E-278 |
| 894 | RG:1647954:10014:D08 | MA163:D08 | | NM_001261 | gi 17017983 ref NM_001261.2 Homo sapiens cyclin-dependent kinase 9 (CDC2-related kinase) (CDK9), mRNA | 1.9E-273 |
| 895 | RG:1664311:10014:F08 | MA163:F08 | | X02761 | gi 31396 emb X02761.1HSF1B1 Human mRNA for fibronectin (FN precursor) | 0 |
| 896 | RG:1671377:10014:G08 | MA163:G08 | | BC013078 | gi 15341811 gb BC013078.1BC013078 Homo sapiens, clone MGC:17534 IMAGE:3459415, mRNA, complete cds | 2.8E-297 |
| 897 | M00043316B:F10 | MA183:C02 | | X16064 | gi 37495 emb X16064.1HSTUMP Human mRNA for translationally controlled tumor protein | 2.7E-269 |
| 898 | M00054545B:A03 | MA185:D02 | | AF151048 | gi 7106817 gb AF151048.1AF151048 Homo sapiens HSPC214 mRNA, complete cds | 4.6E-271 |
| 899 | M00054545B:B09 | MA185:E02 | 0.07415 | X07979 | gi 31441 emb X07979.1HSFNRB Human mRNA for integrin beta 1 subunit | 1.2E-126 |
| 900 | M00054575A:B09 | MA185:D08 | | X16064 | gi 37495 emb X16064.1HSTUMP Human mRNA for translationally controlled tumor protein | 3.2E-278 |
| 901 | M00043374B:H05 | MA183:F08 | 0.11186 | NM_053275 | gi 16933545 ref NM_053275.1 Homo sapiens ribosomal protein, large, P0 (RPLP0), transcript variant 2, mRNA | 3E-136 |
| 902 | M00056641A:G11 | MA186:F02 | | BC003352 | gi 13097158 gb BC003352.1BC003352 Homo sapiens, tumor protein, translationally-controlled 1, clone MGC:5308 IMAGE:2899964, mRNA, co | 3.6E-284 |
| 903 | M00056642A:D08 | MA186:H02 | 0.78693 | | | |
| 904 | M00055403B:B11 | MA199:H02 | | NM_001021 | gi 14591913 ref NM_001021.2 Homo sapiens ribosomal protein S17 (RPS17), mRNA | 5.8E-180 |
| 905 | M00056676B:C11 | MA186:H08 | | AF346968 | gi 13272626 gb AF346968.1AF346968 Homo sapiens mitochondrion, complete genome | 4.6E-165 |
| 906 | M00055530D:B02 | MA169:B03 | | NM_001012 | gi 4506742 ref NM_001012.1 Homo sapiens ribosomal protein S8 (RPS8), mRNA | 1.5E-261 |
| 907 | M00056253A:D06 | MA181:C03 | | BC014166 | gi 15559610 gb BC014166.1BC014166 Homo sapiens, clone IMAGE:4549553, mRNA | 1.2E-274 |

Table 3

| SEQ ID NO | Clone ID | MAClone ID | Mask Prent | GBHit | GBDescription | GBScore |
|-----------|----------------|------------|------------|----------|---|----------|
| 908 | M00056253B:B06 | MA181:D03 | | BC000053 | gi 12652614 gb BC000053.1BC000053 Homo sapiens, LPS-induced TNF-alpha factor, clone IMAGE:3506981, mRNA | 1.7E-270 |
| 909 | M00055642D:F09 | MA169:D09 | | AF203815 | gi 6979641 gb AF203815.1AF203815 Homo sapiens alpha gene sequence | 2.2E-257 |
| 910 | M00055643A:E09 | MA169:E09 | | J03037 | gi 179771 gb J03037.1HUMCAIIA Human carbonic anhydrase II mRNA, complete cds | 3E-247 |
| 911 | M00055643D:E02 | MA169:F09 | | M10050 | gi 182355 gb M10050.1HUMFABPL Human liver fatty acid binding protein (FABP) mRNA, complete cds | 2.1E-251 |
| 912 | M00055376D:D08 | MA197:B09 | | D38112 | gi 644480 dbj D38112.1HUMMTA Homo sapiens mitochondrial DNA, complete sequence | 8.5E-111 |
| 913 | M00056415C:D02 | MA173:B03 | 0.67751 | | | |
| 914 | M00056146D:F05 | MA180:B03 | 0.61693 | | | |
| 915 | M00056417A:F02 | MA173:C03 | | Z85099 | gi 1834810 emb Z85099.1HSZ85099 H.sapiens Ig lambda light chain variable region gene (3-010IIA11) rearranged; Ig-Light-Lambda; VLam | 2.7E-31 |
| 916 | M00056148A:B07 | MA180:C03 | | AK026170 | gi 10438933 dbj AK026170.1AK026170 Homo sapiens cDNA: FLJ22517 fis, clone HRC12186 | 4.8E-134 |
| 917 | M00056420C:E07 | MA173:D03 | | BC010735 | gi 14789596 gb BC010735.1BC010735 Homo sapiens, Similar to eukaryotic translation elongation factor 1 alpha 1, clone MGC:10096 IMAG | 3.7E-262 |
| 918 | M00056150A:E04 | MA180:D03 | 0.82941 | | | |
| 919 | M00056421C:H11 | MA173:F03 | | X60489 | gi 31099 emb X60489.1HSEF1B Human mRNA for elongation factor-1-beta | 3.5E-228 |
| 920 | M00056150C:A10 | MA180:F03 | | AL360191 | gi 8919392 emb AL360191.1HST000237 Homo sapiens mRNA full length insert cDNA clone EUROIMAGE 781354 | 1.1E-237 |
| 921 | M00056421D:H05 | MA173:G03 | | BC017338 | gi 16878283 gb BC017338.1BC017338 Homo sapiens, fucosidase, alpha-L-1, tissue, clone MGC:29579 IMAGE:4871788, mRNA, complete cds | 1.1E-159 |
| 922 | M00056150C:C04 | MA180:G03 | | AJ276249 | gi 7362984 emb AJ276249.1HSA276249 Homo sapiens partial mRNA, clone c1-10e16 | 1.3E-98 |

Table 3

| SEQ ID NO | Clone ID | MAClone ID | Mask Prent | GBHit | GBDescription | GBScore |
|-----------|----------------|------------|------------|-----------|---|----------|
| 923 | M00056422B:D11 | MA173:H03 | | BC001289 | gi 12654890 gb BC001289.1BC001289 Homo sapiens, Sjogren syndrome antigen B (autoantigen La), clone MGC:5194 IMAGE:3454454, mRNA, co | 1.9E-120 |
| 924 | M00056151C:A12 | MA180:H03 | | X59706 | gi 34204 cemb X59706.1HSLA1L11G H.sapiens rearranged Humigla1L1 gene encoding IgG light chain | 1.5E-227 |
| 925 | M00056493C:E06 | MA173:A09 | | AF153608 | gi 5231140 gb AF153608.1AF153608 Homo sapiens sin3 associated polypeptide (SAP18) mRNA, complete cds | 1.3E-280 |
| 926 | M00056205D:E03 | MA180:A09 | 0.78241 | | | |
| 927 | M00056495A:G10 | MA173:B09 | | M63573 | gi 337998 gb M63573.1HUMSCYLP Human secreted cyclophilin-like protein (SCYLP) mRNA, complete cds | 4.5E-100 |
| 928 | M00056206D:B10 | MA180:E09 | | AF001893 | gi 2529723 gb AF001893.1BETA2 Human MEN1 region clone epsilon/beta mRNA, 3' fragment | 1.1E-35 |
| 929 | M00056501D:C08 | MA173:H09 | | Y11339 | gi 7576275 cemb Y11339.2HSY11339 Homo sapiens mRNA for GalNAc alpha-2, 6-sialyltransferase I, long form | 1.9E-220 |
| 930 | M00056209D:H10 | MA180:H09 | 0.08151 | J03037 | gi 179771 gb J03037.1HUMCAIIA Human carbonic anhydrase II mRNA, complete cds | 1.6E-258 |
| 931 | M00054645B:C12 | MA187:B03 | 0.18868 | BC008092 | gi 14198047 gb BC008092.1BC008092 Homo sapiens, ribosomal protein, large, P0, clone MGC:9343 IMAGE:3458803, mRNA, complete cds | 7.3E-105 |
| 932 | M00054646A:B10 | MA187:C03 | | BC007097 | gi 13937968 gb BC007097.1BC007097 Homo sapiens, tissue inhibitor of metalloproteinase 1 (erythroid potentiating activity, collagena | 5.2E-146 |
| 933 | M00054647D:E01 | MA187:G03 | | NM_001026 | gi 14916502 ref NM_001026.2 Homo sapiens ribosomal protein S24 (RPS24), transcript variant 2, mRNA | 6.4E-111 |
| 934 | M00057202C:G06 | MA193:E03 | | | | |
| 935 | M00057202D:C11 | MA193:F03 | | X71973 | gi 311699 cemb X71973.1HSGPX4 H.sapiens GPx-4 mRNA for phospholipid hydroperoxide glutathione peroxidase | 1.3E-26 |
| 936 | M00042549A:G12 | MA167:C03 | | AF153609 | gi 5231142 gb AF153609.1AF153609 Homo sapiens serine/threonine protein kinase sgk mRNA, complete cds | 1.8E-120 |

Table 3

| SEQ ID NO | Clone ID | MA Clone ID | Mask Prent | GBHit | GBDescription | GBScore |
|-----------|---------------------|-------------|------------|-----------|---|----------|
| 937 | M00042549D:F03 | MA167:D03 | | BC011025 | gi 15029635 gb BC011025.1BC011025 Homo sapiens, Similar to sorcin, clone MGC:13597 IMAGE:4281626, mRNA, complete cds | 6.8E-34 |
| 938 | M00042551B:D12 | MA167:E03 | | NM_002295 | gi 9845501 ref NM_002295.2 Homo sapiens laminin receptor 1 (67kD, ribosomal protein SA) (LAMR1), mRNA | 8.3E-226 |
| 939 | M00042513A:D03 | MA171:E03 | | NM_001002 | gi 16933547 ref NM_001002.2 Homo sapiens ribosomal protein, large, P0 (RPLP0), transcript variant 1, mRNA | 2.5E-266 |
| 940 | M00042513D:A12 | MA171:F03 | 0.53205 | | | |
| 941 | M00042551D:D12 | MA167:H03 | | Z48514 | gi 695600 emb Z48514.1HSXGR4551 H.sapiens XG mRNA (clone R4(551)) | 2.8E-191 |
| 942 | M00042717B:D05 | MA167:A09 | 0.47619 | X98311 | gi 1524059 emb X98311.1HSCGM2A NT H.sapiens mRNA for carcinoembryonic antigen family member 2, CGM2 | 1.1E-45 |
| 943 | M00042719D:C09 | MA167:B09 | | L31792 | gi 471076 gb L31792.1HUMCGM2A Homo sapiens carcinoembryonic antigen (CGM2) mRNA, complete cds | 4.2E-144 |
| 944 | M00042803C:F11 | MA171:C09 | | M31520 | gi 337504 gb M31520.1HUMRPS24A Human ribosomal protein S24 mRNA | 7.6E-120 |
| 945 | M00042805D:D12 | MA171:E09 | | BC004324 | gi 13279235 gb BC004324.1BC004324 Homo sapiens, ribosomal protein S16, clone MGC:10931 IMAGE:3628799, mRNA, complete cds | 2.4E-263 |
| 946 | M00042731A:G04 | MA167:F09 | | Z84867 | gi 1834578 emb Z84867.1HSZ84867 H.sapiens Ig lambda light chain variable region gene (14-09DPIA215) rearranged; Ig-Light-Lambda; VL | 5.8E-113 |
| 947 | M00042806C:E09 | MA171:G09 | 0.12055 | U16738 | gi 608516 gb U16738.1HSU16738 Homo sapiens CAG-isl 7 mRNA, complete cds | 1.4E-165 |
| 948 | M00042806D:F08 | MA171:H09 | | Y16241 | gi 3378195 emb Y16241.1HSY16241 Homo sapiens mRNA for ncbullette | 3E-247 |
| 949 | M00056537A:F05 | MA174:C03 | | NM_021130 | gi 10863926 ref NM_021130.1 Homo sapiens peptidylprolyl isomerase A (cyclophilin A) (PPIA), mRNA | 5.1E-249 |
| 950 | M00056537D:A07 | MA174:D03 | | BC019255 | gi 17939424 gb BC019255.1BC019255 Homo sapiens, multifunctional polypeptide similar to SAICAR synthetase and AIR carboxylase, clone | 2.3E-260 |
| 951 | RG:1862584:20001:G0 | MA139:G03 | 0.72829 | | | |

Table 3

| SEQ ID NO | Clone ID | MAClone ID | Mask Prent | GBHit | GBDescription | GBScore |
|-----------|---------------------|------------|------------|-----------|--|----------|
| 952 | M00056585D:D05 | MA174:A09 | | BC007989 | gi 14124931 gb BC007989.1BC007989 Homo sapiens, Similar to heat shock 90kD protein 1, alpha, clone IMAGE:3030617, mRNA, partial cds | 1.3E-283 |
| 953 | M00056586C:B08 | MA174:B09 | | BC013873 | gi 15530196 gb BC013873.1BC013873 Homo sapiens, Similar to centrin, EF-hand protein, 2, clone MGC:10365 IMAGE:3836808, mRNA, comple | 1.2E-184 |
| 954 | M00056592A:B08 | MA174:E09 | | AB018580 | gi 6624210 dbj AB018580.1AB018580 Homo sapiens mRNA for hluPGFS, complete cds | 7.8E-251 |
| 955 | RG:378550:10009:C03 | MA158:C03 | | | | |
| 956 | RG:789040:10011:F09 | MA160:F09 | | M14676 | gi 338227 gb M14676.1HUMSLK Human src-like kinase (slk) mRNA, complete cds | 1E-300 |
| 957 | M00057283A:D01 | MA182:B03 | | AF283772 | gi 10281741 gb AF283772.2AF283772 Homo sapiens clone TCBAP0781 mRNA sequence | 2.5E-266 |
| 958 | M00043505A:E07 | MA184:D03 | | NM_007209 | gi 16117792 ref NM_007209.2 Homo sapiens ribosomal protein L35 (RPL35), mRNA | 5.5E-258 |
| 959 | M00043506B:G10 | MA184:G03 | | BC007945 | gi 14044036 gb BC007945.1BC007945 Homo sapiens, ribosomal protein S11, clone MGC:14322 IMAGE:4297932, mRNA, complete cds | 1E-197 |
| 960 | M00043507A:B02 | MA184:H03 | | | | |
| 961 | M00042353C:F02 | MA182:A09 | | NM_001015 | gi 14277698 ref NM_001015.2 Homo sapiens ribosomal protein S11 (RPS11), mRNA | 3.4E-256 |
| 962 | M00054516B:A08 | MA184:F09 | | BC004459 | gi 13325289 gb BC004459.1BC004459 Homo sapiens, eukaryotic translation initiation factor 4E binding protein 1, clone MGC:4316 IMAGE | 5E-280 |
| 963 | M00054986D:B04 | MA198:A09 | | AJ131712 | gi 7576251 emb AJ131712.1HSA131712 2 Homo sapiens mRNA for nucleolar RNA-helicase (noH61 gene) | 1.2E-168 |
| 964 | M00054987C:B10 | MA198:B09 | 0.09792 | AF097362 | gi 6165617 gb AF097362.1AF097362 Homo sapiens gamma-interferon inducible lysosomal thiol reductase (GILT) mRNA, complete cds | 9.1E-139 |
| 965 | M00054988D:B11 | MA198:C09 | | BC019051 | gi 17403061 gb BC019051.1BC019051 Homo sapiens, clone IMAGE:4636237, mRNA | 1.8E-192 |

Table 3

| SEQ ID NO | Clone ID | MAClone ID | Mask Prent | GBHit | GBDescription | GBScore |
|-----------|----------------|------------|------------|-----------|---|----------|
| 966 | M00055743C:G08 | MA170:E03 | | BC018970 | gi 17512000 gb BC018970.1BC018970 Homo sapiens, ribosomal protein L11, clone MGC:19586 IMAGE:4337066, mRNA, complete cds | 2.8E-216 |
| 967 | M00055196B:C09 | MA196:D03 | | BC018755 | gi 17511806 gb BC018755.1BC018755 Homo sapiens, PDZ and LIM domain 1 (clfin), clone MGC:31954 IMAGE:3610938, mRNA, complete cds | 6.7E-242 |
| 968 | M00055238B:G05 | MA196:B09 | | NM_012423 | gi 14591905 ref NM_012423.2 Homo sapiens ribosomal protein L13a (RPL13A), mRNA | 3.8E-206 |
| 969 | M00056207B:H06 | MA180:G09 | 0.89703 | | | |
| 970 | M00055966C:G04 | MA179:A03 | | BC008492 | gi 14250147 gb BC008492.1BC008492 Homo sapiens, ribosomal protein L3, clone MGC:14821 IMAGE:4251511, mRNA, complete cds | 8.2E-282 |
| 971 | M00056920D:C08 | MA177:A03 | | BC014301 | gi 15679985 gb BC014301.1BC014301 Homo sapiens, Similar to enhancer of rudimentary (Drosophila) homolog, clone MGC:1509 IMAGE:35072 | 8.8E-204 |
| 972 | M00055969D:D01 | MA179:C03 | 0.16904 | X73501 | gi 402644 emb X73501.1HSCYTOK20 H.sapiens gene for cytokeratin 20 | 4E-225 |
| 973 | M00056055D:F06 | MA179:E09 | | AY011168 | gi 12699140 gb AY011168.1 Homo sapiens 16S ribosomal RNA gene, partial sequence; mitochondrial gene for mitochondrial product | 5.4E-149 |
| 974 | M00056956B:G12 | MA177:E09 | 0.87013 | | | |
| 975 | M00056060D:C04 | MA179:F09 | | V00710 | gi 13683 emb V00710.1MIT1HS Human mitochondrial genes for several tRNAs (Phe, Val, Leu) and 12S and 16S ribosomal RNAs | 4E-184 |
| 976 | M00056061C:H04 | MA179:G09 | | U14528 | gi 549987 gb U14528.1HSU14528 Human sulfate transporter (DTD) mRNA, complete cds | 3.4E-219 |
| 977 | M00054743C:E05 | MA188:A03 | | BC001603 | gi 12804402 gb BC001603.1BC001603 Homo sapiens, Similar to ribosomal protein L21, clone MGC:2150 IMAGE:3543702, mRNA, complete cds | 2.3E-179 |
| 978 | M00054744C:B02 | MA188:B03 | | NM_033643 | gi 16117795 ref NM_033643.1 Homo sapiens ribosomal protein L36 (RPL36), transcript variant 1, mRNA | 6.2E-92 |

Table 3

| SEQ ID NO | Clone ID | MA Clone ID | Mask Prent | GBHit | GBDescription | GBScore |
|-----------|----------------|-------------|------------|-----------|---|----------|
| 979 | M00054808A:E02 | MA188:C09 | | BC003030 | gi 12804340 gb BC003030.1BC003030 Homo sapiens, heat shock 60kD protein 1 (chaperonin), clone MGC:4335 IMAGE:2821157, mRNA, complet | 5.5E-174 |
| 980 | M00054811A:G01 | MA188:G09 | | X90583 | gi 1071680 emb X90583.1HSRNATRA P H.sapiens mRNA for rat translocon-associated protein delta homolog | 3.9E-184 |
| 981 | M00054797C:G10 | MA168:A03 | | BC004983 | gi 13436415 gb BC004983.1BC004983 Homo sapiens, nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, alpha | 2.1E-148 |
| 982 | M00042843B:H01 | MA172:A03 | | AF068754 | gi 3283408 gb AF068754.1AF068754 Homo sapiens heat shock factor binding protein 1 HSBP1 mRNA, complete cds | 7.8E-139 |
| 983 | M00042844D:D10 | MA172:D03 | | BC000483 | gi 12653424 gb BC000483.1BC000483 Homo sapiens, clone MGC:8704 IMAGE:2964733, mRNA, complete cds | 2.3E-232 |
| 984 | M00042845D:A12 | MA172:E03 | | BC008329 | gi 14249899 gb BC008329.1BC008329 Homo sapiens, clone MGC:15787 IMAGE:3504130, mRNA, complete cds | 8.5E-229 |
| 985 | M00054800C:H10 | MA168:G03 | | Z85052 | gi 1834763 emb Z85052.1HSZ85052 H.sapiens Ig lambda light chain variable region gene (26-34IT1IIF120) rearranged; Ig-Light-Lambda; | 9E-167 |
| 986 | M00054911D:E09 | MA168:H03 | | NM_000969 | gi 14591908 ref NM_000969.2 Homo sapiens ribosomal protein L5 (RPL5), mRNA | 7.2E-217 |
| 987 | M00055450A:G03 | MA168:A09 | 0.09821 | AF074331 | gi 5052074 gb AF074331.1AF074331 Homo sapiens PAPS synthetase-2 (PAPSS2) mRNA, complete cds | 6.8E-152 |
| 988 | M00055456B:H05 | MA168:D09 | 0.79701 | | | |
| 989 | M00056733C:D03 | MA175:D03 | | X97336 | gi 1666193 emb X97336.1RUMTGEN OM Rhinoceros unicornis complete mitochondrial genome | 3.1E-72 |
| 990 | M00056737D:E08 | MA175:H03 | | D11094 | gi 219930 dbj D11094.1HUMMSS1 Human mRNA for MSS1, complete cds | 5.9E-230 |
| 991 | M00056809B:A12 | MA175:E09 | | L42345 | gi 1160933 gb L42345.1HUMHLAB44 A Homo sapiens lymphocyte antigen HLA-B*4402 and HLA-B*5101 mRNA, exons 1-7, complete cds | 6E-152 |

Table 3

| SEQ ID NO | Clone ID | MAClone ID | Mask Prent | GBHit | GBDescription | GBScore |
|-----------|----------------------|------------|------------|-----------|---|----------|
| 992 | M00056809D:C07 | MA175:G09 | | J03801 | gi 187243 gb J03801.1HUMLSZ Human lysozyme mRNA, complete cds with an Alu repeat in the 3' flank | 9.3E-207 |
| 993 | RG:1664308:10014:F09 | MA163:F09 | | AF011497 | gi 2286216 gb AF011497.1AF011497 Homo sapiens guanine nucleotide binding protein alpha 11 subunit (G11) mRNA, complete cds | 0 |
| 994 | M00043321A:G07 | MA183:B03 | | D49400 | gi 1395161 dbj D49400.1HUMVATPA SE Homo sapiens mRNA for vacuolar ATPase, complete cds | 5.1E-280 |
| 995 | M00054549A:F03 | MA185:C03 | 0.84052 | | | |
| 996 | M00043381A:C08 | MA183:D09 | | NM_001012 | gi 4506742 ref NM_001012.1 Homo sapiens ribosomal protein S8 (RPS8), mRNA | 1.1E-231 |
| 997 | M00056642B:G03 | MA186:A03 | | BC010952 | gi 15012094 gb BC010952.1BC010952 Homo sapiens, Similar to protease inhibitor 3, skin-derived (SKALP), clone MGC:13613 IMAGE:408315 | 1E-300 |
| 998 | M00056688C:A07 | MA186:H09 | | D13748 | gi 219402 dbj D13748.1HUM4AI Human mRNA for eukaryotic initiation factor 4AI | 1E-300 |
| 999 | M00056257C:G03 | MA181:A04 | | AK054673 | gi 16549265 dbj AK054673.1AK054673 Homo sapiens cDNA FLJ30111 fis, clone BNGH42000360, highly similar to 3-KETOACYL-COA THIOLASE MI | 3.6E-228 |
| 1000 | M00055545C:F11 | MA169:G04 | | AY029066 | gi 14017398 gb AY029066.1 Homo sapiens Humanin (HN1) mRNA, complete cds | 1.4E-258 |
| 1001 | M00055653C:F04 | MA169:C10 | | M10050 | gi 182355 gb M10050.1HUMFABPL Human liver fatty acid binding protein (FABP) mRNA, complete cds | 5E-224 |
| 1002 | M00055653D:F01 | MA169:D10 | | M10050 | gi 182355 gb M10050.1HUMFABPL Human liver fatty acid binding protein (FABP) mRNA, complete cds | 1.9E-167 |
| 1003 | M00055385A:C11 | MA197:B10 | | BC013231 | gi 15301504 gb BC013231.1BC013231 Homo sapiens, clone IMAGE:3462987, mRNA | 2.9E-244 |
| 1004 | M00056157A:F11 | MA180:D04 | | X74104 | gi 452756 emb X74104.1HSSSR H.sapiens mRNA for TRAP beta subunit | 4.5E-274 |
| 1005 | M00056160A:F03 | MA180:E04 | 0.89209 | | | |
| 1006 | M00056426A:H07 | MA173:F04 | 0.49541 | | | |
| 1007 | M00056214C:B04 | MA180:C10 | | Y00339 | gi 29586 emb Y00339.1HSCA2 Human mRNA for carbonic anhydrase II (EC 4.2.1.1) | 3E-222 |
| 1008 | M00056216A:F10 | MA180:D10 | 0.75335 | | | |

Table 3

| SEQ ID NO | Clone ID | MA Clone ID | Mask Prent | GBHit | GBDescription | GBScore |
|-----------|----------------|-------------|------------|----------|---|----------|
| 1009 | M00056507A:G11 | MA173:G10 | 0.71615 | | gi 13278665 gb BC004113.1BC004113 Homo sapiens, Similar to non-POU-domain-containing, octamer-binding, clone IMAGE:3835400, mRNA, p | 1.6E-236 |
| 1010 | M00054648C:C10 | MA187:A04 | | BC004113 | | |
| 1011 | M00054862A:H11 | MA189:A04 | 0.60181 | | | |
| 1012 | M00054648D:F12 | MA187:B04 | | BC001118 | gi 12654566 gb BC001118.1BC001118 Homo sapiens, Similar to seven transmembrane domain protein, clone MGC:1936 IMAGE:2989840, mRNA, gi 5931601 dbj AB026723.1AB026723 | 1.5E-289 |
| 1013 | M00054650C:H08 | MA187:D04 | | AB026723 | Homo sapiens SID6-8061 mRNA for pyrophosphatase, complete cds | 1.6E-295 |
| 1014 | M00054868C:C11 | MA189:H04 | 0.09703 | | | |
| 1015 | M00054700C:E02 | MA187:D10 | | BC000530 | gi 12653516 gb BC000530.1BC000530 Homo sapiens, ribosomal protein L19, clone MGC:8653 IMAGE:2961653, mRNA, complete cds | 2.9E-244 |
| 1016 | M00054902D:G11 | MA189:F10 | 0.71088 | | | |
| 1017 | M00054903B:G06 | MA189:G10 | | BC013231 | gi 15301504 gb BC013231.1BC013231 Homo sapiens, clone IMAGE:3462987, mRNA | 1.1E-240 |
| 1018 | M00054706A:D05 | MA187:H10 | | AB060236 | gi 13676490 dbj AB060236.1AB060236 6 Macaca fascicularis brain cDNA clone:Qf1A-11918, full insert sequence gi 6138993 gb AF127763.2AF127763 | 6.9E-71 |
| 1019 | M00057207A:D05 | MA193:C04 | | AF127763 | Homo sapiens mitogenic oxidase mRNA, complete cds | 2.7E-297 |
| 1020 | M00057207C:F06 | MA193:D04 | | BC016756 | gi 16876963 gb BC016756.1BC016756 Homo sapiens, glutathione peroxidase 2 (gastrointestinal), clone IMAGE:3681457, mRNA | 9.4E-291 |
| 1021 | M00057208B:F11 | MA193:F04 | | X60489 | gi 31099 emb X60489.1HSEF1B Human mRNA for elongation factor-1-beta | 8E-279 |
| 1022 | M00057242B:B10 | MA193:C10 | | J03464 | gi 179595 gb J03464.1HUMC1A2 Human collagen alpha-2 type I mRNA, complete cds, clone pHCOL2A1 | 2.1E-282 |
| 1023 | M00042555A:E06 | MA167:C04 | 0.79249 | | | |
| 1024 | M00042561A:H03 | MA167:D04 | | AK057546 | gi 16553292 dbj AK057546.1AK057546 6 Homo sapiens cDNA FLJ32984 fis, clone THYMU1000017, highly similar to Homo sapiens splice varian | 3.1E-278 |

Table 3

| SEQ ID NO | Clone ID | MAClone ID | Mask Prent | GBHit | GBDescription | GBScore |
|-----------|---------------------|------------|------------|-----------|---|----------|
| 1025 | M00042756C:E10 | MA171:E04 | | NM_005348 | gi 13129149 ref NM_005348.1 Homo sapiens heat shock 90kD protein 1, alpha (HSPCA), mRNA | 3E-222 |
| 1026 | M00042758D:F01 | MA171:F04 | | NM_000969 | gi 14591908 ref NM_000969.2 Homo sapiens ribosomal protein L5 (RPL5), mRNA | 3.7E-259 |
| 1027 | M00042759B:E02 | MA171:H04 | | BC000077 | gi 12652658 gb BC000077.1BC000077 Homo sapiens, ribosomal protein L8, clone MGC:3253 IMAGE:3506015, mRNA, complete cds | 5.1E-252 |
| 1028 | M00042808D:D03 | MA171:B10 | | AB048207 | gi 15425668 dbj AB048207.1AB048207 Homo sapiens mRNA for TIGA1, complete cds | 2.2E-257 |
| 1029 | M00042808D:D10 | MA171:C10 | | AK026166 | gi 10438929 dbj AK026166.1AK026166 Homo sapiens cDNA: FLJ22513 fis, clone HRC12111, highly similar to HUMKUP Human Ku (p70/p80) sub | 9.5E-263 |
| 1030 | M00042811B:A05 | MA171:D10 | | AK027191 | gi 10440260 dbj AK027191.1AK027191 Homo sapiens cDNA: FLJ23538 fis, clone LNG08010, highly similar to BETA2 Human MEN1 region clone | 1.6E-121 |
| 1031 | M00042746B:F05 | MA167:E10 | | AK026528 | gi 10439405 dbj AK026528.1AK026528 Homo sapiens cDNA: FLJ22875 fis, clone KAT02879 | 1.6E-77 |
| 1032 | M00042746C:D01 | MA167:G10 | | BC000551 | gi 12653554 gb BC000551.1BC000551 Homo sapiens, lysophospholipase-like, clone MGC:1216 IMAGE:3163689, mRNA, complete cds | 5E-128 |
| 1033 | M00042812D:B04 | MA171:G10 | | NM_000978 | gi 14591907 ref NM_000978.2 Homo sapiens ribosomal protein L23 (RPL23), mRNA | 3.5E-256 |
| 1034 | M00056546B:F12 | MA174:A04 | | AK026570 | gi 10439452 dbj AK026570.1AK026570 Homo sapiens cDNA: FLJ22917 fis, clone KAT06430 | 2.1E-226 |
| 1035 | M00056550A:G09 | MA174:H04 | | X14420 | gi 30057 cemb X14420.1HSCOL3A1 Human mRNA for pro-alpha-1 type 3 collagen | 5.1E-165 |
| 1036 | M00056610C:B08 | MA174:G10 | | D87667 | gi 1620019 dbj D87667.1D87667 Human brain mRNA homologous to 3'UTR of human CD24 gene, partial sequence | 1.4E-199 |
| 1037 | RG:745556:10011:B04 | MA160:B04 | | AK056676 | gi 16552146 dbj AK056676.1AK056676 Homo sapiens cDNA FLJ32114 fis, clone OCBBF2001706 | 8.7E-227 |

Table 3

| SEQ ID NO | Clone ID | MAClone ID | Mask Prent | GBHit | GBDescription | GBScore |
|-----------|---------------------|------------|------------|-----------|---|----------|
| 1038 | RG:446537:10009:G04 | MA158:G04 | | BC001430 | gi 12655150 gb BC001430.1BC001430 Homo sapiens, POP7 (processing of precursor, S. cerevisiae) homolog, clone MGC:1986 IMAGE:3138336 | 0 |
| 1039 | RG:375937:10009:B10 | MA158:B10 | | BC010153 | gi 14603405 gb BC010153.1BC010153 Homo sapiens, cyclin-dependent kinase 4, clone MGC:19704 IMAGE:3531300, mRNA, complete cds | 1.1E-77 |
| 1040 | RG:755120:10011:B10 | MA160:B10 | | BC016725 | gi 16876888 gb BC016725.1BC016725 Homo sapiens, 60S ribosomal protein L30 isolog, clone MGC:24451 IMAGE:4078305, mRNA, complete cds | 3.5E-52 |
| 1041 | RG:781108:10011:D10 | MA160:D10 | | | | |
| 1042 | M00042450C:H10 | MA182:A10 | | S56985 | gi 298485 gb S56985.1S56985 ribosomal protein L19 [human, breast cancer cell line, MCF-7, mRNA, 690 nt] | 1.4E-258 |
| 1043 | M00042451B:B05 | MA182:B10 | | BC013231 | gi 15301504 gb BC013231.1BC013231 Homo sapiens, clone IMAGE:3462987, mRNA | 1.7E-239 |
| 1044 | M00054517D:D12 | MA184:B10 | | NM_000661 | gi 15431302 ref NM_000661.2 Homo sapiens ribosomal protein L9 (RPL9), mRNA | 1E-156 |
| 1045 | M00055002B:G06 | MA198:D10 | | J04164 | gi 177801 gb J04164.1HUM927A Human interferon-inducible protein 9-27 mRNA, complete cds | 1.5E-177 |
| 1046 | M00055749A:C09 | MA170:B04 | 0.08723 | M36532 | gi 179794 gb M36532.1HUMCAIZ Human carbonic anhydrase II mRNA, complete cds | 1.8E-236 |
| 1047 | M00055750A:F10 | MA170:D04 | | X57809 | gi 33714 emb X57809.1HSIGVL009 Human rearranged immunoglobulin lambda light chain mRNA | 4.1E-178 |
| 1048 | M00055757A:H06 | MA170:G04 | | M12759 | gi 532596 gb M12759.1HUMIGJ02 Human Ig J chain gene, exons 3 and 4 | 2.6E-104 |
| 1049 | M00055200B:F03 | MA196:D04 | | AK056446 | gi 16551850 dbj AK056446.1AK056446 Homo sapiens cDNA FLJ31884 fis, clone NT2RP7002906, highly similar to HEAT SHOCK PROTEIN HSP 90- | 2.3E-232 |
| 1050 | M00055203B:F05 | MA196:F04 | | NM_000979 | gi 15431298 ref NM_000979.2 Homo sapiens ribosomal protein L18 (RPL18), mRNA | 3.8E-262 |
| 1051 | M00055980B:F12 | MA179:E04 | | AK000140 | gi 7020034 dbj AK000140.1AK000140 Homo sapiens cDNA FLJ20133 fis, clone COL06539 | 6.8E-270 |
| 1052 | M00056066C:H10 | MA179:B10 | 0.89137 | | | |

Table 3

| SEQ ID NO | Clone ID | MAClone ID | Mask Prent | GBHit | GBDescription | GBScore |
|-----------|----------------|------------|------------|----------|---|----------|
| 1053 | M00056067B:F12 | MA179:C10 | | BC011836 | gi 15080121 gb BC011836.1BC011836 Homo sapiens, clone IMAGE:3945177, mRNA | 7.1E-273 |
| 1054 | M00056075D:H10 | MA179:D10 | | AK027140 | gi 10440192 dbj AK027140.1AK027140 Homo sapiens cDNA: FLJ23487 fis, clone LNG00423 | 3.3E-200 |
| 1055 | M00056962D:A05 | MA177:D10 | | BC017366 | gi 16924194 gb BC017366.1BC017366 Homo sapiens, clone MGC:1191 IMAGE:3506054, mRNA, complete cds | 2.4E-91 |
| 1056 | M00056081D:B09 | MA179:E10 | | AF346964 | gi 13272570 gb AF346964.1AF346964 Homo sapiens mitochondrion, complete genome | 1.9E-93 |
| 1057 | M00056963A:E01 | MA177:E10 | | BC000999 | gi 12803040 gb BC000999.2BC000999 Homo sapiens, Similar to transforming, acidic coiled-coil containing protein 2, clone IMAGE:29849 | 1.9E-276 |
| 1058 | M00056081D:C02 | MA179:F10 | | V00710 | gi 13683 emb V00710.1MIT1HS Human mitochondrial genes for several tRNAs (Phe, Val, Leu) and 12S and 16S ribosomal RNAs | 1.3E-97 |
| 1059 | M00056964D:C08 | MA177:G10 | | M36072 | gi 337494 gb M36072.1HUMRPL7A Human ribosomal protein L7a (surf 3) large subunit mRNA, complete cds | 1.8E-245 |
| 1060 | M00056084A:B08 | MA179:H10 | | U67963 | gi 1763010 gb U67963.1HSU67963 Human lysophospholipase homolog (HU-K5) mRNA, complete cds | 2.3E-136 |
| 1061 | M00054750C:G08 | MA188:B04 | | BC001125 | gi 12654578 gb BC001125.1BC001125 Homo sapiens, peptidylprolyl isomerase B (cyclophilin B), clone MGC:2224 IMAGE:2966791, mRNA, com | 1.1E-190 |
| 1062 | M00054750D:F04 | MA188:C04 | | U30246 | gi 903681 gb U30246.1HSU30246 Human bumetanide-sensitive Na-K-Cl cotransporter (NKCC1) mRNA, complete cds | 3E-247 |
| 1063 | M00054757A:F05 | MA188:G04 | | U86602 | gi 1835785 gb U86602.1HSU86602 Human nucleolar protein p40 mRNA, complete cds | 1E-300 |
| 1064 | M00054760D:B10 | MA188:H04 | | BC014788 | gi 15928638 gb BC014788.1BC014788 Homo sapiens, guanine nucleotide binding protein (G protein), beta polypeptide 2-like 1, clone MG | 1E-300 |
| 1065 | M00042847A:A04 | MA172:A04 | | M61831 | gi 178276 gb M61831.1HUMAHCY Human S-adenosylhomocysteine hydrolase (AHCY) mRNA, complete cds | 5.5E-230 |

Table 3

| SEQ ID NO | Clone ID | MA Clone ID | Mask Prent | GBHit | GBDescription | GBScore |
|-----------|----------------------|-------------|------------|----------|---|----------|
| 1066 | M00042847A:D10 | MA172:B04 | 0.82393 | | gi 177801 gb J04164.1HUM927A | |
| 1067 | M00054917B:G02 | MA168:F04 | | J04164 | Human interferon-inducible protein 9-27 mRNA, complete cds | 6.4E-239 |
| 1068 | M00055468D:D05 | MA168:C10 | | BC001781 | gi 12804704 gb BC001781.1BC001781 Homo sapiens, ribosomal protein L44, clone MGC:2064 IMAGE:3353669, mRNA, complete cds | 2.2E-173 |
| 1069 | M00055469B:E11 | MA168:D10 | 0.52048 | U07969 | gi 483391 gb U07969.1HSU07969 Human intestinal peptide-associated transporter HPT-1 mRNA, complete cds | 7.2E-103 |
| 1070 | M00055492C:C01 | MA168:G10 | | BC003394 | gi 13097278 gb BC003394.1BC003394 Homo sapiens, heterogeneous nuclear ribonucleoprotein C (C1/C2), clone MGC:5418 IMAGE:3447724, mR | 3.2E-253 |
| 1071 | M00055496A:E06 | MA168:H10 | 0.86834 | | | |
| 1072 | M00056742D:D01 | MA175:F04 | | U51924 | gi 1263307 gb U51924.1HSU51924 Human phosphatase 2A inhibitor I2PP2A mRNA, complete cds | 1.3E-199 |
| 1073 | M00056814D:C08 | MA175:G10 | | BC000472 | gi 12653404 gb BC000472.1BC000472 Homo sapiens, ribosomal protein S4, X-linked, clone MGC:8636 IMAGE:2961540, mRNA, complete cds | 2.4E-291 |
| 1074 | RG:1636303:10014:B10 | MA163:B10 | | AJ338808 | gi 15883226 emb AJ338808.1HSA338808 Homo sapiens genomic sequence surrounding NotI site, clone NRI-QA13R | 0 |
| 1075 | RG:1643142:10014:C10 | MA163:C10 | | U14528 | gi 549987 gb U14528.1HSU14528 Human sulfate transporter (DTD) mRNA, complete cds | 5.6E-138 |
| 1076 | RG:1650444:10014:D10 | MA163:D10 | | D10040 | gi 219899 dbj D10040.1HUMLCACS Homo sapiens mRNA for long-chain acyl-CoA synthetase, complete cds | 0 |
| 1077 | RG:1418984:10003:H10 | MA152:H10 | | X52967 | gi 36139 emb X52967.1HSRPL7 Human mRNA for ribosomal protein L7 | 1E-300 |
| 1078 | M00043339C:C12 | MA183:A04 | | X60489 | gi 31099 emb X60489.1HSEF1B Human mRNA for elongation factor-1-beta | 7E-270 |
| 1079 | M00043342C:H03 | MA183:B04 | | AK026558 | gi 10439440 dbj AK026558.1AK026558 Homo sapiens cDNA: FLJ22905 fis, clone KAT05654, highly similar to HUMRPL18A Homo sapiens riboso | 4.1E-159 |

Table 3

| SEQ ID NO | Clone ID | MA Clone ID | Mask Prent | GBHit | GBDescription | GBScore |
|-----------|----------------|-------------|------------|----------|---|----------|
| 1080 | M00043350A:C04 | MA183:D04 | | BC004324 | gi 13279235 gb BC004324.1BC004324 Homo sapiens, ribosomal protein S16, clone MGC:10931 IMAGE:3628799, mRNA, complete cds | 3.7E-231 |
| 1081 | M00056646D:G05 | MA186:B04 | | BC018190 | gi 17390422 gb BC018190.1BC018190 Homo sapiens, Similar to metallothionein 1L, clone MGC:9187 IMAGE:3859643, mRNA, complete cds | 3.4E-172 |
| 1082 | M00055406C:H08 | MA199:D04 | | AF078861 | gi 5531836 gb AF078861.1AF078861 Homo sapiens PTD008 mRNA, complete cds | 1.8E-192 |
| 1083 | M00056653C:F06 | MA186:H04 | | BC005354 | gi 13529169 gb BC005354.1BC005354 Homo sapiens, ribosomal protein, large P2, clone MGC:12453 IMAGE:4052568, mRNA, complete cds | 1.6E-264 |
| 1084 | M00055408A:H06 | MA199:H04 | | AF054183 | gi 4092053 gb AF054183.1AF054183 Homo sapiens GTP binding protein mRNA, complete cds | 1E-187 |
| 1085 | M00055545D:E02 | MA169:A05 | | BC009699 | gi 16307220 gb BC009699.1BC009699 Homo sapiens, Similar to RNA helicase-related protein, clone MGC:9246 IMAGE:3892441, mRNA, comple | 5E-224 |
| 1086 | M00055548B:H07 | MA169:C05 | | AF105253 | gi 7532779 gb AF105253.1AF105253 Homo sapiens neuroendocrine secretory protein 55 mRNA, complete cds | 4.2E-268 |
| 1087 | M00056271C:F02 | MA181:D05 | | BC008323 | gi 14249887 gb BC008323.1BC008323 Homo sapiens, clone MGC:15764 IMAGE:3358085, mRNA, complete cds | 5.8E-202 |
| 1088 | M00055550D:A05 | MA169:F05 | | AF130094 | gi 11493492 gb AF130094.1AF130094 Homo sapiens clone FLC0165 mRNA sequence | 3.4E-225 |
| 1089 | M00055661A:F09 | MA169:E11 | | | | |
| 1090 | M00056427D:A09 | MA173:B05 | | U07550 | gi 469170 gb U07550.1HSU07550 Human chaperonin 10 mRNA, complete cds | 2E-145 |
| 1091 | M00056163C:H09 | MA180:B05 | | AF201944 | gi 9295191 gb AF201944.1AF201944 Homo sapiens HGTD-P (HGTD-P) mRNA, complete cds | 2.2E-285 |
| 1092 | M00056428B:F07 | MA173:C05 | | U30246 | gi 903681 gb U30246.1HSU30246 Human bumetanide-sensitive Na-K-Cl cotransporter (NKCC1) mRNA, complete cds | 9.7E-126 |

Table 3

| SEQ ID NO | Clone ID | MAClone ID | Mask Prent | GBHit | GBDescription | GBScore |
|-----------|----------------|------------|------------|-----------|---|----------|
| 1093 | M00056163D:E01 | MA180:C05 | | BC001829 | gi 12804776 gb BC001829.1BC001829 Homo sapiens, lactate dehydrogenase A, clone MGC:4065 IMAGE:2960999, mRNA, complete cds | 4.4E-240 |
| 1094 | M00056428C:A12 | MA173:E05 | | NM_001016 | gi 14277699 ref NM_001016.2 Homo sapiens ribosomal protein S12 (RPS12), mRNA | 4.2E-212 |
| 1095 | M00056429D:D07 | MA173:F05 | 0.53763 | | | |
| 1096 | M00056175D:B05 | MA180:G05 | | Z62862 | gi 1035240 emb Z62862.1HS74B1R H.sapiens CpG island DNA genomic MseI fragment, clone 74b1, reverse read cpg74b1.rt1a | 6.9E-87 |
| 1097 | M00056507D:D04 | MA173:A11 | 0.65197 | | | |
| 1098 | M00056511D:H07 | MA173:F11 | | BC000419 | gi 12653300 gb BC000419.1BC000419 Homo sapiens, catechol-O-methyltransferase, clone MGC:8663 IMAGE:2964400, mRNA, complete cds | 6.1E-205 |
| 1099 | M00054654A:F12 | MA187:A05 | | NM_000976 | gi 15431291 ref NM_000976.2 Homo sapiens ribosomal protein L12 (RPL12), mRNA | 1E-296 |
| 1100 | M00054868D:F12 | MA189:A05 | | NM_012423 | gi 14591905 ref NM_012423.2 Homo sapiens ribosomal protein L13a (RPL13A), mRNA | 4.4E-140 |
| 1101 | M00054661B:H10 | MA187:D05 | | L47277 | gi 986911 gb L47277.1HUMTOPATR A Homo sapiens (cell line HepG2, HeLa) alpha topoisomerase truncated-form mRNA, 3'UTR | 5.8E-261 |
| 1102 | M00054666B:C07 | MA187:F05 | | AJ250229 | gi 8926686 emb AJ250229.1HSA250229 Homo sapiens mRNA for chromosome 11 hypothetical protein (ORF1) | 6.1E-205 |
| 1103 | M00054870B:H05 | MA189:F05 | | M26326 | gi 186690 gb M26326.1HUMKER18A A Human keratin 18 mRNA, complete cds | 4.8E-121 |
| 1104 | M00054669B:B03 | MA187:G05 | | BC001754 | gi 12804658 gb BC001754.1BC001754 Homo sapiens, male-enhanced antigen, clone MGC:2286 IMAGE:3355279, mRNA, complete cds | 8E-192 |
| 1105 | M00054706B:G04 | MA187:A11 | | AF201944 | gi 9295191 gb AF201944.1AF201944 Homo sapiens HGTD-P (HGTD-P) mRNA, complete cds | 8.3E-251 |
| 1106 | M00054720C:F01 | MA187:D11 | | BC013918 | gi 15530264 gb BC013918.1BC013918 Homo sapiens, Similar to eukaryotic translation elongation factor 1 gamma, clone MGC:22883 IMAGE: | 1.4E-224 |

Table 3

| SEQ ID NO | Clone ID | MAClone ID | Mask Prent | GBHit | GBDescription | GBScore |
|-----------|----------------|------------|------------|-----------|---|----------|
| 1107 | M00054722B:E08 | MA187:E11 | | Z62862 | gi 1035240 emb Z62862.1HS74B1R H.sapiens CpG island DNA genomic MseI fragment, clone 74b1, reverse read cpq74b1.rt1a | 6E-116 |
| 1108 | M00054908A:H08 | MA189:E11 | | L00160 | gi 189904 gb L00160.1HUMPGK2 Human phosphoglycerate kinase (pgk) mRNA, exons 2 to last | 2.4E-291 |
| 1109 | M00054723B:H12 | MA187:G11 | | X60819 | gi 34458 emb X60819.1HSMAOP14 H.sapiens DNA for monoamine oxidase type A (14) (partial) | 1.6E-295 |
| 1110 | M00057210B:G10 | MA193:C05 | | U12404 | gi 531170 gb U12404.1HSU12404 Human Csa-19 mRNA, complete cds | 3.5E-175 |
| 1111 | M00057248D:B05 | MA193:B11 | | NM_001024 | gi 14670385 ref NM_001024.2 Homo sapiens ribosomal protein S21 (RPS21), mRNA | 1.3E-196 |
| 1112 | M00057252A:F06 | MA193:F11 | | AF035555 | gi 3116433 gb AF035555.1AF035555 Homo sapiens short chain L-3-hydroxyacyl-CoA dehydrogenase (SCHAD) mRNA, complete cds | 2.5E-182 |
| 1113 | M00042573B:A02 | MA167:B05 | | BC007583 | gi 14043190 gb BC007583.1BC007583 Homo sapiens, clone MGC:15572 IMAGE:3140342, mRNA, complete cds | 1.6E-102 |
| 1114 | M00042766A:E10 | MA171:F05 | | AF201944 | gi 9295191 gb AF201944.1AF201944 Homo sapiens HGTD-P (HGTD-P) mRNA, complete cds | 2.8E-244 |
| 1115 | M00042882D:G08 | MA167:A11 | | AF346964 | gi 13272570 gb AF346964.1AF346964 Homo sapiens mitochondrion, complete genome | 5.1E-199 |
| 1116 | M00042885C:A12 | MA167:B11 | | NM_001018 | gi 14591911 ref NM_001018.2 Homo sapiens ribosomal protein S15 (RPS15), mRNA | 1.9E-248 |
| 1117 | M00042815A:E07 | MA171:B11 | 0.781 | | | |
| 1118 | M00042817B:E11 | MA171:C11 | | AF077034 | gi 4689115 gb AF077034.1AF077034 Homo sapiens HSPC010 mRNA, complete cds | 5.6E-258 |
| 1119 | M00042887C:A07 | MA167:E11 | | X73502 | gi 406853 emb X73502.1HSENCY20 H. Sapiens mRNA for cytokeratin 20 | 2.1E-195 |
| 1120 | M00042818D:A08 | MA171:G11 | | NM_001002 | gi 16933547 ref NM_001002.2 Homo sapiens ribosomal protein, large, P0 (RPLP0), transcript variant 1, mRNA | 2E-251 |
| 1121 | M00056552A:G08 | MA174:C05 | | AK027892 | gi 14042896 dbj AK027892.1AK027892 2 Homo sapiens cDNA FLJ14986 fis, clone Y79AA1000784, highly similar to Homo sapiens RanBP7/import | 2.4E-291 |

Table 3

| SEQ ID NO | Clone ID | MAClone ID | Mask Prent | GBHit | GBDescription | GBScore |
|-----------|---------------------|------------|------------|----------|---|----------|
| 1122 | M00056552C:D08 | MA174:D05 | | BC017831 | gi 17389602 gb BC017831.1BC017831 Homo sapiens, ribosomal protein L17, clone MGC:22482 IMAGE:4251433, mRNA, complete cds | 2E-279 |
| 1123 | M00056553C:E10 | MA174:E05 | | X14420 | gi 30057 cemb X14420.1HSCOL3AI Human mRNA for pro-alpha-1 type 3 collagen | 5.8E-289 |
| 1124 | M00056555B:C11 | MA174:H05 | | M58458 | gi 337509 gb M58458.1HUMRPS4X Human ribosomal protein S4 (RPS4X) isoform mRNA, complete cds | 1.2E-196 |
| 1125 | M00056611C:D03 | MA174:D11 | | AF081192 | gi 3420798 gb AF081192.1AF081192 Homo sapiens histone H2A.F/Z variant (H2AV) mRNA, complete cds | 3.9E-293 |
| 1126 | M00056611D:B03 | MA174:F11 | | L06498 | gi 292442 gb L06498.1HUMRPS20 Homo sapiens ribosomal protein S20 (RPS20) mRNA, complete cds | 3E-169 |
| 1127 | M00056611D:F08 | MA174:G11 | | M19645 | gi 183644 gb M19645.1HUMGRP78 Human 78 kdalton glucose-regulated protein (GRP78) gene, complete cds | 1.5E-289 |
| 1128 | M00056614C:F06 | MA174:H11 | | AB063318 | gi 14517631 dbj AB063318.1AB063318 Homo sapiens MoDP-2, MoDP-3 mRNA for acute morphine dependence related protein 2, acute morphine | 5.7E-230 |
| 1129 | RG:358387:10009:A05 | MA158:A05 | | BC014270 | gi 15679933 gb BC014270.1BC014270 Homo sapiens, protein kinase C, zeta, clone MGC:10512 IMAGE:3835020, mRNA, complete cds | 2.9E-266 |
| 1130 | M00057302A:F08 | MA182:A05 | | BC007097 | gi 13937968 gb BC007097.1BC007097 Homo sapiens, tissue inhibitor of metalloproteinase 1 (erythroid potentiating activity, collagena | 3.3E-147 |
| 1131 | M00057302C:H09 | MA182:C05 | | BC018210 | gi 17390469 gb BC018210.1BC018210 Homo sapiens, tubulin-specific chaperone a, clone MGC:9129 IMAGE:3861138, mRNA, complete cds | 2.1E-251 |
| 1132 | M00054496A:B09 | MA184:F05 | 0.60245 | BC002589 | gi 12803524 gb BC002589.1BC002589 Homo sapiens, proteasome (prosome, macropain) 26S subunit, ATPase, 2, clone MGC:3004 IMAGE:316179 | 3.5E-64 |

Table 3

| SEQ ID NO | Clone ID | MAClone ID | Mask Prcnt | GBHit | GBDescription | GBScore |
|-----------|----------------|------------|------------|-----------|---|----------|
| 1133 | M00054496A:H05 | MA184:H05 | | BC004138 | gi 13278716 gb BC004138.1BC004138 Homo sapiens, ribosomal protein L6, clone MGC:1635 IMAGE:2823733, mRNA, complete cds | 1.4E-286 |
| 1134 | M00042460B:A08 | MA182:A11 | | NM_000980 | gi 15431299 ref NM_000980.2 Homo sapiens ribosomal protein L18a (RPL18A), mRNA | 8.7E-229 |
| 1135 | M00054524B:B09 | MA184:A11 | | NM_000976 | gi 15431291 ref NM_000976.2 Homo sapiens ribosomal protein L12 (RPL12), mRNA | 4.1E-296 |
| 1136 | M00054526C:E05 | MA184:B11 | | NM_000988 | gi 17017972 ref NM_000988.2 Homo sapiens ribosomal protein L27 (RPL27), mRNA | 7E-189 |
| 1137 | M00042516B:A08 | MA182:C11 | | NM_000976 | gi 15431291 ref NM_000976.2 Homo sapiens ribosomal protein L12 (RPL12), mRNA | 2E-248 |
| 1138 | M00042517D:H10 | MA182:D11 | | BC000386 | gi 12653234 gb BC000386.1BC000386 Homo sapiens, eukaryotic translation initiation factor 3, subunit 3 (gamma, 40kD), clone MGC:8431 | 3.8E-178 |
| 1139 | M00054527B:H11 | MA184:D11 | | AF155235 | gi 6318598 gb AF155235.1AF155235 Homo sapiens 15.5 kD RNA binding protein mRNA, complete cds | 4.5E-240 |
| 1140 | M00042517D:H11 | MA182:E11 | | BC016756 | gi 16876963 gb BC016756.1BC016756 Homo sapiens, glutathione peroxidase 2 (gastrointestinal), clone IMAGE:3681457, mRNA | 1.4E-230 |
| 1141 | M00054529C:G04 | MA184:G11 | | NM_022551 | gi 14165467 ref NM_022551.2 Homo sapiens ribosomal protein S18 (RPS18), mRNA | 2.7E-213 |
| 1142 | M00043300D:A06 | MA182:H11 | | BC012146 | gi 15082460 gb BC012146.1BC012146 Homo sapiens, Similar to ribosomal protein L3, clone MGC:20359 IMAGE:4549682, mRNA, complete cds | 3.6E-259 |
| 1143 | M00054958A:G10 | MA198:C05 | | AY007723 | gi 15431041 gb AY007723.1 Homo sapiens MAL2 protecolipid (MAL2) mRNA, complete cds | 2.6E-185 |
| 1144 | M00054958B:B07 | MA198:D05 | 0.12023 | AF012108 | gi 2331249 gb AF012108.1AF012108 Homo sapiens Amplified in Breast Cancer (AIB1) mRNA, complete cds | 2.6E-111 |
| 1145 | M00054961D:E08 | MA198:H05 | | NM_005617 | gi 14141191 ref NM_005617.2 Homo sapiens ribosomal protein S14 (RPS14), mRNA | 3.2E-172 |
| 1146 | M00055015C:H02 | MA198:C11 | | X58965 | gi 35069 emb X58965.1HSNM23H2G H.sapiens RNA for nm23-H2 gene | 4.4E-187 |

Table 3

| SEQ ID NO | Clone ID | MA Clone ID | Mask Prent | GBHit | GBDescription | GBScore |
|-----------|----------------|-------------|------------|-----------|--|----------|
| 1147 | M00055016B:D03 | MA198:E11 | | NM_001010 | gi 17158043 ref NM_001010.2 Homo sapiens ribosomal protein S6 (RPS6), mRNA | 1.7E-186 |
| 1148 | M00055764D:D05 | MA170:E05 | | BC001708 | gi 12804576 gb BC001708.1BC001708 Homo sapiens, ribosomal protein S3A, clone MGC:1626 IMAGE:3544072, mRNA, complete cds | 9.8E-210 |
| 1149 | M00055815C:E08 | MA170:B11 | | AK025459 | gi 10437979 dbj AK025459.1AK025459 Homo sapiens cDNA: FLJ21806 fis, clone HEP00829, highly similar to HSTRA1 Human tra1 mRNA for hu | 4.8E-249 |
| 1150 | M00055819B:B12 | MA170:F11 | | AF014838 | gi 2281706 gb AF014838.1AF014838 Homo sapiens galectin-4 mRNA, complete cds | 8.3E-254 |
| 1151 | M00055820C:H11 | MA170:H11 | | NM_000967 | gi 16507968 ref NM_000967.2 Homo sapiens ribosomal protein L3 (RPL3), mRNA | 3.4E-175 |
| 1152 | M00055204B:C04 | MA196:A05 | | X57351 | gi 311373 emb X57351.1HS18D Human 1-8D gene from interferon-inducible gene family | 1.2E-218 |
| 1153 | M00055209A:C09 | MA196:D05 | | AF028832 | gi 3287488 gb AF028832.1AF028832 Homo sapiens Hsp89-alpha-delta-N mRNA, complete cds | 9.1E-232 |
| 1154 | M00055252C:G12 | MA196:D11 | 0.1038 | U16738 | gi 608516 gb U16738.1HSU16738 Homo sapiens CAG-isl 7 mRNA, complete cds | 1E-172 |
| 1155 | M00056934C:D08 | MA177:A05 | | Z69043 | gi 2398656 emb Z69043.1HSTRAPRN A H.sapiens mRNA translocon-associated protein delta subunit precursor | 3.2E-281 |
| 1156 | M00055989C:D03 | MA179:B05 | 0.8 | | | |
| 1157 | M00056937C:G12 | MA177:D05 | | AK055020 | gi 16549662 dbj AK055020.1AK055020 Homo sapiens cDNA FLJ30458 fis, clone BRACE2009421, highly similar to NUCLEOSOME ASSEMBLY PROTEIN | 3.2E-219 |
| 1158 | M00055997B:A02 | MA179:H05 | 0.89264 | | | |
| 1159 | M00056087A:G01 | MA179:C11 | | AF150754 | gi 12484558 gb AF150754.2AF150754 Homo sapiens 3'phosphoadenosine 5'-phosphosulfate synthase 2b isoform mRNA, complete cds | 2.4E-96 |
| 1160 | M00056091A:H05 | MA179:D11 | | BC013724 | gi 15489238 gb BC013724.1BC013724 Homo sapiens, ferritin, heavy polypeptide 1, clone MGC:17255 IMAGE:3857790, mRNA, complete cds | 3.9E-265 |

Table 3

| SEQ ID NO | Clone ID | MAClone ID | Mask Prent | GBHit | GBDescription | GBScore |
|-----------|----------------|------------|------------|-----------|---|----------|
| 1161 | M00056966B:A05 | MA177:E11 | | AF346974 | gi 13272710 gb AF346974.1AF346974 Homo sapiens mitochondrion, complete genome | 5.6E-108 |
| 1162 | M00056093A:F08 | MA179:F11 | 0.26754 | | | |
| 1163 | M00056096C:H10 | MA179:H11 | 0.77419 | | | |
| 1164 | M00054766B:E10 | MA188:H05 | | BC005328 | gi 13529103 gb BC005328.1BC005328 Homo sapiens, ribosomal protein S27a, clone MGC:12414, mRNA, complete cds | 5.8E-258 |
| 1165 | M00054817B:H09 | MA188:B11 | | BC015465 | gi 15930040 gb BC015465.1BC015465 Homo sapiens, HSPC023 protein, clone MGC:8754 IMAGE:3914049, mRNA, complete cds | 8.4E-254 |
| 1166 | M00054818D:G04 | MA188:D11 | | BC008495 | gi 14250151 gb BC008495.1BC008495 Homo sapiens, nucleophosmin (nucleolar phosphoprotein B23, numatrin), clone MGC:14826 IMAGE:42766 | 1.4E-258 |
| 1167 | M00042851D:H04 | MA172:A05 | | NM_001000 | gi 16306563 ref NM_001000.2 Homo sapiens ribosomal protein L39 (RPL39), mRNA | 3.7E-156 |
| 1168 | M00042853A:F01 | MA172:B05 | | NM_000970 | gi 16753226 ref NM_000970.2 Homo sapiens ribosomal protein L6 (RPL6), mRNA | 3.4E-284 |
| 1169 | M00055426A:G06 | MA168:E05 | | AF272149 | gi 9971873 gb AF272149.1AF272149 Homo sapiens hepatocellular carcinoma associated-gene TB6, mRNA sequence | 1.3E-61 |
| 1170 | M00055496A:G12 | MA168:B11 | | AF203815 | gi 6979641 gb AF203815.1AF203815 Homo sapiens alpha gene sequence | 5.6E-202 |
| 1171 | M00055509C:C02 | MA168:F11 | 0.76684 | AL590401 | gi 14422235 emb AL590401.6AL590401 Human DNA sequence from clone RP11-466P12 on chromosome 6, complete sequence [Homo sapiens] | 1.8E-35 |
| 1172 | M00055510B:F08 | MA168:G11 | | AF067174 | gi 4894381 gb AF067174.1AF067174 Homo sapiens retinol dehydrogenase homolog mRNA, complete cds | 2.2E-257 |
| 1173 | M00055510D:A08 | MA168:H11 | | AK026649 | gi 10439547 dbj AK026649.1AK026649 Homo sapiens cDNA: FLJ22996 fis, clone KAT11938 | 1.6E-161 |
| 1174 | M00056748C:B08 | MA175:B05 | | AF054183 | gi 4092053 gb AF054183.1AF054183 Homo sapiens GTP binding protein mRNA, complete cds | 1.2E-165 |
| 1175 | M00056749A:F01 | MA175:C05 | | Y14736 | gi 2765422 emb Y14736.1HSIGG1KL Homo sapiens mRNA for immunoglobulin kappa light chain | 1.2E-249 |

Table 3

| SEQ ID NO | Clone ID | MAClone ID | Mask Prent | GBHit | GBDescription | GBScore |
|-----------|----------------------|------------|------------|-----------|---|----------|
| 1176 | M00056754B:A10 | MA175:G05 | | V00710 | gi 13683 emb V00710.1MIT1HS Human mitochondrial genes for several tRNAs (Phe, Val, Leu) and 12S and 16S ribosomal RNAs | 6.3E-292 |
| 1177 | M00056754B:H06 | MA175:H05 | | D38112 | gi 644480 dbj D38112.1HUMMTA Homo sapiens mitochondrial DNA, complete sequence | 1.4E-252 |
| 1178 | RG:1653390:10014:E05 | MA163:E05 | | M15353 | gi 306486 gb M15353.1HUMIF4E Homo sapiens cap-binding protein mRNA, complete cds | 1.5E-138 |
| 1179 | RG:1669553:10014:G05 | MA163:G05 | | X03663 | gi 29899 emb X03663.1HSCFMS Human mRNA for c-fms proto-oncogene | 5.8E-221 |
| 1180 | M00043355A:H12 | MA183:B05 | | M94314 | gi 292436 gb M94314.1HUMRPL30A Homo sapiens ribosomal protein L30 mRNA, complete cds | 7.9E-66 |
| 1181 | M00043355B:F10 | MA183:C05 | | AK055653 | gi 16550433 dbj AK055653.1AK055653 Homo sapiens cDNA FLJ31091 fis, clone IMR321000155, highly similar to 60S RIBOSOMAL PROTEIN L35A | 1.1E-165 |
| 1182 | M00043357B:B10 | MA183:G05 | | NM_000978 | gi 14591907 ref NM_000978.2 Homo sapiens ribosomal protein L23 (RPL23), mRNA | 3.7E-206 |
| 1183 | M00054557C:D09 | MA185:G05 | | NM_012423 | gi 14591905 ref NM_012423.2 Homo sapiens ribosomal protein L13a (RPL13A), mRNA | 9.6E-167 |
| 1184 | M00043358B:G11 | MA183:H05 | | M60854 | gi 338446 gb M60854.1HUMSRAA Human ribosomal protein S16 mRNA, complete cds | 5.2E-280 |
| 1185 | M00043396D:B04 | MA183:A11 | | AF026166 | gi 4090928 gb AF026166.1AF026166 Homo sapiens chapronin-containing TCP-1 beta subunit homolog mRNA, complete cds | 4.1E-237 |
| 1186 | M00054612D:D11 | MA185:H11 | | NM_006013 | gi 15718685 ref NM_006013.2 Homo sapiens ribosomal protein L10 (RPL10), mRNA | 1.2E-171 |
| 1187 | M00055409B:D08 | MA199:A05 | | BC016748 | gi 16876941 gb BC016748.1BC016748 Homo sapiens, ribosomal protein L37a, clone MGC:26772 IMAGE:4831278, mRNA, complete cds | 3.6E-55 |
| 1188 | M00055409D:F06 | MA199:B05 | | V00572 | gi 35434 emb V00572.1HSPGK1 Human mRNA encoding phosphoglycerate kinase | 1.6E-186 |
| 1189 | M00055410A:A06 | MA199:C05 | 0.80422 | | | |
| 1190 | M00056659A:D08 | MA186:F05 | | M15470 | gi 187680 gb M15470.1HUMMHB44 Human MHC class I HLA-B44 mRNA, partial cds | 3E-275 |

Table 3

| SEQ ID NO | Clone ID | MAClone ID | Mask Prent | GBHit | GBDescription | GBScore |
|-----------|----------------|------------|------------|----------|---|----------|
| 1191 | M00056704C:H08 | MA186:D11 | | BC001125 | gi 12654578 gb BC001125.1BC001125 Homo sapiens, peptidylprolyl isomerase B (cyclophilin B), clone MGC:2224 IMAGE:2966791, mRNA, com | 8.2E-282 |
| 1192 | M00055553C:B06 | MA169:A06 | | | | |
| 1193 | M00056280B:D10 | MA181:A06 | 0.72079 | | | |
| 1194 | M00056282D:G10 | MA181:C06 | 0.05211 | AJ420520 | gi 17066384 cemb AJ420520.1HSA420520 Homo sapiens mRNA full length insert cDNA clone EUROIMAGE 1979495 | 1.5E-88 |
| 1195 | M00056288B:A12 | MA181:G06 | | D14530 | gi 414348 dbj D14530.1HUMRSPT Human homolog of yeast ribosomal protein S28, complete cds | 9.8E-23 |
| 1196 | M00055686D:E11 | MA169:B12 | | L02785 | gi 291963 gb L02785.1HUMDRA Homo sapiens colon mucosa-associated (DRA) mRNA, complete cds | 5.9E-202 |
| 1197 | M00042346B:F09 | MA181:C12 | 0.23093 | AK000168 | gi 7020079 dbj AK000168.1AK000168 Homo sapiens cDNA FLJ20161 fis, clone COL09252, highly similar to L33930 Homo sapiens CD24 signal | 7.4E-202 |
| 1198 | M00055698C:E05 | MA169:E12 | 0.82609 | | | |
| 1199 | M00042347C:D07 | MA181:E12 | | M12759 | gi 532596 gb M12759.1HUMIGJ02 Human Ig J chain gene, exons 3 and 4 | 3.2E-166 |
| 1200 | M00055702C:C04 | MA169:F12 | 0.85 | | | |
| 1201 | M00042348C:F03 | MA181:G12 | | X60489 | gi 31099 cemb X60489.1HSEF1B Human mRNA for elongation factor-1-beta | 6.8E-233 |
| 1202 | M00055335D:E01 | MA197:D06 | | BC003510 | gi 13097578 gb BC003510.1BC003510 Homo sapiens, prothymosin, alpha (gene sequence 28), clone MGC:10549 IMAGE:3610808, mRNA, complet | 2.6E-176 |
| 1203 | M00056180C:E06 | MA180:B06 | | BC018190 | gi 17390422 gb BC018190.1BC018190 Homo sapiens, Similar to metallothionein 1L, clone MGC:9187 IMAGE:3859643, mRNA, complete cds | 5.3E-171 |
| 1204 | M00056184B:G11 | MA180:D06 | | Y00345 | gi 35569 cemb Y00345.1HSPOLYAB Human mRNA for polyA binding protein | 8.2E-254 |
| 1205 | M00056514A:F06 | MA173:A12 | | AJ335311 | gi 15879729 cemb AJ335311.1HSA335311 Homo sapiens genomic sequence surrounding NotI site, clone NRI-WB8C | 7.7E-54 |

Table 3

| SEQ ID NO | Clone ID | MAClone ID | Mask Prent | GBHit | GBDescription | GBScore |
|-----------|----------------|------------|------------|-----------|---|----------|
| 1206 | M00056514C:H11 | MA173:D12 | | BC000386 | gi 12653234 gb BC000386.1BC000386 Homo sapiens, eukaryotic translation initiation factor 3, subunit 3 (gamma, 40kD), clone MGC:8431 | 1.8E-242 |
| 1207 | M00054674D:C05 | MA187:C06 | | D14530 | gi 414348 dbj D14530.1HUMRSPT Human homolog of yeast ribosomal protein S28, complete cds | 8.3E-198 |
| 1208 | M00054675A:H07 | MA187:D06 | | X00474 | gi 35706 emb X00474.1HSPS2 Human pS2 mRNA induced by estrogen from human breast cancer cell line MCF-7 | 7.8E-170 |
| 1209 | M00054878A:G12 | MA189:D06 | | AL359678 | gi 15215911 emb AL359678.15AL359678 Human DNA sequence from clone RP11-550J21 on chromosome 9, complete sequence [Homo sapiens] | 2.4E-207 |
| 1210 | M00054676B:D07 | MA187:H06 | | BC000749 | gi 13879207 gb BC000749.1BC000749 Homo sapiens, lactate dehydrogenase A, clone MGC:2417 IMAGE:2960999, mRNA, complete cds | 2.9E-129 |
| 1211 | M00054725A:E09 | MA187:B12 | | NM_022551 | gi 14165467 ref NM_022551.2 Homo sapiens ribosomal protein S18 (RPS18), mRNA | 2.7E-241 |
| 1212 | M00054924C:B09 | MA189:C12 | 0.63711 | | | |
| 1213 | M00054726D:B04 | MA187:D12 | | X16064 | gi 37495 emb X16064.1HSTUMP Human mRNA for translationally controlled tumor protein | 1.1E-271 |
| 1214 | M00054927A:H09 | MA189:E12 | | X06705 | gi 35511 emb X06705.1HSPLAX Human PLA-X mRNA | 2.7E-297 |
| 1215 | M00054727C:F11 | MA187:F12 | 0.7234 | | | |
| 1216 | M00054728A:H05 | MA187:H12 | | X16064 | gi 37495 emb X16064.1HSTUMP Human mRNA for translationally controlled tumor protein | 1.3E-168 |
| 1217 | M00054930B:G05 | MA189:H12 | | U15008 | gi 600747 gb U15008.1HSU15008 Human SnRNP core protein Sm D2 mRNA, complete cds | 7E-270 |
| 1218 | M00057214C:G11 | MA193:B06 | | U55206 | gi 2957143 gb U55206.1HSU55206 Homo sapiens human gamma-glutamyl hydrolase (hGH) mRNA, complete cds | 4.1E-115 |
| 1219 | M00057216C:G01 | MA193:D06 | | BC000695 | gi 12653812 gb BC000695.1BC000695 Homo sapiens, Similar to tetraspan 1, clone IMAGE:3349380, mRNA | 7.3E-28 |

Table 3

| SEQ ID NO | Clone ID | MA Clone ID | Mask Prent | GBHit | GBDescription | GBScore |
|-----------|----------------|-------------|------------|-----------|--|----------|
| 1220 | M00057217C:B07 | MA193:F06 | | AK057120 | gi 16552707 dbj AK057120.1AK057120 Homo sapiens cDNA FLJ32558 fis, clone SPLEN1000143, highly similar to HIGH MOBILITY GROUP PROTEIN | 3.6E-206 |
| 1221 | M00042695A:H04 | MA167:B06 | | BC007075 | gi 13937928 gb BC007075.1BC007075 Homo sapiens, hemoglobin, beta, clone MGC:14540 IMAGE:4292125, mRNA, complete cds | 9.6E-37 |
| 1222 | M00042695D:D09 | MA167:C06 | | BC018749 | gi 17511797 gb BC018749.1BC018749 Homo sapiens, Similar to immunoglobulin lambda joining 3, clone MGC:31942 IMAGE:4854511, mRNA, co | 3.5E-194 |
| 1223 | M00042771A:D01 | MA171:D06 | | BC007659 | gi 14043327 gb BC007659.1BC007659 Homo sapiens, diaphorase (NADH/NADPH) (cytochrome b-5 reductase), clone MGC:2073 IMAGE:3349257, m | 6.7E-239 |
| 1224 | M00042772D:F02 | MA171:E06 | | NM_002295 | gi 9845501 ref NM_002295.2 Homo sapiens laminin receptor 1 (67kD, ribosomal protein SA) (LAMR1), mRNA | 2.2E-254 |
| 1225 | M00042773A:A12 | MA171:F06 | | AK000009 | gi 7019813 dbj AK000009.1AK000009 Homo sapiens cDNA FLJ20002 fis, clone ADKA01577 | 2.6E-213 |
| 1226 | M00042699B:B10 | MA167:G06 | | X98311 | gi 1524059 emb X98311.1HSCGM2A NT H.sapiens mRNA for carcinoembryonic antigen family member 2, CGM2 | 1.5E-31 |
| 1227 | M00042889A:H07 | MA167:A12 | | NM_005950 | gi 10835229 ref NM_005950.1 Homo sapiens metallothionein 1G (MT1G), mRNA | 6E-202 |
| 1228 | M00042819A:C09 | MA171:A12 | | BC009220 | gi 14327996 gb BC009220.1BC009220 Homo sapiens, clone MGC:16362 IMAGE:3927795, mRNA, complete cds | 5.2E-218 |
| 1229 | M00042819C:B03 | MA171:B12 | | NM_000995 | gi 16117786 ref NM_000995.2 Homo sapiens ribosomal protein L34 (RPL34), transcript variant 1, mRNA | 9.4E-207 |
| 1230 | M00042895B:C02 | MA167:C12 | | AF217186 | gi 11526786 gb AF217186.1AF217186 Homo sapiens inorganic pyrophosphatase 1 (PPA1) mRNA, complete cds | 1.4E-283 |
| 1231 | M00042823B:A02 | MA171:C12 | | AF212248 | gi 13182770 gb AF212248.1AF212248 Homo sapiens CDA09 mRNA, complete cds | 5.1E-252 |

Table 3

| SEQ ID NO | Clone ID | MAClone ID | Mask Prent | GBHit | GBDescription | GBScore |
|-----------|---------------------|------------|------------|----------|---|----------|
| 1232 | M00042895D:B04 | MA167:E12 | | U83908 | gi 1825561 gb U83908.1HSU83908 Human nuclear antigen H731 mRNA, complete cds | 2.4E-229 |
| 1233 | M00056564B:F11 | MA174:F06 | | AL136593 | gi 7018431 emb AL136593.1HSM8015 67 Homo sapiens mRNA; cDNA DKFZp761K102 (from clone DKFZp761K102); complete cds | 3.4E-284 |
| 1234 | M00056564C:E08 | MA174:G06 | | Z74616 | gi 1418929 emb Z74616.1HSPPA2ICO H.sapiens mRNA for prepro-alpha2(I) collagen | 1.4E-286 |
| 1235 | M00056615D:A01 | MA174:A12 | | X12881 | gi 34036 emb X12881.1HSKER18R Human mRNA for cytokeratin 18 | 1.8E-273 |
| 1236 | M00056620D:F02 | MA174:G12 | | AK000335 | gi 7020350 dbj AK000335.1AK000335 Homo sapiens cDNA FLJ20328 fis, clone HEP10039 | 3.5E-287 |
| 1237 | RG:359184:10009:A06 | MA158:A06 | | M35663 | gi 189505 gb M35663.1HUMP68A Human p68 kinase mRNA, complete cds | 1.6E-258 |
| 1238 | RG:428530:10009:D12 | MA158:D12 | | AF321918 | gi 12958659 gb AF321918.1AF321918 Homo sapiens testicular acid phosphatase (ACPT) gene, complete cds, alternatively spliced product | 0 |
| 1239 | M00057310A:A07 | MA182:A06 | | AF054187 | gi 4092059 gb AF054187.1AF054187 Homo sapiens alpha NAC mRNA, complete cds | 7.3E-143 |
| 1240 | M00054503C:H10 | MA184:F06 | | BC018828 | gi 17402971 gb BC018828.1BC018828 Homo sapiens, clone IMAGE:3343539, mRNA | 2E-276 |
| 1241 | M00043302C:D03 | MA182:C12 | | BC006791 | gi 13905015 gb BC006791.1BC006791 Homo sapiens, ribosomal protein L10a, clone MGC:5203 IMAGE:2901249, mRNA, complete cds | 8.3E-282 |
| 1242 | M00054535B:F10 | MA184:F12 | | S35960 | gi 249370 gb S35960.1S35960 laminin receptor homolog {3' region} [human, mRNA Partial, 739 nt] | 4.1E-112 |
| 1243 | M00054535C:D10 | MA184:G12 | | BC008063 | gi 14165520 gb BC008063.1BC008063 Homo sapiens, Similar to KIAA0102 gene product, clone MGC:2249 IMAGE:2967488, mRNA, complete cds | 4.7E-274 |
| 1244 | M00054535C:H09 | MA184:H12 | | AB020680 | gi 4240234 dbj AB020680.1AB020680 Homo sapiens mRNA for KIAA0873 protein, partial cds | 3.1E-275 |

Table 3

| SEQ ID NO | Clone ID | MAClone ID | Mask Prent | GBHit | GBDescription | GBScore |
|-----------|----------------|------------|------------|-----------|---|----------|
| 1245 | M00054964B:A08 | MA198:C06 | | BC017189 | gi 16877928 gb BC017189.1BC017189 Homo sapiens, myo-inositol 1-phosphate synthase A1, clone MGC:726 IMAGE:3140452, mRNA, complete c | 1.1E-190 |
| 1246 | M00054966C:H01 | MA198:D06 | | BC018828 | gi 17402971 gb BC018828.1BC018828 Homo sapiens, clone IMAGE:3343539, mRNA | 4.4E-190 |
| 1247 | M00055022D:F01 | MA198:D12 | | NM_000975 | gi 15431289 ref NM_000975.2 Homo sapiens ribosomal protein L11 (RPL11), mRNA | 2.5E-182 |
| 1248 | M00055026C:C12 | MA198:G12 | | NM_007209 | gi 16117792 ref NM_007209.2 Homo sapiens ribosomal protein L35 (RPL35), mRNA | 4E-184 |
| 1249 | M00055027B:C11 | MA198:H12 | | AF283772 | gi 10281741 gb AF283772.2AF283772 Homo sapiens clone TCBAPO781 mRNA sequence | 1E-187 |
| 1250 | M00055826D:C11 | MA170:E12 | 0.7443 | | | |
| 1251 | M00055828C:D10 | MA170:G12 | | V00662 | gi 13003 emb V00662.1MIHSXX H.sapiens mitochondrial genome | 9.5E-229 |
| 1252 | M00055828D:F12 | MA170:H12 | 0.71968 | BC001573 | gi 16306770 gb BC001573.1BC001573 Homo sapiens, clone MGC:5522 IMAGE:3454199, mRNA, complete cds | 2.8E-37 |
| 1253 | M00055215C:E11 | MA196:B06 | | BC001118 | gi 12654566 gb BC001118.1BC001118 Homo sapiens, Similar to seven transmembrane domain protein, clone MGC:1936 IMAGE:2989840, mRNA, | 2.4E-288 |
| 1254 | M00055217C:E09 | MA196:D06 | | BC010187 | gi 14603477 gb BC010187.1BC010187 Homo sapiens, ribosomal protein S11, clone MGC:20218 IMAGE:4547934, mRNA, complete cds | 4.3E-215 |
| 1255 | M00055221B:C01 | MA196:E06 | | NM_001016 | gi 14277699 ref NM_001016.2 Homo sapiens ribosomal protein S12 (RPS12), mRNA | 4.7E-246 |
| 1256 | M00055222A:E02 | MA196:G06 | | NM_000987 | gi 17017970 ref NM_000987.2 Homo sapiens ribosomal protein L26 (RPL26), mRNA | 2.1E-226 |
| 1257 | M00056226D:F03 | MA180:B12 | | BC011835 | gi 15080118 gb BC011835.1BC011835 Homo sapiens, Similar to ATPase, Na+/K+ transporting, beta 3 polypeptide, clone MGC:20152 IMAGE:3 | 1.7E-57 |
| 1258 | M00055258A:G02 | MA196:F12 | | BC016753 | gi 16876954 gb BC016753.1BC016753 Homo sapiens, clone MGC:1138 IMAGE:2987963, mRNA, complete cds | 1.3E-102 |

Table 3

| SEQ ID NO | Clone ID | MAClone ID | Mask Prent | GBHit | GBDescription | GBScore |
|-----------|----------------|------------|------------|-----------|---|----------|
| 1259 | M00055998A:A02 | MA179:A06 | | AF343729 | gi 13649973 gb AF343729.1AF343729 Homo sapiens 3-alpha hydroxysteroid dehydrogenase mRNA, complete cds | 1.4E-283 |
| 1260 | M00056945A:B11 | MA177:A06 | 0.89778 | | | |
| 1261 | M00056945D:H03 | MA177:C06 | 0.71282 | | | |
| 1262 | M00056001A:F11 | MA179:D06 | | BC015983 | gi 16359036 gb BC015983.1BC015983 Homo sapiens, clone IMAGE:4074053, mRNA | 4.5E-165 |
| 1263 | M00056946D:B04 | MA177:F06 | | AF028832 | gi 3287488 gb AF028832.1AF028832 Homo sapiens Hsp89-alpha-delta-N mRNA, complete cds | 1E-296 |
| 1264 | M00056101B:B02 | MA179:A12 | | AL049999 | gi 4884252 emb AL049999.1HSM8003 47 Homo sapiens mRNA; cDNA DKFZp564M182 (from clone DKFZp564M182); partial cds | 3E-100 |
| 1265 | M00056110C:D09 | MA179:E12 | | AK024903 | gi 10437317 dbj AK024903.1AK024903 3 Homo sapiens cDNA: FLJ21250 fis, clone COL01253, highly similar to AB020527 Homo sapiens mRNA fo | 1E-209 |
| 1266 | M00056111B:H03 | MA179:F12 | 0.81436 | | | |
| 1267 | M00054772B:H06 | MA188:G06 | | L19185 | gi 440307 gb L19185.1HUMNKEFB Human natural killer cell enhancing factor (NKEFB) mRNA, complete cds | 3.6E-178 |
| 1268 | M00054825B:B05 | MA188:C12 | 0.09038 | NM_005348 | gi 13129149 ref NM_005348.1 Homo sapiens heat shock 90kD protein 1, alpha (HSPCA), mRNA | 4.1E-222 |
| 1269 | M00054831A:G04 | MA188:D12 | | AL359585 | gi 8655645 emb AL359585.1HSM8026 87 Homo sapiens mRNA; cDNA DKFZp762B195 (from clone DKFZp762B195) | 6.2E-116 |
| 1270 | M00054831D:B07 | MA188:F12 | | U43701 | gi 1399085 gb U43701.1HSU43701 Human ribosomal protein L23a mRNA, complete cds | 4.2E-296 |
| 1271 | M00042862D:A12 | MA172:B06 | | BC007097 | gi 13937968 gb BC007097.1BC007097 Homo sapiens, tissue inhibitor of metalloproteinase 1 (erythroid potentiating activity, collagena | 1.9E-248 |
| 1272 | M00042864A:E05 | MA172:E06 | 0.59184 | | | |
| 1273 | M00042864D:E06 | MA172:F06 | | NM_007099 | gi 6005987 ref NM_007099.1 Homo sapiens acid phosphatase 1, soluble (ACP1), transcript variant b, mRNA | 3.5E-228 |
| 1274 | M00055514B:A05 | MA168:E12 | | BC001190 | gi 12654700 gb BC001190.1BC001190 Homo sapiens, Similar to creatine kinase, brain, clone MGC:3160 IMAGE:3354679, mRNA, complete cds | 1.4E-230 |

Table 3

| SEQ ID NO | Clone ID | MAClone ID | Mask Prent | GBHit | GBDescription | GBScore |
|-----------|----------------------|------------|------------|-----------|--|----------|
| 1275 | M00056763B:A12 | MA175:D06 | | NM_004417 | gi 7108342 ref NM_004417.2 Homo sapiens dual specificity phosphatase 1 (DUSP1), mRNA | 6.4E-267 |
| 1276 | M00056767D:F06 | MA175:F06 | | AF203815 | gi 6979641 gb AF203815.1 AF203815 Homo sapiens alpha gene sequence | 8.6E-285 |
| 1277 | M00056821A:D08 | MA175:A12 | | NM_001016 | gi 14277699 ref NM_001016.2 Homo sapiens ribosomal protein S12 (RPS12), mRNA | 8.3E-220 |
| 1278 | M00056822C:G03 | MA175:C12 | | NM_000970 | gi 16753226 ref NM_000970.2 Homo sapiens ribosomal protein L6 (RPL6), mRNA | 3.4E-284 |
| 1279 | M00056823D:H02 | MA175:E12 | | BC018828 | gi 17402971 gb BC018828.1 BC018828 Homo sapiens, clone IMAGE:3343539, mRNA | 1.9E-276 |
| 1280 | RG:1609994:10014:A06 | MA163:A06 | | BC006322 | gi 13623444 gb BC006322.1 BC006322 Homo sapiens, activating transcription factor 3, clone MGC:12746 IMAGE:4138076, mRNA, complete cd | 1E-300 |
| 1281 | RG:1667183:10014:F12 | MA163:F12 | | BC000013 | gi 12652546 gb BC000013.1 BC000013 Homo sapiens, insulin-like growth factor binding protein 3, clone MGC:2305 IMAGE:3506666, mRNA, c | 5.4E-58 |
| 1282 | M00043358D:C06 | MA183:A06 | | AF113008 | gi 6642739 gb AF113008.1 AF113008 Homo sapiens clone FLB0708 mRNA sequence | 1.5E-152 |
| 1283 | M00054558B:E05 | MA185:A06 | 0.69811 | BC014498 | gi 15680272 gb BC014498.1 BC014498 Homo sapiens, clone IMAGE:4856273, mRNA | 1.1E-27 |
| 1284 | M00043361B:G03 | MA183:E06 | | NM_001025 | gi 14790142 ref NM_001025.2 Homo sapiens ribosomal protein S23 (RPS23), mRNA | 1.3E-218 |
| 1285 | M00043408C:D11 | MA183:G12 | | U14967 | gi 550014 gb U14967.1 HSU14967 Human ribosomal protein L21 mRNA, complete cds | 1.4E-283 |
| 1286 | M00054632A:E11 | MA185:H12 | 0.18764 | X73459 | gi 313660 emb X73459.1 HSSRP14A H.sapiens mRNA for signal recognition particle subunit 14 | 2E-140 |
| 1287 | M00056661A:G05 | MA186:A06 | | L18960 | gi 306724 gb L18960.1 HUMEIF4C Human protein synthesis factor (eIF-4C) mRNA, complete cds | 5.2E-280 |
| 1288 | M00056661C:C11 | MA186:B06 | | S72481 | gi 632789 gb S72481.1 S72481 pantophysin [human, keratinocyte line HaCaT, mRNA, 2106 nt] | 3.4E-281 |
| 1289 | M00055412D:E05 | MA199:B06 | | M26697 | gi 189311 gb M26697.1 HUMNUMB23 Human nucleolar protein (B23) mRNA, complete cds | 8.9E-176 |

Table 3

| SEQ ID NO | Clone ID | MAClone ID | Mask Prent | GBHit | GBDescription | GBScore |
|-----------|---------------------|------------|------------|-----------|---|----------|
| 1290 | M00055413A:G12 | MA199:C06 | | BC012354 | gi 15214456 gb BC012354.1BC012354 Homo sapiens, clone MGC:20390 IMAGE:4564801, mRNA, complete cds | 1.9E-95 |
| 1291 | M00055414D:A09 | MA199:D06 | | X06705 | gi 35511 emb X06705.1HSPLAX Human PLA-X mRNA | 4.1E-187 |
| 1292 | M00056707B:C01 | MA186:C12 | | AF178581 | gi 10800410 gb AF178581.2AF178581 Homo sapiens nasopharyngeal carcinoma gene sequence | 1.3E-252 |
| 1293 | M00056237D:C10 | MA181:D01 | 0.64821 | | | |
| 1294 | M00056238B:D03 | MA181:E01 | | AF083241 | gi 5106776 gb AF083241.1HSPC024 Homo sapiens HSPC024 mRNA, complete cds | 9.4E-257 |
| 1295 | M00056239B:D05 | MA181:G01 | 0.89873 | | | |
| 1296 | M00056241B:H07 | MA181:H01 | 0.625 | NM_033340 | gi 15718701 ref NM_033340.1 Homo sapiens caspase 7, apoptosis-related cysteine protease (CASP7), transcript variant beta, mRNA | 2.2E-50 |
| 1297 | I:2921194:04B02:C06 | MA118:C06 | | AB006780 | gi 2385451 dbj AB006780.1AB006780 Homo sapiens mRNA for galectin-3, complete cds | 3.1E-222 |
| 1298 | I:1624865:04B02:G06 | MA118:G06 | | U15009 | gi 600749 gb U15009.1HSU15009 Human SnRNP core protein Sm D3 mRNA, complete cds | 4.7E-246 |
| 1299 | I:1728607:04A02:H06 | MA116:H06 | | BC016164 | gi 16740573 gb BC016164.1BC016164 Homo sapiens, small inducible cytokine subfamily D (Cys-X3-Cys), member 1 (fractalkine, neurotact | 1E-262 |
| 1300 | I:2827453:04B02:H06 | MA118:H06 | | U27143 | gi 862932 gb U27143.1HSU27143 Human protein kinase C inhibitor-I cDNA, complete cds | 2.5E-113 |
| 1301 | I:2070593:04B02:D12 | MA118:D12 | | D83004 | gi 1181557 dbj D83004.1D83004 Human epidermoid carcinoma mRNA for ubiquitin-conjugating enzyme E2 similar to Drosophila bendless ge | 1.5E-233 |
| 1302 | I:2683114:04A02:H12 | MA116:H12 | | L20493 | gi 306754 gb L20493.1HUMGAGLUT D Human gamma-glutamyl transpeptidase mRNA, complete cds | 1E-300 |
| 1303 | I:1809336:02A02:G06 | MA108:G06 | | U09117 | gi 483919 gb U09117.1HSU09117 Human phospholipase c delta 1 mRNA, complete cds | 1.3E-280 |

Table 4

| SEQ ID NO | SpotID | Clone ID | MAClone ID | >=2x | >=5x | <=halfx | Num Ratios |
|--------------|--------|----------------|------------|-------------|-------------|-------------|---------------|
| 1 | 18 | M00026919B:A10 | MA40:F01 | 41.17647059 | 20.58823529 | 0 | 34 |
| 2 | 20 | M00026919B:E07 | MA40:G01 | 0 | 0 | 20.58823529 | 34 |
| 3 | 22 | M00026919D:F04 | MA40:H01 | 20.58823529 | 8.823529412 | 0 | 34 |
| 4 | 54 | M00026914D:G06 | MA40:A01 | 0 | 0 | 58.82352941 | 34 |
| 5 | 56 | M00026950A:A09 | MA40:D07 | 0 | 0 | 32.35294118 | 34 |
| 6 | 67 | M00003820C:A09 | MA244:B01 | 0 | 0 | 23.52941176 | 34 |
| 7 | 73 | M00001673A:G03 | MA244:E01 | 23.52941176 | 0 | 5.882352941 | 34 |
| 8 | 115 | M00007939A:A12 | MA27:B07 | 55.88235294 | 5.882352941 | 0 | 34 |
| 9 | 119 | M00007939A:B11 | MA27:D07 | 0 | 0 | 29.41176471 | 34 |
| 10 | 127 | M00007939B:G03 | MA27:H07 | 0 | 0 | 55.88235294 | 34 |
| 11 | 166 | M00007997D:G08 | MA29:C01 | 0 | 0 | 47.05882353 | 34 |
| 12 | 220 | M00026894C:E11 | MA39:F07 | 38.23529412 | 0 | 0 | 34 |
| 13 | 238 | M00001391A:C05 | MA15:G01 | 5.882352941 | 0 | 38.23529412 | 34 |
| 14 | 294 | M00006818A:A06 | MA240:C01 | 20.58823529 | 0 | 0 | 34 |
| 15 | 393 | M00023278A:F09 | MA36:E01 | 0 | 0 | 41.17647059 | 34 |
| 16 | 405 | M00023299A:G01 | MA36:C07 | 70.58823529 | 8.823529412 | 0 | 34 |
| 17 | 411 | M00023301A:A11 | MA36:F07 | 26.47058824 | 0 | 0 | 34 |
| 18 | 453 | M00008050A:D12 | MA30:C01 | 23.52941176 | 2.941176471 | 0 | 34 |
| 19 | 460 | M00022135A:C04 | MA35:F01 | 0 | 0 | 23.52941176 | 34 |
| 20 | 462 | M00022137A:A05 | MA35:G01 | 26.47058824 | 11.76470588 | 0 | 34 |
| 21 | 466 | M00022176C:A07 | MA35:A07 | 8.823529412 | 0 | 20.58823529 | 34 |
| 22 | 471 | M00008077B:A08 | MA30:D07 | 41.17647059 | 2.941176471 | 0 | 34 |
| 23 | 477 | M00008077C:D09 | MA30:G07 | 26.47058824 | 0 | 0 | 34 |
| 24 | 492 | M00022081C:E09 | MA34:F01 | 32.35294118 | 0 | 0 | 34 |
| 25 | 495 | M00001662A:G06 | MA24:H01 | 0 | 0 | 20.58823529 | 34 |
| 26 | 504 | M00022102B:B11 | MA34:D07 | 35.29411765 | 8.823529412 | 0 | 34 |
| 27 | 506 | M00022102B:E08 | MA34:E07 | 0 | 0 | 29.41176471 | 34 |
| 28 | 556 | M00022569D:G06 | MA22:F01 | 8.823529412 | 0 | 35.29411765 | 34 |
| 29 | 577 | M00001358B:B11 | MA14:A01 | 52.94117647 | 2.941176471 | 0 | 34 |
| 30 | 578 | M00001429A:G04 | MA16:A01 | 79.41176471 | 29.41176471 | 0 | 34 |
| 31 | 579 | M00001358B:F05 | MA14:B01 | 82.35294118 | 32.35294118 | 0 | 34 |
| 32 | 582 | M00001429C:C03 | MA16:C01 | 44.11764706 | 2.941176471 | 0 | 34 |
| 33 | 585 | M00001359D:B04 | MA14:E01 | 38.23529412 | 0 | 0 | 34 |
| 34 | 587 | M00001360A:E10 | MA14:F01 | 50 | 0 | 0 | 34 |
| 35 | 589 | M00001360C:B05 | MA14:G01 | 61.76470588 | 8.823529412 | 2.941176471 | 34 |
| 36 | 590 | M00001430B:F01 | MA16:G01 | 38.23529412 | 0 | 0 | 34 |
| 37 | 592 | M00001430C:A02 | MA16:H01 | 44.11764706 | 0 | 0 | 34 |
| 38 | 594 | M00001445C:H05 | MA16:A07 | 50 | 2.941176471 | 0 | 34 |
| 39 | 596 | M00001445D:D07 | MA16:B07 | 0 | 0 | 47.05882353 | 34 |
| 40 | 605 | M00001374D:D10 | MA14:G07 | 70.58823529 | 5.882352941 | 0 | 34 |
| 41 | 607 | M00001375A:A08 | MA14:H07 | 38.23529412 | 8.823529412 | 14.70588235 | 34 |
| 42 | 643 | M00006600A:E07 | MA241:B01 | 61.76470588 | 5.882352941 | 0 | 34 |
| 43 | 661 | M00006690A:F06 | MA241:C07 | 0 | 0 | 20.58823529 | 34 |
| 44 | 739 | M00023325D:A08 | MA37:B02 | 2.941176471 | 0 | 23.52941176 | 34 |
| 45 | 742 | M00026921D:F12 | MA40:C02 | 38.23529412 | 8.823529412 | 0 | 34 |
| 46 | 743 | M00023325D:F06 | MA37:D02 | 32.35294118 | 2.941176471 | 0 | 34 |
| 47 | 750 | M00026924A:E09 | MA40:G02 | 79.41176471 | 0 | 0 | 34 |
| 48 | 823 | M00007940C:A04 | MA27:D08 | 0 | 0 | 23.52941176 | 34 |
| 49 | 827 | M00007941C:H03 | MA27:F08 | 38.23529412 | 5.882352941 | 0 | 34 |

Table 4

| SEQ ID NO | SpotID | Clone ID | MAClone ID | >=2x | >=5x | <=halfx | Num Ratios |
|--------------|--------|----------------|------------|-------------|-------------|-------------|---------------|
| 50 | 828 | M00021638B:F03 | MA31:F08 | 0 | 0 | 58.82352941 | 34 |
| 51 | 831 | M00007941D:C04 | MA27:H08 | 55.88235294 | 2.941176471 | 0 | 34 |
| 52 | 842 | M00004054D:D02 | | 0 | 0 | 26.47058824 | 34 |
| 53 | 857 | M00001507A:A10 | MA23:E08 | 23.52941176 | 23.52941176 | 0 | 34 |
| 54 | 858 | M00004198D:A01 | | 26.47058824 | 5.882352941 | 0 | 34 |
| 55 | 861 | M00001528C:B08 | MA23:G08 | 0 | 0 | 29.41176471 | 34 |
| 56 | 868 | M00008002C:A05 | MA29:B03 | 50 | 0 | 0 | 34 |
| 57 | 880 | M00008006C:H05 | MA29:H03 | 0 | 0 | 52.94117647 | 34 |
| 58 | 898 | M00026850C:A01 | MA39:A02 | 0 | 0 | 20.58823529 | 34 |
| 59 | 908 | M00026853D:C07 | MA39:F02 | 38.23529412 | 0 | 0 | 34 |
| 60 | 920 | M00026896A:C09 | MA39:D08 | 32.35294118 | 2.941176471 | 2.941176471 | 34 |
| 61 | 934 | M00001391B:D02 | MA15:C02 | 73.52941176 | 11.76470588 | 0 | 34 |
| 62 | 938 | M00001391B:H05 | MA15:E02 | 26.47058824 | 5.882352941 | 0 | 34 |
| 63 | 940 | M00001391D:C07 | MA15:F02 | 41.17647059 | 2.941176471 | 0 | 34 |
| 64 | 942 | M00001392B:B01 | MA15:G02 | 52.94117647 | 5.882352941 | 0 | 34 |
| 65 | 954 | M00001407B:C03 | MA15:E08 | 55.88235294 | 2.941176471 | 0 | 34 |
| 66 | 1011 | M00005635B:E02 | MA242:B08 | 0 | 0 | 29.41176471 | 34 |
| 67 | 1017 | M00005636B:B06 | MA242:E08 | 70.58823529 | 5.882352941 | 0 | 34 |
| 68 | 1018 | M00006971A:E06 | MA240:E08 | 64.70588235 | 11.76470588 | 0 | 34 |
| 69 | 1019 | M00005636D:B08 | MA242:F08 | 52.94117647 | 2.941176471 | 0 | 34 |
| 70 | 1107 | M00023302C:A04 | MA36:B08 | 20.58823529 | 8.823529412 | 2.941176471 | 34 |
| 71 | 1117 | M00023305A:C02 | MA36:G08 | 23.52941176 | 2.941176471 | 2.941176471 | 34 |
| 72 | 1172 | M00022180A:E08 | MA35:B08 | 0 | 0 | 58.82352941 | 34 |
| 73 | 1178 | M00022181C:H11 | MA35:E08 | 20.58823529 | 5.882352941 | 0 | 34 |
| 74 | 1193 | M00001673A:C11 | | 41.17647059 | 2.941176471 | 0 | 34 |
| 75 | 1201 | M00003853B:C07 | | 23.52941176 | 11.76470588 | 0 | 34 |
| 76 | 1204 | M00022106B:D04 | MA34:B08 | 32.35294118 | 0 | 0 | 34 |
| 77 | 1209 | M00003858B:G01 | MA24:E08 | 0 | 0 | 23.52941176 | 34 |
| 78 | 1214 | M00022109B:A11 | MA34:G08 | 0 | 0 | 32.35294118 | 34 |
| 79 | 1260 | M00022921A:H05 | MA22:F02 | 0 | 0 | 29.41176471 | 34 |
| 80 | 1282 | M00001430D:H07 | MA16:A02 | 73.52941176 | 11.76470588 | 0 | 34 |
| 81 | 1283 | M00001360D:H10 | MA14:B02 | 85.29411765 | 29.41176471 | 0 | 34 |
| 82 | 1284 | M00001431A:E01 | MA16:B02 | 41.17647059 | 5.882352941 | 2.941176471 | 34 |
| 83 | 1285 | M00001361A:A02 | MA14:C02 | 64.70588235 | 2.941176471 | 0 | 34 |
| 84 | 1295 | M00001362A:B03 | MA14:H02 | 44.11764706 | 2.941176471 | 0 | 34 |
| 85 | 1297 | M00001376C:C01 | MA14:A08 | 0 | 0 | 76.47058824 | 34 |
| 86 | 1300 | M00001449A:D02 | MA16:B08 | 55.88235294 | 2.941176471 | 0 | 34 |
| 87 | 1301 | M00001378B:A02 | MA14:C08 | 67.64705882 | 2.941176471 | 0 | 34 |
| 88 | 1302 | M00001450A:D12 | MA16:C08 | 26.47058824 | 0 | 0 | 34 |
| 89 | 1303 | M00001378C:D08 | MA14:D08 | 50 | 0 | 0 | 34 |
| 90 | 1310 | M00001451D:F01 | MA16:G08 | 44.11764706 | 8.823529412 | 0 | 34 |
| 91 | 1349 | M00006628B:A02 | MA241:C02 | 20.58823529 | 0 | 0 | 34 |
| 92 | 1444 | M00026926C:F03 | MA40:B03 | 73.52941176 | 11.76470588 | 0 | 34 |
| 93 | 1458 | M00026963B:H03 | MA40:A09 | 0 | 0 | 29.41176471 | 34 |
| 94 | 1464 | M00026964A:E10 | MA40:D09 | 29.41176471 | 5.882352941 | 0 | 34 |
| 95 | 1468 | M00026965C:A11 | MA40:F09 | 67.64705882 | 26.47058824 | 0 | 34 |
| 96 | 1493 | M00001398A:D11 | MA244:C09 | 50 | 2.941176471 | 0 | 34 |
| 97 | 1512 | M00008095C:H08 | MA31:D03 | 20.58823529 | 5.882352941 | 2.941176471 | 34 |
| 98 | 1523 | M00007942A:F12 | MA27:B09 | 52.94117647 | 5.882352941 | 0 | 34 |

Table 4

| SEQ ID NO | SpotID | Clone ID | MAClone ID | >=2x | >=5x | <=halfx | Num Ratios |
|--------------|--------|----------------|------------|-------------|-------------|-------------|---------------|
| 99 | 1554 | M00004212B:B12 | MA25:A09 | 0 | 0 | 20.58823529 | 34 |
| 100 | 1576 | M00008014C:E11 | MA29:D05 | 0 | 0 | 23.52941176 | 34 |
| 101 | 1578 | M00008015A:B05 | MA29:E05 | 58.82352941 | 2.941176471 | 0 | 34 |
| 102 | 1586 | M00022049A:B08 | MA33:A05 | 29.41176471 | 0 | 0 | 34 |
| 103 | 1602 | M00026856B:F08 | MA39:A03 | 0 | 0 | 50 | 34 |
| 104 | 1604 | M00026856C:H12 | MA39:B03 | 0 | 0 | 32.35294118 | 34 |
| 105 | 1628 | M00026900D:A03 | MA39:F09 | 50 | 5.882352941 | 0 | 34 |
| 106 | 1630 | M00026900D:C12 | MA39:G09 | 52.94117647 | 8.823529412 | 0 | 34 |
| 107 | 1632 | M00026901D:A03 | MA39:H09 | 32.35294118 | 5.882352941 | 5.882352941 | 34 |
| 108 | 1642 | M00001393A:G03 | MA15:E03 | 50 | 0 | 0 | 34 |
| 109 | 1656 | M00001409B:D03 | MA15:D09 | 29.41176471 | 2.941176471 | 0 | 34 |
| 110 | 1658 | M00001409B:G01 | MA15:E09 | 55.88235294 | 8.823529412 | 0 | 34 |
| 111 | 1660 | M00001410C:C09 | MA15:F09 | 41.17647059 | 0 | 0 | 34 |
| 112 | 1662 | M00001410D:A03 | MA15:G09 | 26.47058824 | 11.76470588 | 11.76470588 | 34 |
| 113 | 1697 | M00005504D:F06 | MA242:A03 | 0 | 0 | 23.52941176 | 34 |
| 114 | 1709 | M00005510D:H10 | MA242:G03 | 0 | 0 | 32.35294118 | 34 |
| 115 | 1726 | M00006990D:D06 | MA240:G09 | 38.23529412 | 2.941176471 | 0 | 34 |
| 116 | 1761 | SL146 | MA248:A03 | 0 | 0 | 20.58823529 | 34 |
| 117 | 1775 | SL153 | MA248:H03 | 0 | 0 | 23.52941176 | 34 |
| 118 | 1785 | SL198 | MA248:E09 | 0 | 0 | 67.64705882 | 34 |
| 119 | 1787 | SL199 | MA248:F09 | 0 | 0 | 26.47058824 | 34 |
| 120 | 1789 | SL200 | MA248:G09 | 0 | 0 | 32.35294118 | 34 |
| 121 | 1797 | M00023283D:C03 | MA36:C03 | 26.47058824 | 5.882352941 | 0 | 34 |
| 122 | 1799 | M00023283D:D03 | MA36:D03 | 0 | 0 | 85.29411765 | 34 |
| 123 | 1801 | M00023284A:D09 | MA36:E03 | 70.58823529 | 8.823529412 | 2.941176471 | 34 |
| 124 | 1807 | M00023285D:C05 | MA36:H03 | 67.64705882 | 29.41176471 | 0 | 34 |
| 125 | 1809 | M00023306C:H11 | MA36:A09 | 41.17647059 | 0 | 0 | 34 |
| 126 | 1813 | M00023308D:B06 | MA36:C09 | 32.35294118 | 5.882352941 | 11.76470588 | 34 |
| 127 | 1817 | M00023309D:H04 | MA36:E09 | 0 | 0 | 23.52941176 | 34 |
| 128 | 1819 | M00023310A:D07 | MA36:F09 | 0 | 0 | 29.41176471 | 34 |
| 129 | 1875 | M00008079C:H04 | MA30:B09 | 20.58823529 | 11.76470588 | 2.941176471 | 34 |
| 130 | 1883 | M00008080B:B10 | MA30:F09 | 20.58823529 | 14.70588235 | 0 | 34 |
| 131 | 1884 | M00022198D:C02 | MA35:F09 | 23.52941176 | 8.823529412 | 0 | 34 |
| 132 | 1886 | M00022198D:G03 | MA35:G09 | 38.23529412 | 8.823529412 | 0 | 34 |
| 133 | 1895 | M00003768B:B09 | MA24:D03 | 58.82352941 | 2.941176471 | 0 | 34 |
| 134 | 1910 | M00022110C:A08 | MA34:C09 | 0 | 0 | 26.47058824 | 34 |
| 135 | 1913 | M00003886C:H08 | MA24:E09 | 0 | 0 | 20.58823529 | 34 |
| 136 | 1960 | M00023297B:A10 | MA22:D03 | 5.882352941 | 2.941176471 | 52.94117647 | 34 |
| 137 | 1966 | M00023314C:G05 | MA22:G03 | 20.58823529 | 0 | 0 | 34 |
| 138 | 1991 | M00001363B:C04 | MA14:D03 | 0 | 0 | 47.05882353 | 34 |
| 139 | 1992 | M00001434D:F08 | MA16:D03 | 73.52941176 | 8.823529412 | 0 | 34 |
| 140 | 1994 | M00001435B:A04 | MA16:E03 | 23.52941176 | 5.882352941 | 0 | 34 |
| 141 | 1996 | M00001435B:B09 | MA16:F03 | 55.88235294 | 5.882352941 | 0 | 34 |
| 142 | 2000 | M00001435C:F08 | MA16:H03 | 58.82352941 | 11.76470588 | 0 | 34 |
| 143 | 2001 | M00001381A:F03 | MA14:A09 | 47.05882353 | 8.823529412 | 0 | 34 |
| 144 | 2004 | M00001453B:E11 | MA16:B09 | 29.41176471 | 2.941176471 | 0 | 34 |
| 145 | 2008 | M00001453C:D02 | MA16:D09 | 61.76470588 | 5.882352941 | 0 | 34 |
| 146 | 2050 | M00007121D:A05 | MA243:A03 | 35.29411765 | 0 | 0 | 34 |
| 147 | 2052 | M00007122C:F03 | MA243:B03 | 26.47058824 | 0 | 0 | 34 |

Table 4

| SEQ ID NO | SpotID | Clone ID | MAClone ID | >=2x | >=5x | <=halfx | Num Ratios |
|--------------|--------|----------------|------------|-------------|-------------|-------------|---------------|
| 148 | 2053 | M00006638A:G02 | MA241:C03 | 47.05882353 | 0 | 0 | 34 |
| 149 | 2059 | M00006639B:H09 | MA241:F03 | 0 | 0 | 32.35294118 | 34 |
| 150 | 2064 | M00007127C:C11 | MA243:H03 | 2.941176471 | 0 | 20.58823529 | 34 |
| 151 | 2073 | M00006720D:C11 | MA241:E09 | 47.05882353 | 5.882352941 | 0 | 34 |
| 152 | 2075 | M00006728C:E07 | MA241:F09 | 38.23529412 | 0 | 0 | 34 |
| 153 | 2156 | M00026931D:E08 | MA40:F04 | 32.35294118 | 5.882352941 | 0 | 34 |
| 154 | 2158 | M00026932D:B08 | MA40:G04 | 58.82352941 | 5.882352941 | 0 | 34 |
| 155 | 2168 | M00026969D:D02 | MA40:D10 | 29.41176471 | 2.941176471 | 0 | 34 |
| 156 | 2169 | M00023393B:E02 | MA37:E10 | 35.29411765 | 2.941176471 | 0 | 34 |
| 157 | 2185 | M00003782D:D06 | MA244:E04 | 32.35294118 | 0 | 0 | 34 |
| 158 | 2189 | M00004105D:B04 | MA244:G04 | 67.64705882 | 20.58823529 | 0 | 34 |
| 159 | 2199 | M00001556D:B11 | MA244:D10 | 0 | 0 | 23.52941176 | 34 |
| 160 | 2234 | M00021664B:G03 | MA31:E10 | 0 | 0 | 32.35294118 | 34 |
| 161 | 2242 | M00004078A:A07 | | 0 | 0 | 20.58823529 | 34 |
| 162 | 2263 | M00001561A:B03 | MA23:D10 | 0 | 0 | 20.58823529 | 34 |
| 163 | 2284 | M00008023C:A06 | MA29:F07 | 32.35294118 | 0 | 0 | 34 |
| 164 | 2286 | M00008024C:F02 | MA29:G07 | 61.76470588 | 5.882352941 | 0 | 34 |
| 165 | 2288 | M00008024C:G06 | MA29:H07 | 2.941176471 | 0 | 23.52941176 | 34 |
| 166 | 2292 | M00022057C:H10 | MA33:B07 | 55.88235294 | 2.941176471 | 0 | 34 |
| 167 | 2294 | M00022059B:B06 | MA33:C07 | 2.941176471 | 0 | 58.82352941 | 34 |
| 168 | 2324 | M00026902B:F10 | MA39:B10 | 26.47058824 | 8.823529412 | 23.52941176 | 34 |
| 169 | 2342 | M00001394D:B08 | MA15:C04 | 23.52941176 | 2.941176471 | 0 | 34 |
| 170 | 2354 | M00001415A:G05 | MA15:A10 | 41.17647059 | 0 | 0 | 34 |
| 171 | 2356 | M00001416B:E03 | MA15:B10 | 50 | 5.882352941 | 0 | 34 |
| 172 | 2368 | M00001421B:B12 | MA15:H10 | 47.05882353 | 2.941176471 | 0 | 34 |
| 173 | 2413 | M00005528C:E02 | MA242:G04 | 50 | 0 | 0 | 34 |
| 174 | 2513 | M00023312D:F10 | MA36:A10 | 41.17647059 | 5.882352941 | 0 | 34 |
| 175 | 2566 | M00022157A:C06 | MA35:C04 | 35.29411765 | 0 | 0 | 34 |
| 176 | 2576 | M00022165A:A11 | MA35:H04 | 44.11764706 | 8.823529412 | 0 | 34 |
| 177 | 2584 | M00022206A:B10 | MA35:D10 | 0 | 0 | 67.64705882 | 34 |
| 178 | 2601 | M00003811B:F09 | | 26.47058824 | 2.941176471 | 0 | 34 |
| 179 | 2605 | M00003812D:A11 | | 73.52941176 | 11.76470588 | 0 | 34 |
| 180 | 2606 | M00022088D:C10 | MA34:G04 | 29.41176471 | 0 | 0 | 34 |
| 181 | 2613 | M00003910B:C12 | | 20.58823529 | 2.941176471 | 0 | 34 |
| 182 | 2689 | M00001366A:F06 | MA14:A04 | 23.52941176 | 0 | 0 | 34 |
| 183 | 2692 | M00001435C:F12 | MA16:B04 | 58.82352941 | 5.882352941 | 0 | 34 |
| 184 | 2694 | M00001436B:E11 | MA16:C04 | 41.17647059 | 2.941176471 | 11.76470588 | 34 |
| 185 | 2695 | M00001366B:E01 | MA14:D04 | 38.23529412 | 2.941176471 | 0 | 34 |
| 186 | 2696 | M00001436C:C03 | MA16:D04 | 35.29411765 | 2.941176471 | 0 | 34 |
| 187 | 2700 | M00001437A:B01 | MA16:F04 | 26.47058824 | 0 | 0 | 34 |
| 188 | 2702 | M00001437B:B08 | MA16:G04 | 67.64705882 | 8.823529412 | 0 | 34 |
| 189 | 2712 | M00001467B:H05 | | 64.70588235 | 5.882352941 | 0 | 34 |
| 190 | 2716 | M00001468A:D02 | MA16:F10 | 0 | 0 | 20.58823529 | 34 |
| 191 | 2756 | M00007131B:B11 | MA243:B04 | 23.52941176 | 2.941176471 | 0 | 34 |
| 192 | 2761 | M00006650A:A10 | MA241:E04 | 0 | 0 | 23.52941176 | 34 |
| 193 | 2765 | M00006653C:B09 | MA241:G04 | 55.88235294 | 14.70588235 | 0 | 34 |
| 194 | 2766 | M00007154B:H08 | MA243:G04 | 0 | 0 | 47.05882353 | 34 |
| 195 | 2769 | M00006740A:E02 | MA241:A10 | 0 | 0 | 32.35294118 | 34 |
| 196 | 2770 | M00021621A:D04 | MA243:A10 | 58.82352941 | 2.941176471 | 0 | 34 |

Table 4

| SEQ ID NO | SpotID | Clone ID | MAClone ID | >=2x | >=5x | <=halfx | Num Ratios |
|--------------|--------|----------------|------------|-------------|-------------|-------------|---------------|
| 197 | 2771 | M00006740B:F11 | MA241:B10 | 0 | 0 | 20.58823529 | 34 |
| 198 | 2773 | M00006741C:A01 | MA241:C10 | 50 | 2.941176471 | 0 | 34 |
| 199 | 2780 | M00022171C:A04 | MA243:F10 | 29.41176471 | 0 | 0 | 34 |
| 200 | 2858 | M00026937C:B08 | MA40:E05 | 23.52941176 | 8.823529412 | 0 | 34 |
| 201 | 2861 | M00023367A:H06 | MA37:G05 | 61.76470588 | 0 | 0 | 34 |
| 202 | 2876 | M00026985C:E12 | MA40:F11 | 29.41176471 | 2.941176471 | 0 | 34 |
| 203 | 2916 | M00008100A:A07 | MA31:B05 | 41.17647059 | 2.941176471 | 0 | 34 |
| 204 | 2921 | M00007936B:H07 | MA27:E05 | 47.05882353 | 5.882352941 | 2.941176471 | 34 |
| 205 | 2924 | M00008100C:E05 | MA31:F05 | 20.58823529 | 0 | 0 | 34 |
| 206 | 2937 | M00007947B:B02 | MA27:E11 | 61.76470588 | 0 | 0 | 34 |
| 207 | 2956 | M00004105A:C09 | MA25:F05 | 52.94117647 | 0 | 0 | 34 |
| 208 | 2957 | M00001433C:D09 | MA23:G05 | 29.41176471 | 14.70588235 | 0 | 34 |
| 209 | 2980 | M00008027B:D09 | MA29:B09 | 0 | 0 | 64.70588235 | 34 |
| 210 | 2984 | M00008028D:B01 | MA29:D09 | 0 | 0 | 26.47058824 | 34 |
| 211 | 2988 | M00008039A:C09 | MA29:F09 | 52.94117647 | 5.882352941 | 0 | 34 |
| 212 | 3026 | M00026905A:A10 | MA39:A11 | 29.41176471 | 0 | 5.882352941 | 34 |
| 213 | 3030 | M00026905D:C05 | MA39:C11 | 0 | 0 | 35.29411765 | 34 |
| 214 | 3054 | M00001401B:A06 | MA15:G05 | 52.94117647 | 0 | 0 | 34 |
| 215 | 3056 | M00001402A:A08 | MA15:H05 | 61.76470588 | 2.941176471 | 0 | 34 |
| 216 | 3105 | M00005534C:E12 | MA242:A05 | 0 | 0 | 26.47058824 | 34 |
| 217 | 3111 | M00005542A:D09 | MA242:D05 | 47.05882353 | 0 | 0 | 34 |
| 218 | 3132 | M00007031D:E02 | MA240:F11 | 23.52941176 | 2.941176471 | 0 | 34 |
| 219 | 3134 | M00007032A:D04 | MA240:G11 | 26.47058824 | 5.882352941 | 0 | 34 |
| 220 | 3135 | M00005813C:F12 | MA242:H11 | 23.52941176 | 2.941176471 | 0 | 34 |
| 221 | 3171 | SL163 | MA248:B05 | 0 | 0 | 32.35294118 | 34 |
| 222 | 3173 | SL164 | MA248:C05 | 0 | 0 | 20.58823529 | 34 |
| 223 | 3179 | SL167 | MA248:F05 | 0 | 0 | 32.35294118 | 34 |
| 224 | 3181 | SL168 | MA248:G05 | 0 | 0 | 26.47058824 | 34 |
| 225 | 3183 | SL169 | MA248:H05 | 0 | 0 | 20.58823529 | 34 |
| 226 | 3231 | M00023320B:A03 | MA36:H11 | 44.11764706 | 8.823529412 | 0 | 34 |
| 227 | 3238 | M00005350B:F10 | MA246:C05 | 35.29411765 | 0 | 0 | 34 |
| 228 | 3267 | M00008069D:F01 | MA30:B05 | 20.58823529 | 2.941176471 | 0 | 34 |
| 229 | 3268 | M00022165B:C08 | MA35:B05 | 20.58823529 | 2.941176471 | 0 | 34 |
| 230 | 3272 | M00022165C:E12 | MA35:D05 | 50 | 2.941176471 | 0 | 34 |
| 231 | 3274 | M00022166C:E07 | MA35:E05 | 0 | 0 | 23.52941176 | 34 |
| 232 | 3275 | M00008072D:E12 | MA30:F05 | 35.29411765 | 20.58823529 | 2.941176471 | 34 |
| 233 | 3282 | M00022211B:D05 | MA35:A11 | 20.58823529 | 11.76470588 | 0 | 34 |
| 234 | 3293 | M00008089A:E09 | MA30:G11 | 20.58823529 | 17.64705882 | 0 | 34 |
| 235 | 3317 | M00003974D:E04 | MA24:C11 | 2.941176471 | 0 | 55.88235294 | 34 |
| 236 | 3323 | M00003980D:F10 | MA24:F11 | 47.05882353 | 11.76470588 | 0 | 34 |
| 237 | 3327 | M00003984D:C08 | MA24:H11 | 20.58823529 | 0 | 0 | 34 |
| 238 | 3370 | M00023373D:A01 | MA22:E05 | 0 | 0 | 88.23529412 | 34 |
| 239 | 3376 | M00023396D:D01 | MA22:H05 | 0 | 0 | 38.23529412 | 34 |
| 240 | 3394 | M00001437D:E12 | MA16:A05 | 5.882352941 | 0 | 47.05882353 | 34 |
| 241 | 3396 | M00001438A:B09 | MA16:B05 | 5.882352941 | 0 | 44.11764706 | 34 |
| 242 | 3401 | M00001369A:C07 | MA14:E05 | 76.47058824 | 14.70588235 | 0 | 34 |
| 243 | 3404 | M00001439C:A07 | MA16:F05 | 55.88235294 | 5.882352941 | 0 | 34 |
| 244 | 3407 | M00001369C:A05 | MA14:H05 | 38.23529412 | 5.882352941 | 0 | 34 |
| 245 | 3410 | M00001468D:B11 | MA16:A11 | 44.11764706 | 0 | 0 | 34 |

Table 4

| SEQ ID NO | SpotID | Clone ID | MAClone ID | >=2x | >=5x | <=halfx | Num Ratios |
|--------------|--------|----------------|------------|-------------|-------------|-------------|---------------|
| 246 | 3411 | M00001386B:F08 | MA14:B11 | 23.52941176 | 0 | 0 | 34 |
| 247 | 3419 | M00001387A:A08 | MA14:F11 | 73.52941176 | 20.58823529 | 2.941176471 | 34 |
| 248 | 3460 | M00007163A:B10 | MA243:B05 | 32.35294118 | 2.941176471 | 0 | 34 |
| 249 | 3465 | M00006675C:A06 | MA241:E05 | 0 | 0 | 35.29411765 | 34 |
| 250 | 3470 | M00007191C:A06 | MA243:G05 | 58.82352941 | 8.823529412 | 0 | 34 |
| 251 | 3471 | M00006678A:D02 | MA241:H05 | 26.47058824 | 2.941176471 | 0 | 34 |
| 252 | 3562 | M00026941C:A12 | MA40:E06 | 50 | 23.52941176 | 0 | 34 |
| 253 | 3578 | M00026996A:E01 | MA40:E12 | 20.58823529 | 0 | 0 | 34 |
| 254 | 3581 | M00023401B:E06 | MA37:G12 | 0 | 0 | 35.29411765 | 34 |
| 255 | 3584 | M00027005B:D03 | MA40:H12 | 0 | 0 | 20.58823529 | 34 |
| 256 | 3621 | M00007937B:A02 | MA27:C06 | 23.52941176 | 17.64705882 | 0 | 34 |
| 257 | 3622 | M00021612C:E11 | MA31:C06 | 0 | 0 | 32.35294118 | 34 |
| 258 | 3629 | M00007938C:C12 | MA27:G06 | 35.29411765 | 0 | 0 | 34 |
| 259 | 3675 | M00001623C:A06 | MA23:F12 | 61.76470588 | 5.882352941 | 0 | 34 |
| 260 | 3677 | M00001630D:A11 | MA23:G12 | 0 | 0 | 64.70588235 | 34 |
| 261 | 3682 | M00008044B:E11 | MA29:A11 | 41.17647059 | 0 | 0 | 34 |
| 262 | 3684 | M00008044C:C10 | MA29:B11 | 32.35294118 | 20.58823529 | 0 | 34 |
| 263 | 3686 | M00008044D:B08 | MA29:C11 | 58.82352941 | 29.41176471 | 0 | 34 |
| 264 | 3688 | M00008044D:C05 | MA29:D11 | 50 | 2.941176471 | 0 | 34 |
| 265 | 3706 | M00022074C:A04 | MA33:E11 | 0 | 0 | 32.35294118 | 34 |
| 266 | 3738 | M00026910C:D12 | MA39:E12 | 0 | 0 | 70.58823529 | 34 |
| 267 | 3742 | M00026913A:D06 | MA39:G12 | 50 | 8.823529412 | 0 | 34 |
| 268 | 3752 | M00001402C:H08 | MA15:D06 | 67.64705882 | 11.76470588 | 0 | 34 |
| 269 | 3756 | M00001404C:C11 | MA15:F06 | 70.58823529 | 20.58823529 | 0 | 34 |
| 270 | 3813 | M00005587B:G05 | MA242:C06 | 50 | 0 | 0 | 34 |
| 271 | 3814 | M00006934D:D10 | MA240:C06 | 0 | 0 | 29.41176471 | 34 |
| 272 | 3885 | SL176 | MA248:G06 | 0 | 0 | 20.58823529 | 34 |
| 273 | 3905 | M00023295D:E05 | MA36:A06 | 50 | 2.941176471 | 0 | 34 |
| 274 | 3921 | M00023320B:C02 | MA36:A12 | 0 | 0 | 44.11764706 | 34 |
| 275 | 3956 | M00005401B:F12 | MA246:B12 | 0 | 0 | 23.52941176 | 34 |
| 276 | 3979 | M00008074D:C05 | MA30:F06 | 26.47058824 | 11.76470588 | 11.76470588 | 34 |
| 277 | 3982 | M00022175B:F06 | MA35:G06 | 38.23529412 | 23.52941176 | 0 | 34 |
| 278 | 3998 | M00022230B:C10 | MA35:G12 | 41.17647059 | 5.882352941 | 0 | 34 |
| 279 | 4006 | M00022093C:C08 | MA34:C06 | 70.58823529 | 0 | 0 | 34 |
| 280 | 4008 | M00022093C:C12 | MA34:D06 | 20.58823529 | 0 | 26.47058824 | 34 |
| 281 | 4028 | M00022132A:H07 | MA34:F12 | 0 | 0 | 32.35294118 | 34 |
| 282 | 4066 | M00023397B:D04 | MA22:A06 | 32.35294118 | 0 | 0 | 34 |
| 283 | 4074 | M00023399D:G04 | MA22:E06 | 29.41176471 | 0 | 2.941176471 | 34 |
| 284 | 4098 | M00001439D:C09 | MA16:A06 | 41.17647059 | 0 | 0 | 34 |
| 285 | 4100 | M00001441A:A09 | MA16:B06 | 0 | 0 | 58.82352941 | 34 |
| 286 | 4101 | M00001369D:E02 | MA14:C06 | 26.47058824 | 2.941176471 | 0 | 34 |
| 287 | 4105 | M00001371D:H10 | MA14:E06 | 38.23529412 | 2.941176471 | 5.882352941 | 34 |
| 288 | 4107 | M00001372A:D01 | MA14:F06 | 47.05882353 | 2.941176471 | 0 | 34 |
| 289 | 4110 | M00001444C:F03 | MA16:G06 | 52.94117647 | 2.941176471 | 0 | 34 |
| 290 | 4112 | M00001445A:B02 | | 50 | 0 | 0 | 34 |
| 291 | 4119 | M00001388D:F11 | MA14:D12 | 47.05882353 | 0 | 0 | 34 |
| 292 | 4124 | M00001481C:A12 | MA16:F12 | 38.23529412 | 0 | 0 | 34 |
| 293 | 4125 | M00001389B:B05 | MA14:G12 | 0 | 0 | 20.58823529 | 34 |
| 294 | 4127 | M00001389C:G01 | MA14:H12 | 26.47058824 | 5.882352941 | 2.941176471 | 34 |

Table 4

| SEQ ID NO | SpotID | Clone ID | MAClone ID | >=2x | >=5x | <=halfx | Num Ratios |
|--------------|--------|---------------------|------------|-------------|-------------|-------------|---------------|
| 295 | 4128 | M00001482D:D11 | MA16:H12 | 64.70588235 | 5.882352941 | 0 | 34 |
| 296 | 4183 | M00006809B:F04 | MA241:D12 | 0 | 0 | 26.47058824 | 34 |
| 297 | 8513 | I:3325119:07A01:A01 | MA127:A01 | 2.173913043 | 0 | 23.91304348 | 46 |
| 298 | 8517 | I:3033345:07A01:C01 | MA127:C01 | 43.47826087 | 2.173913043 | 0 | 46 |
| 299 | 8537 | I:3176222:07A01:E07 | MA127:E07 | 2.173913043 | 0 | 34.7826087 | 46 |
| 300 | 8542 | I:2510627:07B01:G07 | MA129:G07 | 28.26086957 | 0 | 0 | 46 |
| 301 | 8546 | I:1705208:06B01:A01 | MA125:A01 | 8.695652174 | 4.347826087 | 23.91304348 | 46 |
| 302 | 8566 | I:1672781:06B01:C07 | MA125:C07 | 32.60869565 | 4.347826087 | 0 | 46 |
| 303 | 8568 | I:1712888:06B01:D07 | MA125:D07 | 0 | 0 | 36.95652174 | 46 |
| 304 | 8570 | I:1696224:06B01:E07 | MA125:E07 | 13.04347826 | 4.347826087 | 39.13043478 | 46 |
| 305 | 8576 | I:3935034:06B01:H07 | MA125:H07 | 34.7826087 | 2.173913043 | 0 | 46 |
| 306 | 8617 | I:1800114:03A01:E01 | MA111:E01 | 0 | 0 | 80.43478261 | 46 |
| 307 | 8631 | I:1976029:03A01:D07 | MA111:D07 | 54.34782609 | 2.173913043 | 0 | 46 |
| 308 | 8634 | I:1439934:03B01:E07 | MA113:E07 | 4.347826087 | 0 | 26.08695652 | 46 |
| 309 | 8645 | I:2512879:01A01:C01 | MA103:C01 | 2.173913043 | 0 | 86.95652174 | 46 |
| 310 | 8660 | I:2900277:01B01:B07 | MA105:B07 | 23.91304348 | 10.86956522 | 23.91304348 | 46 |
| 311 | 8661 | I:1479255:01A01:C07 | MA103:C07 | 4.347826087 | 0 | 26.08695652 | 46 |
| 312 | 8738 | I:2648612:04B01:A01 | MA117:A01 | 60.86956522 | 13.04347826 | 0 | 46 |
| 313 | 8741 | I:1889867:04A01:C01 | MA115:C01 | 23.91304348 | 2.173913043 | 0 | 46 |
| 314 | 8743 | I:1858905:04A01:D01 | MA115:D01 | 4.347826087 | 0 | 21.73913043 | 46 |
| 315 | 8752 | I:2591494:04B01:H01 | MA117:H01 | 0 | 0 | 89.13043478 | 46 |
| 316 | 8754 | I:2916261:04B01:A07 | MA117:A07 | 28.26086957 | 2.173913043 | 0 | 46 |
| 317 | 8756 | I:2397815:04B01:B07 | MA117:B07 | 34.7826087 | 6.52173913 | 0 | 46 |
| 318 | 8760 | I:2182095:04B01:D07 | MA117:D07 | 23.91304348 | 15.2173913 | 8.695652174 | 46 |
| 319 | 8769 | I:2506194:02A01:A01 | MA107:A01 | 36.95652174 | 2.173913043 | 0 | 46 |
| 320 | 8773 | I:1806219:02A01:C01 | MA107:C01 | 0 | 0 | 82.60869565 | 46 |
| 321 | 8797 | I:1729724:02A01:G07 | MA107:G07 | 0 | 0 | 21.73913043 | 46 |
| 322 | 8845 | I:1886842:05A02:G01 | MA120:G01 | 34.7826087 | 2.173913043 | 2.173913043 | 46 |
| 323 | 8851 | I:1352669:05A02:B07 | MA120:B07 | 0 | 0 | 23.91304348 | 46 |
| 324 | 8854 | I:1755847:05B02:C07 | MA122:C07 | 2.173913043 | 0 | 21.73913043 | 46 |
| 325 | 8856 | I:1803418:05B02:D07 | MA122:D07 | 0 | 0 | 34.7826087 | 46 |
| 326 | 8860 | I:1568725:05B02:F07 | MA122:F07 | 2.173913043 | 0 | 21.73913043 | 46 |
| 327 | 8861 | I:1857708:05A02:G07 | MA120:G07 | 34.7826087 | 10.86956522 | 0 | 46 |
| 328 | 8862 | I:1687060:05B02:G07 | MA122:G07 | 8.695652174 | 0 | 28.26086957 | 46 |
| 329 | 8881 | I:3407289:07A02:A07 | MA128:A07 | 0 | 0 | 43.47826087 | 46 |
| 330 | 8883 | I:1235535:07A02:B07 | MA128:B07 | 23.91304348 | 2.173913043 | 2.173913043 | 46 |
| 331 | 8984 | I:1525795:03B02:D07 | MA114:D07 | 39.13043478 | 2.173913043 | 0 | 46 |
| 332 | 8991 | I:3744592:03A02:H07 | MA112:H07 | 28.26086957 | 0 | 0 | 46 |
| 333 | 8995 | I:1485817:01A02:B01 | MA104:B01 | 41.30434783 | 4.347826087 | 0 | 46 |
| 334 | 8996 | I:2365149:01B02:B01 | MA106:B01 | 2.173913043 | 0 | 30.43478261 | 46 |
| 335 | 8999 | I:1439677:01A02:D01 | MA104:D01 | 0 | 0 | 26.08695652 | 46 |
| 336 | 9006 | I:2372275:01B02:G01 | MA106:G01 | 23.91304348 | 8.695652174 | 0 | 46 |
| 337 | 9008 | I:3211615:01B02:H01 | MA106:H01 | 2.173913043 | 0 | 23.91304348 | 46 |
| 338 | 9012 | I:2368282:01B02:B07 | MA106:B07 | 21.73913043 | 8.695652174 | 23.91304348 | 46 |
| 339 | 9095 | I:1737833:04A02:D01 | MA116:D01 | 34.7826087 | 0 | 0 | 46 |
| 340 | 9100 | I:2382192:04B02:F01 | MA118:F01 | 28.26086957 | 21.73913043 | 2.173913043 | 46 |
| 341 | 9111 | I:1958902:04A02:D07 | MA116:D07 | 21.73913043 | 4.347826087 | 2.173913043 | 46 |
| 342 | 9118 | I:1704472:04B02:G07 | MA118:G07 | 26.08695652 | 0 | 0 | 46 |
| 343 | 9119 | I:1903767:04A02:H07 | MA116:H07 | 32.60869565 | 6.52173913 | 2.173913043 | 46 |

Table 4

| SEQ ID NO | SpotID | Clone ID | MAClone ID | >=2x | >=5x | <=halfx | Num Ratios |
|--------------|--------|---------------------|------------|-------------|-------------|-------------|---------------|
| 344 | 9125 | I:1268080:02A02:C01 | MA108:C01 | 0 | 0 | 45.65217391 | 46 |
| 345 | 9141 | I:1347384:02A02:C07 | MA108:C07 | 0 | 0 | 28.26086957 | 46 |
| 346 | 9168 | I:2344817:08B01:H02 | MA133:H02 | 0 | 0 | 28.26086957 | 46 |
| 347 | 9171 | I:3236109:08A01:B08 | MA131:B08 | 2.173913043 | 0 | 32.60869565 | 46 |
| 348 | 9247 | I:2832506:07A01:H08 | MA127:H08 | 56.52173913 | 6.52173913 | 0 | 46 |
| 349 | 9252 | I:1673876:06B01:B02 | MA125:B02 | 45.65217391 | 6.52173913 | 0 | 46 |
| 350 | 9258 | I:3686211:06B01:E02 | MA125:E02 | 0 | 0 | 26.08695652 | 46 |
| 351 | 9264 | I:2449837:06B01:H02 | MA125:H02 | 45.65217391 | 2.173913043 | 0 | 46 |
| 352 | 9270 | I:1613874:06B01:C08 | MA125:C08 | 28.26086957 | 2.173913043 | 0 | 46 |
| 353 | 9317 | I:1813409:03A01:C02 | MA111:C02 | 36.95652174 | 8.695652174 | 6.52173913 | 46 |
| 354 | 9329 | I:1975514:03A01:A08 | MA111:A08 | 4.347826087 | 0 | 28.26086957 | 46 |
| 355 | 9347 | I:1403294:01A01:B02 | MA103:B02 | 0 | 0 | 43.47826087 | 46 |
| 356 | 9352 | I:2414624:01B01:D02 | MA105:D02 | 34.7826087 | 17.39130435 | 0 | 46 |
| 357 | 9360 | I:2901811:01B01:H02 | MA105:H02 | 0 | 0 | 47.82608696 | 46 |
| 358 | 9364 | I:2683564:01B01:B08 | MA105:B08 | 23.91304348 | 4.347826087 | 8.695652174 | 46 |
| 359 | 9366 | I:2725511:01B01:C08 | MA105:C08 | 0 | 0 | 30.43478261 | 46 |
| 360 | 9441 | I:1431273:04A01:A02 | MA115:A02 | 0 | 0 | 45.65217391 | 46 |
| 361 | 9442 | I:1636639:04B01:A02 | MA117:A02 | 6.52173913 | 0 | 26.08695652 | 46 |
| 362 | 9448 | I:2455617:04B01:D02 | MA117:D02 | 28.26086957 | 8.695652174 | 0 | 46 |
| 363 | 9452 | I:2952504:04B01:F02 | MA117:F02 | 39.13043478 | 2.173913043 | 0 | 46 |
| 364 | 9457 | I:1483847:04A01:A08 | MA115:A08 | 43.47826087 | 2.173913043 | 0 | 46 |
| 365 | 9460 | I:2923150:04B01:B08 | MA117:B08 | 21.73913043 | 15.2173913 | 8.695652174 | 46 |
| 366 | 9467 | I:1813133:04A01:F08 | MA115:F08 | 47.82608696 | 4.347826087 | 0 | 46 |
| 367 | 9472 | I:2510171:04B01:H08 | MA117:H08 | 34.7826087 | 4.347826087 | 26.08695652 | 46 |
| 368 | 9487 | I:2190284:02A01:H02 | MA107:H02 | 36.95652174 | 4.347826087 | 0 | 46 |
| 369 | 9540 | I:1522716:05B02:B02 | MA122:B02 | 21.73913043 | 2.173913043 | 19.56521739 | 46 |
| 370 | 9549 | I:1901271:05A02:G02 | MA120:G02 | 2.173913043 | 0 | 30.43478261 | 46 |
| 371 | 9552 | I:1820522:05B02:H02 | MA122:H02 | 30.43478261 | 0 | 2.173913043 | 46 |
| 372 | 9553 | I:2365295:05A02:A08 | MA120:A08 | 10.86956522 | 4.347826087 | 56.52173913 | 46 |
| 373 | 9557 | I:1335140:05A02:C08 | MA120:C08 | 50 | 0 | 2.173913043 | 46 |
| 374 | 9560 | I:1822577:05B02:D08 | MA122:D08 | 39.13043478 | 4.347826087 | 4.347826087 | 46 |
| 375 | 9618 | I:1306814:06B02:A08 | MA126:A08 | 28.26086957 | 2.173913043 | 4.347826087 | 46 |
| 376 | 9624 | I:3034694:06B02:D08 | MA126:D08 | 36.95652174 | 4.347826087 | 2.173913043 | 46 |
| 377 | 9666 | I:1453049:03B02:A02 | MA114:A02 | 2.173913043 | 0 | 32.60869565 | 46 |
| 378 | 9672 | I:1453748:03B02:D02 | MA114:D02 | 0 | 0 | 21.73913043 | 46 |
| 379 | 9677 | I:3001492:03A02:G02 | MA112:G02 | 2.173913043 | 0 | 21.73913043 | 46 |
| 380 | 9685 | I:3876715:03A02:C08 | MA112:C08 | 2.173913043 | 0 | 23.91304348 | 46 |
| 381 | 9687 | I:2992851:03A02:D08 | MA112:D08 | 0 | 0 | 26.08695652 | 46 |
| 382 | 9694 | I:1500649:03B02:G08 | MA114:G08 | 36.95652174 | 6.52173913 | 0 | 46 |
| 383 | 9699 | I:1512943:01A02:B02 | MA104:B02 | 0 | 0 | 23.91304348 | 46 |
| 384 | 9703 | I:1467565:01A02:D02 | MA104:D02 | 41.30434783 | 0 | 0 | 46 |
| 385 | 9720 | I:2455118:01B02:D08 | MA106:D08 | 50 | 10.86956522 | 0 | 46 |
| 386 | 9722 | I:2840251:01B02:E08 | MA106:E08 | 0 | 0 | 23.91304348 | 46 |
| 387 | 9770 | I:2911347:10B02:E02 | MA67:E02 | 2.173913043 | 0 | 36.95652174 | 46 |
| 388 | 9790 | I:1812030:10B02:G08 | MA67:G08 | 0 | 0 | 26.08695652 | 46 |
| 389 | 9820 | I:2663606:04B02:F08 | MA118:F08 | 36.95652174 | 0 | 2.173913043 | 46 |
| 390 | 9833 | I:1308333:02A02:E02 | MA108:E02 | 0 | 0 | 67.39130435 | 46 |
| 391 | 9834 | I:1578941:02B02:E02 | MA110:E02 | 0 | 0 | 36.95652174 | 46 |
| 392 | 9847 | I:1535439:02A02:D08 | MA108:D08 | 56.52173913 | 6.52173913 | 0 | 46 |

Table 4

| SEQ ID NO | SpotID | Clone ID | MAClone ID | >=2x | >=5x | <=halfx | Num Ratios |
|--------------|--------|---------------------|------------|-------------|-------------|-------------|---------------|
| 393 | 9856 | I:1857475:02B02:H08 | MA110:H08 | 0 | 0 | 34.7826087 | 46 |
| 394 | 9884 | I:2908878:08B01:F09 | MA133:F09 | 2.173913043 | 0 | 36.95652174 | 46 |
| 395 | 9925 | I:2830575:07A01:C03 | MA127:C03 | 32.60869565 | 0 | 0 | 46 |
| 396 | 9934 | I:1557906:07B01:G03 | MA129:G03 | 8.695652174 | 4.347826087 | 34.7826087 | 46 |
| 397 | 9964 | I:2200604:06B01:F03 | MA125:F03 | 34.7826087 | 0 | 0 | 46 |
| 398 | 9973 | I:1653326:06A01:C09 | MA123:C09 | 21.73913043 | 0 | 2.173913043 | 46 |
| 399 | 9981 | I:1720149:06A01:G09 | MA123:G09 | 2.173913043 | 0 | 52.17391304 | 46 |
| 400 | 10030 | I:1560987:03B01:G03 | MA113:G03 | 0 | 0 | 43.47826087 | 46 |
| 401 | 10046 | I:1510714:03B01:G09 | MA113:G09 | 0 | 0 | 65.2173913 | 46 |
| 402 | 10050 | I:2501484:01B01:A03 | MA105:A03 | 0 | 0 | 21.73913043 | 46 |
| 403 | 10051 | I:1379063:01A01:B03 | MA103:B03 | 2.173913043 | 0 | 41.30434783 | 46 |
| 404 | 10054 | I:2797902:01B01:C03 | MA105:C03 | 0 | 0 | 39.13043478 | 46 |
| 405 | 10062 | I:1805613:01B01:G03 | MA105:G03 | 0 | 0 | 78.26086957 | 46 |
| 406 | 10063 | I:1524885:01A01:H03 | MA103:H03 | 67.39130435 | 13.04347826 | 0 | 46 |
| 407 | 10064 | I:2888464:01B01:H03 | MA105:H03 | 2.173913043 | 0 | 58.69565217 | 46 |
| 408 | 10148 | I:1992788:04B01:B03 | MA117:B03 | 41.30434783 | 0 | 0 | 46 |
| 409 | 10155 | I:1413451:04A01:F03 | MA115:F03 | 0 | 0 | 50 | 46 |
| 410 | 10166 | I:2779515:04B01:C09 | MA117:C09 | 78.26086957 | 19.56521739 | 0 | 46 |
| 411 | 10206 | I:1583076:02B01:G09 | MA109:G09 | 2.173913043 | 0 | 69.56521739 | 46 |
| 412 | 10243 | I:3070110:05A02:B03 | MA120:B03 | 2.173913043 | 0 | 30.43478261 | 46 |
| 413 | 10255 | I:1904493:05A02:H03 | MA120:H03 | 30.43478261 | 4.347826087 | 2.173913043 | 46 |
| 414 | 10257 | I:2860815:05A02:A09 | MA120:A09 | 4.347826087 | 2.173913043 | 67.39130435 | 46 |
| 415 | 10285 | I:1930135:07A02:G03 | MA128:G03 | 4.347826087 | 4.347826087 | 67.39130435 | 46 |
| 416 | 10318 | I:3747901:06B02:G03 | MA126:G03 | 34.7826087 | 2.173913043 | 0 | 46 |
| 417 | 10321 | I:1720946:06A02:A09 | MA124:A09 | 39.13043478 | 2.173913043 | 0 | 46 |
| 418 | 10328 | I:2877413:06B02:D09 | MA126:D09 | 21.73913043 | 4.347826087 | 0 | 46 |
| 419 | 10330 | I:3035279:06B02:E09 | MA126:E09 | 32.60869565 | 0 | 0 | 46 |
| 420 | 10393 | I:2503913:03A02:E09 | MA112:E09 | 21.73913043 | 4.347826087 | 19.56521739 | 46 |
| 421 | 10403 | I:1517380:01A02:B03 | MA104:B03 | 0 | 0 | 23.91304348 | 46 |
| 422 | 10406 | I:3138128:01B02:C03 | MA106:C03 | 2.173913043 | 0 | 23.91304348 | 46 |
| 423 | 10409 | I:2453722:01A02:E03 | MA104:E03 | 21.73913043 | 0 | 2.173913043 | 46 |
| 424 | 10417 | I:1414260:01A02:A09 | MA104:A09 | 0 | 0 | 41.30434783 | 46 |
| 425 | 10418 | I:2891247:01B02:A09 | MA106:A09 | 26.08695652 | 0 | 2.173913043 | 46 |
| 426 | 10427 | I:1682176:01A02:F09 | MA104:F09 | 0 | 0 | 32.60869565 | 46 |
| 427 | 10503 | I:2739076:04A02:D03 | MA116:D03 | 73.91304348 | 10.86956522 | 0 | 46 |
| 428 | 10508 | I:1900378:04B02:F03 | MA118:F03 | 0 | 0 | 30.43478261 | 46 |
| 429 | 10509 | I:1603391:04A02:G03 | MA116:G03 | 36.95652174 | 0 | 0 | 46 |
| 430 | 10517 | I:2018222:04A02:C09 | MA116:C09 | 34.7826087 | 6.52173913 | 4.347826087 | 46 |
| 431 | 10523 | I:1327263:04A02:F09 | MA116:F09 | 0 | 0 | 43.47826087 | 46 |
| 432 | 10547 | I:1734393:02A02:B09 | MA108:B09 | 0 | 0 | 91.30434783 | 46 |
| 433 | 10553 | I:2190607:02A02:E09 | MA108:E09 | 45.65217391 | 0 | 0 | 46 |
| 434 | 10569 | I:2447969:08A01:E04 | MA131:E04 | 2.173913043 | 0 | 23.91304348 | 46 |
| 435 | 10592 | I:1753033:08B01:H10 | MA133:H10 | 32.60869565 | 26.08695652 | 0 | 46 |
| 436 | 10650 | I:2456393:07B01:E10 | MA129:E10 | 0 | 0 | 23.91304348 | 46 |
| 437 | 10658 | I:1719920:06B01:A04 | MA125:A04 | 0 | 0 | 26.08695652 | 46 |
| 438 | 10672 | I:2927362:06B01:H04 | MA125:H04 | 34.7826087 | 2.173913043 | 2.173913043 | 46 |
| 439 | 10684 | I:4082816:06B01:F10 | MA125:F10 | 52.17391304 | 13.04347826 | 2.173913043 | 46 |
| 440 | 10721 | I:1803446:03A01:A04 | MA111:A04 | 32.60869565 | 0 | 0 | 46 |
| 441 | 10725 | I:1557490:03A01:C04 | MA111:C04 | 41.30434783 | 0 | 0 | 46 |

Table 4

| SEQ ID NO | SpotID | Clone ID | MAClone ID | >=2x | >=5x | <=halfx | Num Ratios |
|--------------|--------|---------------------|------------|-------------|-------------|-------------|---------------|
| 442 | 10746 | I:1445895:03B01:E10 | MA113:E10 | 2.173913043 | 0 | 23.91304348 | 46 |
| 443 | 10767 | I:1336836:01A01:H04 | MA103:H04 | 0 | 0 | 32.60869565 | 46 |
| 444 | 10778 | I:1802745:01B01:E10 | MA105:E10 | 2.173913043 | 0 | 23.91304348 | 46 |
| 445 | 10784 | I:2503003:01B01:H10 | MA105:H10 | 23.91304348 | 2.173913043 | 4.347826087 | 46 |
| 446 | 10827 | I:1655377:10A01:F04 | MA64:F04 | 0 | 0 | 43.47826087 | 46 |
| 447 | 10849 | I:1430662:04A01:A04 | MA115:A04 | 30.43478261 | 2.173913043 | 0 | 46 |
| 448 | 10861 | I:3335055:04A01:G04 | MA115:G04 | 45.65217391 | 2.173913043 | 0 | 46 |
| 449 | 10868 | I:2457671:04B01:B10 | MA117:B10 | 47.82608696 | 4.347826087 | 0 | 46 |
| 450 | 10901 | I:1641421:02A01:C10 | MA107:C10 | 0 | 0 | 47.82608696 | 46 |
| 451 | 10906 | I:1655225:02B01:E10 | MA109:E10 | 21.73913043 | 0 | 0 | 46 |
| 452 | 10947 | I:1313325:05A02:B04 | MA120:B04 | 23.91304348 | 6.52173913 | 0 | 46 |
| 453 | 10962 | I:1558081:05B02:A10 | MA122:A10 | 0 | 0 | 41.30434783 | 46 |
| 454 | 10975 | I:1889191:05A02:H10 | MA120:H10 | 26.08695652 | 2.173913043 | 2.173913043 | 46 |
| 455 | 10997 | I:3495906:07A02:C10 | MA128:C10 | 2.173913043 | 0 | 21.73913043 | 46 |
| 456 | 11095 | I:3704132:03A02:D10 | MA112:D10 | 0 | 0 | 30.43478261 | 46 |
| 457 | 11100 | I:1636553:03B02:F10 | MA114:F10 | 0 | 0 | 28.26086957 | 46 |
| 458 | 11104 | I:1402228:03B02:H10 | MA114:H10 | 45.65217391 | 8.695652174 | 0 | 46 |
| 459 | 11107 | I:1361963:01A02:B04 | MA104:B04 | 30.43478261 | 0 | 0 | 46 |
| 460 | 11111 | I:1510424:01A02:D04 | MA104:D04 | 39.13043478 | 34.7826087 | 2.173913043 | 46 |
| 461 | 11112 | I:2918558:01B02:D04 | MA106:D04 | 0 | 0 | 26.08695652 | 46 |
| 462 | 11127 | I:1731061:01A02:D10 | MA104:D10 | 45.65217391 | 8.695652174 | 2.173913043 | 46 |
| 463 | 11201 | I:2579602:04A02:A04 | MA116:A04 | 60.86956522 | 10.86956522 | 0 | 46 |
| 464 | 11202 | I:2824181:04B02:A04 | MA118:A04 | 36.95652174 | 4.347826087 | 0 | 46 |
| 465 | 11203 | I:2123183:04A02:B04 | MA116:B04 | 26.08695652 | 0 | 0 | 46 |
| 466 | 11221 | I:1958560:04A02:C10 | MA116:C10 | 10.86956522 | 2.173913043 | 28.26086957 | 46 |
| 467 | 11229 | I:1447903:04A02:G10 | MA116:G10 | 43.47826087 | 2.173913043 | 0 | 46 |
| 468 | 11257 | I:1875576:02A02:E10 | MA108:E10 | 54.34782609 | 0 | 0 | 46 |
| 469 | 11262 | I:1709457:02B02:G10 | MA110:G10 | 26.08695652 | 2.173913043 | 0 | 46 |
| 470 | 11278 | I:2155675:08B01:G05 | MA133:G05 | 0 | 0 | 23.91304348 | 46 |
| 471 | 11329 | I:1635069:07A01:A05 | MA127:A05 | 0 | 0 | 73.91304348 | 46 |
| 472 | 11341 | I:1453445:07A01:G05 | MA127:G05 | 2.173913043 | 0 | 34.7826087 | 46 |
| 473 | 11351 | I:3002566:07A01:D11 | MA127:D11 | 45.65217391 | 10.86956522 | 0 | 46 |
| 474 | 11365 | I:1631511:06A01:C05 | MA123:C05 | 0 | 0 | 26.08695652 | 46 |
| 475 | 11375 | I:1610523:06A01:H05 | MA123:H05 | 39.13043478 | 8.695652174 | 0 | 46 |
| 476 | 11386 | I:3297656:06B01:E11 | MA125:E11 | 52.17391304 | 10.86956522 | 2.173913043 | 46 |
| 477 | 11392 | I:2509730:06B01:H11 | MA125:H11 | 28.26086957 | 4.347826087 | 0 | 46 |
| 478 | 11432 | I:2121863:03B01:D05 | MA113:D05 | 17.39130435 | 4.347826087 | 21.73913043 | 46 |
| 479 | 11434 | I:1413704:03B01:E05 | MA113:E05 | 34.7826087 | 4.347826087 | 0 | 46 |
| 480 | 11441 | I:1626232:03A01:A11 | MA111:A11 | 10.86956522 | 10.86956522 | 32.60869565 | 46 |
| 481 | 11460 | I:2354446:01B01:B05 | MA105:B05 | 0 | 0 | 23.91304348 | 46 |
| 482 | 11466 | I:2916753:01B01:E05 | MA105:E05 | 41.30434783 | 6.52173913 | 0 | 46 |
| 483 | 11473 | I:2555034:01A01:A11 | MA103:A11 | 2.173913043 | 0 | 26.08695652 | 46 |
| 484 | 11480 | I:2804190:01B01:D11 | MA105:D11 | 0 | 0 | 50 | 46 |
| 485 | 11481 | I:1814488:01A01:E11 | MA103:E11 | 41.30434783 | 0 | 0 | 46 |
| 486 | 11482 | I:2474163:01B01:E11 | MA105:E11 | 0 | 0 | 95.65217391 | 46 |
| 487 | 11485 | I:1402967:01A01:G11 | MA103:G11 | 43.47826087 | 6.52173913 | 0 | 46 |
| 488 | 11543 | I:2821541:10A01:D11 | MA64:D11 | 2.173913043 | 0 | 23.91304348 | 46 |
| 489 | 11554 | I:2888814:04B01:A05 | MA117:A05 | 54.34782609 | 6.52173913 | 0 | 46 |
| 490 | 11557 | I:1451005:04A01:C05 | MA115:C05 | 34.7826087 | 2.173913043 | 0 | 46 |

Table 4

| SEQ ID NO | SpotID | Clone ID | MAClone ID | >=2x | >=5x | <=halfx | Num Ratios |
|--------------|--------|---------------------|------------|-------------|-------------|-------------|---------------|
| 491 | 11567 | I:1457726:04A01:H05 | MA115:H05 | 0 | 0 | 30.43478261 | 46 |
| 492 | 11568 | I:2883195:04B01:H05 | MA117:H05 | 58.69565217 | 6.52173913 | 4.347826087 | 46 |
| 493 | 11581 | I:1603605:04A01:G11 | MA115:G11 | 2.173913043 | 0 | 21.73913043 | 46 |
| 494 | 11583 | I:2832224:04A01:H11 | MA115:H11 | 43.47826087 | 2.173913043 | 2.173913043 | 46 |
| 495 | 11585 | I:2231364:02A01:A05 | MA107:A05 | 0 | 0 | 73.91304348 | 46 |
| 496 | 11612 | I:1595081:02B01:F11 | MA109:F11 | 0 | 0 | 32.60869565 | 46 |
| 497 | 11654 | I:1877913:05B02:C05 | MA122:C05 | 0 | 0 | 39.13043478 | 46 |
| 498 | 11660 | I:1666130:05B02:F05 | MA122:F05 | 30.43478261 | 6.52173913 | 0 | 46 |
| 499 | 11664 | I:1709995:05B02:H05 | MA122:H05 | 45.65217391 | 4.347826087 | 0 | 46 |
| 500 | 11683 | I:3872557:07A02:B05 | MA128:B05 | 15.2173913 | 0 | 26.08695652 | 46 |
| 501 | 11705 | I:2734906:07A02:E11 | MA128:E11 | 28.26086957 | 0 | 2.173913043 | 46 |
| 502 | 11715 | I:1798585:06A02:B05 | MA124:B05 | 0 | 0 | 39.13043478 | 46 |
| 503 | 11723 | I:1683389:06A02:F05 | MA124:F05 | 36.95652174 | 4.347826087 | 0 | 46 |
| 504 | 11725 | I:1704517:06A02:G05 | MA124:G05 | 32.60869565 | 2.173913043 | 0 | 46 |
| 505 | 11728 | I:2792982:06B02:H05 | MA126:H05 | 0 | 0 | 39.13043478 | 46 |
| 506 | 11736 | I:3511355:06B02:D11 | MA126:D11 | 32.60869565 | 0 | 2.173913043 | 46 |
| 507 | 11777 | I:1738060:03A02:A05 | MA112:A05 | 45.65217391 | 2.173913043 | 2.173913043 | 46 |
| 508 | 11780 | I:1810821:03B02:B05 | MA114:B05 | 28.26086957 | 6.52173913 | 2.173913043 | 46 |
| 509 | 11785 | I:2451279:03A02:E05 | MA112:E05 | 26.08695652 | 4.347826087 | 0 | 46 |
| 510 | 11786 | I:1431166:03B02:E05 | MA114:E05 | 0 | 0 | 26.08695652 | 46 |
| 511 | 11794 | I:2949427:03B02:A11 | MA114:A11 | 91.30434783 | 67.39130435 | 0 | 46 |
| 512 | 11802 | I:1458366:03B02:E11 | MA114:E11 | 4.347826087 | 0 | 36.95652174 | 46 |
| 513 | 11806 | I:1525881:03B02:G11 | MA114:G11 | 0 | 0 | 32.60869565 | 46 |
| 514 | 11817 | I:2071473:01A02:E05 | MA104:E05 | 78.26086957 | 23.91304348 | 0 | 46 |
| 515 | 11829 | I:2481012:01A02:C11 | MA104:C11 | 26.08695652 | 2.173913043 | 2.173913043 | 46 |
| 516 | 11830 | I:2816931:01B02:C11 | MA106:C11 | 26.08695652 | 0 | 0 | 46 |
| 517 | 11836 | I:1806769:01B02:F11 | MA106:F11 | 0 | 0 | 84.7826087 | 46 |
| 518 | 11922 | I:2636634:04B02:A11 | MA118:A11 | 30.43478261 | 8.695652174 | 2.173913043 | 46 |
| 519 | 11962 | I:1649959:02B02:E11 | MA110:E11 | 2.173913043 | 0 | 21.73913043 | 46 |
| 520 | 11964 | I:1633719:02B02:F11 | MA110:F11 | 0 | 0 | 54.34782609 | 46 |
| 521 | 11966 | I:1901035:02B02:G11 | MA110:G11 | 34.7826087 | 2.173913043 | 0 | 46 |
| 522 | 11990 | I:2503879:08B01:C12 | MA133:C12 | 28.26086957 | 2.173913043 | 2.173913043 | 46 |
| 523 | 12036 | I:2383065:07B01:B06 | MA129:B06 | 39.13043478 | 4.347826087 | 0 | 46 |
| 524 | 12043 | I:3357245:07A01:F06 | MA127:F06 | 2.173913043 | 0 | 21.73913043 | 46 |
| 525 | 12045 | I:2832314:07A01:G06 | MA127:G06 | 54.34782609 | 6.52173913 | 2.173913043 | 46 |
| 526 | 12055 | I:3667096:07A01:D12 | MA127:D12 | 28.26086957 | 0 | 0 | 46 |
| 527 | 12071 | I:1798283:06A01:D06 | MA123:D06 | 21.73913043 | 0 | 2.173913043 | 46 |
| 528 | 12131 | I:1648206:03A01:B06 | MA111:B06 | 26.08695652 | 2.173913043 | 0 | 46 |
| 529 | 12148 | I:3360476:03B01:B12 | MA113:B12 | 0 | 0 | 26.08695652 | 46 |
| 530 | 12150 | I:2500511:03B01:C12 | MA113:C12 | 0 | 0 | 32.60869565 | 46 |
| 531 | 12152 | I:1730806:03B01:D12 | MA113:D12 | 30.43478261 | 4.347826087 | 0 | 46 |
| 532 | 12166 | I:2479074:01B01:C06 | MA105:C06 | 30.43478261 | 6.52173913 | 0 | 46 |
| 533 | 12170 | I:1635004:01B01:E06 | MA105:E06 | 0 | 0 | 89.13043478 | 46 |
| 534 | 12174 | I:2378569:01B01:G06 | MA105:G06 | 32.60869565 | 0 | 0 | 46 |
| 535 | 12183 | I:2207849:01A01:D12 | MA103:D12 | 21.73913043 | 6.52173913 | 6.52173913 | 46 |
| 536 | 12187 | I:1504554:01A01:F12 | MA103:F12 | 2.173913043 | 0 | 23.91304348 | 46 |
| 537 | 12258 | I:2989991:04B01:A06 | MA117:A06 | 32.60869565 | 6.52173913 | 6.52173913 | 46 |
| 538 | 12260 | I:2852561:04B01:B06 | MA117:B06 | 56.52173913 | 8.695652174 | 0 | 46 |
| 539 | 12277 | I:2832839:04A01:C12 | MA115:C12 | 45.65217391 | 4.347826087 | 0 | 46 |

Table 4

| SEQ ID NO | SpotID | Clone ID | MAClone ID | >=2x | >=5x | <=halfx | Num Ratios |
|--------------|--------|----------------------|------------|-------------|-------------|-------------|---------------|
| 540 | 12282 | I:2845548:04B01:E12 | MA117:E12 | 34.7826087 | 2.173913043 | 0 | 46 |
| 541 | 12292 | I:1251819:02B01:B06 | MA109:B06 | 36.95652174 | 4.347826087 | 0 | 46 |
| 542 | 12296 | I:1672930:02B01:D06 | MA109:D06 | 43.47826087 | 2.173913043 | 0 | 46 |
| 543 | 12298 | I:2122820:02B01:E06 | MA109:E06 | 2.173913043 | 0 | 26.08695652 | 46 |
| 544 | 12303 | I:2174920:02A01:H06 | MA107:H06 | 0 | 0 | 58.69565217 | 46 |
| 545 | 12362 | I:1875994:05B02:E06 | MA122:E06 | 30.43478261 | 2.173913043 | 2.173913043 | 46 |
| 546 | 12365 | I:1858644:05A02:G06 | MA120:G06 | 34.7826087 | 6.52173913 | 0 | 46 |
| 547 | 12425 | I:1700047:06A02:E06 | MA124:E06 | 28.26086957 | 4.347826087 | 0 | 46 |
| 548 | 12426 | I:1718257:06B02:E06 | MA126:E06 | 39.13043478 | 0 | 0 | 46 |
| 549 | 12427 | I:1612306:06A02:F06 | MA124:F06 | 32.60869565 | 4.347826087 | 0 | 46 |
| 550 | 12443 | I:1637427:06A02:F12 | MA124:F12 | 23.91304348 | 2.173913043 | 0 | 46 |
| 551 | 12499 | I:2513883:03A02:B12 | MA112:B12 | 0 | 0 | 89.13043478 | 46 |
| 552 | 12525 | I:2645840:01A02:G06 | MA104:G06 | 26.08695652 | 13.04347826 | 2.173913043 | 46 |
| 553 | 12529 | I:1737403:01A02:A12 | MA104:A12 | 0 | 0 | 50 | 46 |
| 554 | 12544 | I:1733522:01B02:H12 | MA106:H12 | 2.173913043 | 0 | 34.7826087 | 46 |
| 555 | 17049 | RG:160664:10006:E07 | MA155:E07 | 10 | 2.5 | 70 | 40 |
| 556 | 17065 | I:747335:16A01:E01 | MA87:E01 | 30 | 2.5 | 0 | 40 |
| 557 | 17071 | I:2085191:16A01:H01 | MA87:H01 | 0 | 0 | 30 | 40 |
| 558 | 17081 | I:1211126:16A01:E07 | MA87:E07 | 30 | 7.5 | 2.5 | 40 |
| 559 | 17157 | RG:669310:10010:C01 | MA159:C01 | 20 | 0 | 0 | 40 |
| 560 | 17167 | RG:730402:10010:H01 | MA159:H01 | 22.5 | 20 | 0 | 40 |
| 561 | 17174 | RG:1047541:10012:C07 | MA161:C07 | 22.5 | 2.5 | 0 | 40 |
| 562 | 17178 | RG:1161753:10012:E07 | MA161:E07 | 30 | 2.5 | 5 | 40 |
| 563 | 17194 | I:1218464:17B01:E01 | MA93:E01 | 0 | 0 | 35 | 40 |
| 564 | 17214 | I:958633:17B01:G07 | MA93:G07 | 45 | 2.5 | 0 | 40 |
| 565 | 17236 | I:1602726:09B01:B07 | MA137:B07 | 0 | 0 | 35 | 40 |
| 566 | 17379 | RG:205212:10007:B01 | MA156:B01 | 45 | 7.5 | 2.5 | 40 |
| 567 | 17395 | RG:207395:10007:B07 | MA156:B07 | 55 | 25 | 2.5 | 40 |
| 568 | 17422 | I:349535:16B02:G01 | MA90:G01 | 0 | 0 | 22.5 | 40 |
| 569 | 17423 | I:2323525:16A02:H01 | MA88:H01 | 0 | 0 | 20 | 40 |
| 570 | 17432 | I:1965049:16B02:D07 | MA90:D07 | 0 | 0 | 80 | 40 |
| 571 | 17437 | I:2054436:16A02:G07 | MA88:G07 | 2.5 | 0 | 22.5 | 40 |
| 572 | 17515 | RG:1506197:10013:F01 | MA162:F01 | 37.5 | 7.5 | 0 | 40 |
| 573 | 17518 | RG:1871436:10015:G01 | MA164:G01 | 57.5 | 10 | 0 | 40 |
| 574 | 17524 | RG:1705470:10015:B07 | MA164:B07 | 2.5 | 0 | 27.5 | 40 |
| 575 | 17556 | I:546910:17B02:B07 | MA94:B07 | 0 | 0 | 20 | 40 |
| 576 | 17580 | I:1799023:09B02:F01 | MA138:F01 | 0 | 0 | 25 | 40 |
| 577 | 17584 | I:2380380:09B02:H01 | MA138:H01 | 0 | 0 | 25 | 40 |
| 578 | 17675 | I:2319269:18A01:F02 | MA95:F02 | 25 | 0 | 0 | 40 |
| 579 | 17687 | I:2296344:18A01:D08 | MA95:D08 | 0 | 0 | 35 | 40 |
| 580 | 17737 | RG:155066:10006:E02 | MA155:E02 | 5 | 0 | 20 | 40 |
| 581 | 17741 | RG:180135:10006:G02 | MA155:G02 | 62.5 | 2.5 | 0 | 40 |
| 582 | 17755 | RG:178093:10006:F08 | MA155:F08 | 37.5 | 2.5 | 0 | 40 |
| 583 | 17757 | RG:184042:10006:G08 | MA155:G08 | 47.5 | 0 | 0 | 40 |
| 584 | 17761 | I:1741643:16A01:A02 | MA87:A02 | 30 | 0 | 0 | 40 |
| 585 | 17860 | RG:928026:10012:B02 | MA161:B02 | 30 | 7.5 | 2.5 | 40 |
| 586 | 17862 | RG:1032969:10012:C02 | MA161:C02 | 22.5 | 0 | 0 | 40 |
| 587 | 17872 | RG:1322660:10012:H02 | MA161:H02 | 0 | 0 | 52.5 | 40 |
| 588 | 17876 | RG:968474:10012:B08 | MA161:B08 | 2.5 | 0 | 35 | 40 |

Table 4

| SEQ ID NO | SpotID | Clone ID | MAClone ID | >=2x | >=5x | <=halfx | Num Ratios |
|--------------|--------|----------------------|------------|------|------|---------|---------------|
| 589 | 17878 | RG:1047592:10012:C08 | MA161:C08 | 2.5 | 0 | 57.5 | 40 |
| 590 | 17914 | I:617750:17B01:E08 | MA93:E08 | 2.5 | 0 | 30 | 40 |
| 591 | 17934 | I:2808775:09B01:G02 | MA137:G02 | 0 | 0 | 22.5 | 40 |
| 592 | 18035 | I:966692:18A02:B08 | MA96:B08 | 2.5 | 0 | 32.5 | 40 |
| 593 | 18085 | RG:209240:10007:C02 | MA156:C02 | 27.5 | 2.5 | 10 | 40 |
| 594 | 18087 | RG:223355:10007:D02 | MA156:D02 | 0 | 0 | 25 | 40 |
| 595 | 18095 | RG:267629:10007:H02 | MA156:H02 | 25 | 0 | 0 | 40 |
| 596 | 18134 | I:2246234:16B02:C08 | MA90:C08 | 2.5 | 0 | 20 | 40 |
| 597 | 18212 | RG:1696513:10015:B02 | MA164:B02 | 30 | 17.5 | 0 | 40 |
| 598 | 18216 | RG:1733895:10015:D02 | MA164:D02 | 27.5 | 5 | 0 | 40 |
| 599 | 18225 | RG:1353930:10013:A08 | MA162:A08 | 22.5 | 2.5 | 0 | 40 |
| 600 | 18238 | RG:1881947:10015:G08 | MA164:G08 | 42.5 | 20 | 5 | 40 |
| 601 | 18443 | RG:166575:10006:F03 | MA155:F03 | 2.5 | 2.5 | 30 | 40 |
| 602 | 18465 | I:1998994:16A01:A03 | MA87:A03 | 35 | 0 | 0 | 40 |
| 603 | 18471 | I:1953051:16A01:D03 | MA87:D03 | 25 | 0 | 0 | 40 |
| 604 | 18473 | I:518826:16A01:E03 | MA87:E03 | 35 | 2.5 | 2.5 | 40 |
| 605 | 18483 | I:81490:16A01:B09 | MA87:B09 | 0 | 0 | 22.5 | 40 |
| 606 | 18572 | RG:1256163:10012:F03 | MA161:F03 | 45 | 2.5 | 0 | 40 |
| 607 | 18584 | RG:1132085:10012:D09 | MA161:D09 | 55 | 2.5 | 0 | 40 |
| 608 | 18614 | I:2132717:17B01:C09 | MA93:C09 | 25 | 0 | 12.5 | 40 |
| 609 | 18620 | I:1998428:17B01:F09 | MA93:F09 | 2.5 | 0 | 22.5 | 40 |
| 610 | 18787 | RG:206694:10007:B03 | MA156:B03 | 2.5 | 0 | 25 | 40 |
| 611 | 18811 | RG:261714:10007:F09 | MA156:F09 | 0 | 0 | 32.5 | 40 |
| 612 | 18821 | I:1461515:16A02:C03 | MA88:C03 | 0 | 0 | 20 | 40 |
| 613 | 18831 | I:338859:16A02:H03 | MA88:H03 | 0 | 0 | 30 | 40 |
| 614 | 18845 | I:1425861:16A02:G09 | MA88:G09 | 5 | 0 | 37.5 | 40 |
| 615 | 18848 | I:1928644:16B02:H09 | MA90:H09 | 0 | 0 | 22.5 | 40 |
| 616 | 18917 | RG:1404414:10013:C03 | MA162:C03 | 30 | 0 | 0 | 40 |
| 617 | 18919 | RG:1415437:10013:D03 | MA162:D03 | 7.5 | 0 | 65 | 40 |
| 618 | 18920 | RG:1734353:10015:D03 | MA164:D03 | 5 | 0 | 62.5 | 40 |
| 619 | 18926 | RG:1872251:10015:G03 | MA164:G03 | 0 | 0 | 32.5 | 40 |
| 620 | 18929 | RG:1354408:10013:A09 | MA162:A09 | 2.5 | 0 | 27.5 | 40 |
| 621 | 18930 | RG:1690198:10015:A09 | MA164:A09 | 2.5 | 0 | 27.5 | 40 |
| 622 | 18937 | RG:1476452:10013:E09 | MA162:E09 | 40 | 0 | 2.5 | 40 |
| 623 | 18988 | I:2069305:09B02:F03 | MA138:F03 | 57.5 | 5 | 0 | 40 |
| 624 | 19088 | I:1966067:18B01:H04 | MA97:H04 | 27.5 | 5 | 5 | 40 |
| 625 | 19090 | I:2128547:18B01:A10 | MA97:A10 | 25 | 2.5 | 0 | 40 |
| 626 | 19143 | RG:149960:10006:D04 | MA155:D04 | 0 | 0 | 42.5 | 40 |
| 627 | 19147 | RG:171569:10006:F04 | MA155:F04 | 0 | 0 | 50 | 40 |
| 628 | 19163 | RG:178638:10006:F10 | MA155:F10 | 0 | 0 | 30 | 40 |
| 629 | 19167 | RG:195122:10006:H10 | MA155:H10 | 45 | 2.5 | 0 | 40 |
| 630 | 19195 | I:814216:16A01:F10 | MA87:F10 | 65 | 32.5 | 0 | 40 |
| 631 | 19265 | RG:491163:10010:A04 | MA159:A04 | 0 | 0 | 45 | 40 |
| 632 | 19266 | RG:827185:10012:A04 | MA161:A04 | 0 | 0 | 42.5 | 40 |
| 633 | 19272 | RG:1129102:10012:D04 | MA161:D04 | 45 | 7.5 | 0 | 40 |
| 634 | 19279 | RG:730938:10010:H04 | MA159:H04 | 22.5 | 0 | 0 | 40 |
| 635 | 19282 | RG:925984:10012:A10 | MA161:A10 | 0 | 0 | 45 | 40 |
| 636 | 19283 | RG:668442:10010:B10 | MA159:B10 | 22.5 | 0 | 0 | 40 |
| 637 | 19284 | RG:1028911:10012:B10 | MA161:B10 | 42.5 | 2.5 | 0 | 40 |

Table 4

| SEQ ID NO | SpotID | Clone ID | MAClone ID | >=2x | >=5x | <=halfx | Num Ratios |
|-----------|--------|----------------------|------------|------|------|---------|------------|
| 638 | 19285 | RG:684866:10010:C10 | MA159:C10 | 0 | 0 | 27.5 | 40 |
| 639 | 19292 | RG:1283076:10012:F10 | MA161:F10 | 40 | 0 | 0 | 40 |
| 640 | 19309 | I:627654:17A01:G04 | MA91:G04 | 42.5 | 5 | 0 | 40 |
| 641 | 19319 | I:1833801:17A01:D10 | MA91:D10 | 0 | 0 | 55 | 40 |
| 642 | 19328 | I:961473:17B01:H10 | MA93:H10 | 0 | 0 | 25 | 40 |
| 643 | 19348 | I:2556708:09B01:B10 | MA137:B10 | 0 | 0 | 35 | 40 |
| 644 | 19511 | RG:243565:10007:D10 | MA156:D10 | 27.5 | 5 | 2.5 | 40 |
| 645 | 19517 | RG:266649:10007:G10 | MA156:G10 | 47.5 | 0 | 2.5 | 40 |
| 646 | 19524 | I:2013513:16B02:B04 | MA90:B04 | 0 | 0 | 27.5 | 40 |
| 647 | 19539 | I:2312442:16A02:B10 | MA88:B10 | 2.5 | 0 | 30 | 40 |
| 648 | 19543 | I:2060626:16A02:D10 | MA88:D10 | 25 | 0 | 0 | 40 |
| 649 | 19623 | RG:1415858:10013:D04 | MA162:D04 | 57.5 | 7.5 | 0 | 40 |
| 650 | 19627 | RG:1517435:10013:F04 | MA162:F04 | 22.5 | 7.5 | 2.5 | 40 |
| 651 | 19632 | RG:1914716:10015:H04 | MA164:H04 | 30 | 2.5 | 0 | 40 |
| 652 | 19633 | RG:1354528:10013:A10 | MA162:A10 | 37.5 | 5 | 0 | 40 |
| 653 | 19636 | RG:1706414:10015:B10 | MA164:B10 | 2.5 | 0 | 20 | 40 |
| 654 | 19653 | I:1998510:17A02:C04 | MA92:C04 | 0 | 0 | 60 | 40 |
| 655 | 19678 | I:899118:17B02:G10 | MA94:G10 | 30 | 0 | 7.5 | 40 |
| 656 | 19684 | I:2680168:09B02:B04 | MA138:B04 | 0 | 0 | 42.5 | 40 |
| 657 | 19690 | I:1354558:09B02:E04 | MA138:E04 | 0 | 0 | 20 | 40 |
| 658 | 19708 | I:1665871:09B02:F10 | MA138:F10 | 25 | 0 | 0 | 40 |
| 659 | 19782 | I:1922084:18B01:C05 | MA97:C05 | 0 | 0 | 77.5 | 40 |
| 660 | 19795 | I:2307946:18A01:B11 | MA95:B11 | 25 | 2.5 | 0 | 40 |
| 661 | 19798 | I:1923572:18B01:C11 | MA97:C11 | 0 | 0 | 30 | 40 |
| 662 | 19851 | RG:171993:10006:F05 | MA155:F05 | 0 | 0 | 20 | 40 |
| 663 | 19859 | RG:129317:10006:B11 | MA155:B11 | 0 | 0 | 40 | 40 |
| 664 | 19863 | RG:153244:10006:D11 | MA155:D11 | 52.5 | 2.5 | 0 | 40 |
| 665 | 19871 | RG:196236:10006:H11 | MA155:H11 | 35 | 5 | 5 | 40 |
| 666 | 19893 | I:557538:16A01:C11 | MA87:C11 | 27.5 | 0 | 0 | 40 |
| 667 | 19899 | I:782235:16A01:F11 | MA87:F11 | 67.5 | 30 | 0 | 40 |
| 668 | 19980 | RG:1257341:10012:F05 | MA161:F05 | 42.5 | 2.5 | 0 | 40 |
| 669 | 19981 | RG:727387:10010:G05 | MA159:G05 | 32.5 | 2.5 | 0 | 40 |
| 670 | 19992 | RG:1145235:10012:D11 | MA161:D11 | 25 | 2.5 | 0 | 40 |
| 671 | 19995 | RG:725145:10010:F11 | MA159:F11 | 10 | 0 | 25 | 40 |
| 672 | 19999 | RG:740079:10010:H11 | MA159:H11 | 57.5 | 7.5 | 0 | 40 |
| 673 | 20042 | I:1873176:09B01:E05 | MA137:E05 | 27.5 | 0 | 0 | 40 |
| 674 | 20056 | I:2081974:09B01:D11 | MA137:D11 | 30 | 5 | 2.5 | 40 |
| 675 | 20141 | I:2107723:18A02:G05 | MA96:G05 | 37.5 | 7.5 | 0 | 40 |
| 676 | 20211 | RG:207777:10007:B11 | MA156:B11 | 22.5 | 0 | 2.5 | 40 |
| 677 | 20213 | RG:221172:10007:C11 | MA156:C11 | 42.5 | 7.5 | 0 | 40 |
| 678 | 20230 | I:1968436:16B02:C05 | MA90:C05 | 2.5 | 0 | 25 | 40 |
| 679 | 20253 | I:2060973:16A02:G11 | MA88:G11 | 22.5 | 0 | 2.5 | 40 |
| 680 | 20323 | RG:1369494:10013:B05 | MA162:B05 | 32.5 | 12.5 | 0 | 40 |
| 681 | 20330 | RG:1752177:10015:E05 | MA164:E05 | 22.5 | 2.5 | 2.5 | 40 |
| 682 | 20331 | RG:1519327:10013:F05 | MA162:F05 | 10 | 0 | 60 | 40 |
| 683 | 20338 | RG:1694569:10015:A11 | MA164:A11 | 50 | 2.5 | 0 | 40 |
| 684 | 20346 | RG:1839794:10015:E11 | MA164:E11 | 0 | 0 | 45 | 40 |
| 685 | 20359 | I:514124:17A02:D05 | MA92:D05 | 0 | 0 | 22.5 | 40 |
| 686 | 20365 | I:997782:17A02:G05 | MA92:G05 | 0 | 0 | 25 | 40 |

Table 4

| SEQ ID NO | SpotID | Clone ID | MAClone ID | >=2x | >=5x | <=halfx | Num Ratios |
|--------------|--------|----------------------|------------|-------------|-------------|-------------|---------------|
| 687 | 20412 | I:1709364:09B02:F11 | MA138:F11 | 2.5 | 0 | 30 | 40 |
| 688 | 20485 | I:2004896:18A01:C06 | MA95:C06 | 0 | 0 | 22.5 | 40 |
| 689 | 20555 | RG:172982:10006:F06 | MA155:F06 | 2.5 | 0 | 32.5 | 40 |
| 690 | 20557 | RG:180978:10006:G06 | MA155:G06 | 20 | 2.5 | 2.5 | 40 |
| 691 | 20563 | RG:129528:10006:B12 | MA155:B12 | 20 | 7.5 | 0 | 40 |
| 692 | 20573 | RG:186511:10006:G12 | MA155:G12 | 30 | 0 | 0 | 40 |
| 693 | 20580 | I:2005910:16B01:B06 | MA89:B06 | 0 | 0 | 20 | 40 |
| 694 | 20583 | I:620871:16A01:D06 | MA87:D06 | 30 | 0 | 0 | 40 |
| 695 | 20593 | I:1920819:16A01:A12 | MA87:A12 | 27.5 | 0 | 0 | 40 |
| 696 | 20601 | I:990375:16A01:E12 | MA87:E12 | 0 | 0 | 82.5 | 40 |
| 697 | 20605 | I:690313:16A01:G12 | MA87:G12 | 47.5 | 10 | 0 | 40 |
| 698 | 20674 | RG:878195:10012:A06 | MA161:A06 | 25 | 0 | 0 | 40 |
| 699 | 20679 | RG:687128:10010:D06 | MA159:D06 | 0 | 0 | 25 | 40 |
| 700 | 20712 | I:884855:17B01:D06 | MA93:D06 | 25 | 2.5 | 0 | 40 |
| 701 | 20716 | I:1218621:17B01:F06 | MA93:F06 | 0 | 0 | 35 | 40 |
| 702 | 20719 | I:620371:17A01:H06 | MA91:H06 | 35 | 5 | 0 | 40 |
| 703 | 20744 | I:1681610:09B01:D06 | MA137:D06 | 0 | 0 | 22.5 | 40 |
| 704 | 20909 | RG:265206:10007:G06 | MA156:G06 | 50 | 2.5 | 0 | 40 |
| 705 | 20911 | RG:268073:10007:H06 | MA156:H06 | 0 | 0 | 20 | 40 |
| 706 | 20939 | I:2117221:16A02:F06 | MA88:F06 | 0 | 0 | 35 | 40 |
| 707 | 20942 | I:1760693:16B02:G06 | MA90:G06 | 2.5 | 0 | 35 | 40 |
| 708 | 20948 | I:776793:16B02:B12 | MA90:B12 | 0 | 0 | 25 | 40 |
| 709 | 21029 | RG:1405692:10013:C06 | MA162:C06 | 62.5 | 5 | 0 | 40 |
| 710 | 21044 | RG:1707747:10015:B12 | MA164:B12 | 65 | 15 | 0 | 40 |
| 711 | 21046 | RG:1722789:10015:C12 | MA164:C12 | 30 | 2.5 | 0 | 40 |
| 712 | 21066 | I:2112348:17B02:E06 | MA94:E06 | 25 | 2.5 | 0 | 40 |
| 713 | 21067 | I:630458:17A02:F06 | MA92:F06 | 35 | 5 | 0 | 40 |
| 714 | 21071 | I:901577:17A02:H06 | MA92:H06 | 20 | 7.5 | 0 | 40 |
| 715 | 21082 | I:2298081:17B02:E12 | MA94:E12 | 0 | 0 | 37.5 | 40 |
| 716 | 21120 | I:2718565:09B02:H12 | MA138:H12 | 0 | 0 | 20 | 40 |
| 717 | 21122 | M00056237C:E03 | MA181:A01 | 2.173913043 | 0 | 28.26086957 | 46 |
| 718 | 21130 | M00055261C:F04 | MA197:E01 | 28.26086957 | 0 | 0 | 46 |
| 719 | 21144 | M00055353D:A04 | MA197:D07 | 78.26086957 | 54.34782609 | 0 | 46 |
| 720 | 21152 | M00055357B:B10 | MA197:H07 | 69.56521739 | 34.7826087 | 0 | 46 |
| 721 | 21189 | M00056386D:H12 | MA173:C01 | 52.17391304 | 2.173913043 | 0 | 46 |
| 722 | 21191 | M00056394B:B04 | MA173:D01 | 54.34782609 | 8.695652174 | 0 | 46 |
| 723 | 21193 | M00056395A:B04 | MA173:E01 | 26.08695652 | 0 | 0 | 46 |
| 724 | 21195 | M00056396B:G05 | MA173:F01 | 26.08695652 | 0 | 0 | 46 |
| 725 | 21198 | M00056137A:A05 | MA180:G01 | 0 | 0 | 76.08695652 | 46 |
| 726 | 21199 | M00056401C:C03 | MA173:H01 | 36.95652174 | 8.695652174 | 6.52173913 | 46 |
| 727 | 21209 | M00056484A:F06 | MA173:E07 | 26.08695652 | 2.173913043 | 0 | 46 |
| 728 | 21212 | M00056193B:C11 | MA180:F07 | 2.173913043 | 0 | 41.30434783 | 46 |
| 729 | 21213 | M00056484B:B07 | MA173:G07 | 2.173913043 | 0 | 39.13043478 | 46 |
| 730 | 21214 | M00056193B:D06 | MA180:G07 | 4.347826087 | 2.173913043 | 45.65217391 | 46 |
| 731 | 21216 | M00056194B:G06 | MA180:H07 | 8.695652174 | 0 | 21.73913043 | 46 |
| 732 | 21217 | M00054633D:B07 | MA187:A01 | 30.43478261 | 0 | 0 | 46 |
| 733 | 21219 | M00054633D:E06 | MA187:B01 | 26.08695652 | 6.52173913 | 17.39130435 | 46 |
| 734 | 21232 | M00054848A:C03 | MA189:H01 | 34.7826087 | 0 | 2.173913043 | 46 |
| 735 | 21234 | M00054882C:C06 | MA189:A07 | 0 | 0 | 23.91304348 | 46 |

Table 4

| SEQ ID NO | SpotID | Clone ID | MAClone ID | >=2x | >=5x | <=halfx | Num Ratios |
|--------------|--------|---------------------|------------|-------------|-------------|-------------|---------------|
| 736 | 21237 | M00054678D:A03 | MA187:C07 | 30.43478261 | 0 | 0 | 46 |
| 737 | 21239 | M00054679B:B03 | MA187:D07 | 23.91304348 | 13.04347826 | 28.26086957 | 46 |
| 738 | 21245 | M00054680B:D06 | MA187:G07 | 71.73913043 | 15.2173913 | 0 | 46 |
| 739 | 21247 | M00054680C:A06 | MA187:H07 | 0 | 0 | 43.47826087 | 46 |
| 740 | 21252 | M00057176B:F11 | MA193:B01 | 32.60869565 | 0 | 0 | 46 |
| 741 | 21254 | M00057181A:D01 | MA193:C01 | 43.47826087 | 0 | 0 | 46 |
| 742 | 21272 | M00057219D:B04 | MA193:D07 | 43.47826087 | 0 | 0 | 46 |
| 743 | 21281 | M00042341A:D12 | MA167:A01 | 0 | 0 | 76.08695652 | 46 |
| 744 | 21284 | M00042433B:G09 | MA171:B01 | 39.13043478 | 0 | 0 | 46 |
| 745 | 21288 | M00042435A:F08 | MA171:D01 | 45.65217391 | 0 | 0 | 46 |
| 746 | 21290 | M00042437B:G03 | MA171:E01 | 10.86956522 | 6.52173913 | 67.39130435 | 46 |
| 747 | 21291 | M00042525D:E07 | MA167:F01 | 54.34782609 | 0 | 0 | 46 |
| 748 | 21292 | M00042438B:D01 | MA171:F01 | 0 | 0 | 58.69565217 | 46 |
| 749 | 21293 | M00042529C:G07 | MA167:G01 | 0 | 0 | 82.60869565 | 46 |
| 750 | 21295 | M00042529D:B12 | MA167:H01 | 0 | 0 | 76.08695652 | 46 |
| 751 | 21297 | M00042700A:E05 | MA167:A07 | 58.69565217 | 6.52173913 | 0 | 46 |
| 752 | 21300 | M00042777D:G05 | MA171:B07 | 21.73913043 | 13.04347826 | 28.26086957 | 46 |
| 753 | 21304 | M00042781C:F03 | MA171:D07 | 76.08695652 | 13.04347826 | 0 | 46 |
| 754 | 21306 | M00042783C:F10 | MA171:E07 | 2.173913043 | 0 | 23.91304348 | 46 |
| 755 | 21307 | M00042702D:B02 | MA167:F07 | 10.86956522 | 6.52173913 | 73.91304348 | 46 |
| 756 | 21312 | M00042785B:F11 | MA171:H07 | 15.2173913 | 10.86956522 | 26.08695652 | 46 |
| 757 | 21329 | M00056566C:C03 | MA174:A07 | 26.08695652 | 0 | 0 | 46 |
| 758 | 21333 | M00056567B:A09 | MA174:C07 | 43.47826087 | 0 | 0 | 46 |
| 759 | 21341 | M00056569B:D09 | MA174:G07 | 23.91304348 | 0 | 0 | 46 |
| 760 | 21343 | M00056571D:E05 | MA174:H07 | 52.17391304 | 2.173913043 | 2.173913043 | 46 |
| 761 | 21349 | RG:376801:10009:C01 | MA158:C01 | 34.7826087 | 2.173913043 | 2.173913043 | 46 |
| 762 | 21363 | RG:365436:10009:B07 | MA158:B07 | 41.30434783 | 13.04347826 | 0 | 46 |
| 763 | 21367 | RG:416839:10009:D07 | MA158:D07 | 2.173913043 | 0 | 47.82608696 | 46 |
| 764 | 21370 | RG:784224:10011:E07 | MA160:E07 | 30.43478261 | 2.173913043 | 4.347826087 | 46 |
| 765 | 21374 | RG:796852:10011:G07 | MA160:G07 | 28.26086957 | 6.52173913 | 2.173913043 | 46 |
| 766 | 21386 | M00043412A:F04 | MA184:E01 | 34.7826087 | 0 | 0 | 46 |
| 767 | 21391 | M00057273B:H10 | MA182:H01 | 36.95652174 | 0 | 0 | 46 |
| 768 | 21396 | M00054506C:B10 | MA184:B07 | 32.60869565 | 0 | 0 | 46 |
| 769 | 21404 | M00054507D:G03 | MA184:F07 | 43.47826087 | 0 | 0 | 46 |
| 770 | 21418 | M00054935B:B03 | MA198:E01 | 0 | 0 | 23.91304348 | 46 |
| 771 | 21424 | M00054935D:C11 | MA198:H01 | 23.91304348 | 4.347826087 | 0 | 46 |
| 772 | 21432 | M00054976A:E09 | MA198:D07 | 39.13043478 | 4.347826087 | 0 | 46 |
| 773 | 21461 | M00055788B:F08 | MA170:C07 | 2.173913043 | 0 | 36.95652174 | 46 |
| 774 | 21469 | M00055791A:E10 | MA170:G07 | 2.173913043 | 0 | 36.95652174 | 46 |
| 775 | 21497 | M00055224C:H11 | MA196:E07 | 32.60869565 | 6.52173913 | 2.173913043 | 46 |
| 776 | 21539 | M00055932A:C02 | MA179:B01 | 58.69565217 | 4.347826087 | 4.347826087 | 46 |
| 777 | 21542 | M00056908A:F12 | MA177:C01 | 0 | 0 | 21.73913043 | 46 |
| 778 | 21543 | M00055935D:B06 | MA179:D01 | 60.86956522 | 21.73913043 | 0 | 46 |
| 779 | 21546 | M00056908D:D08 | MA177:E01 | 23.91304348 | 0 | 2.173913043 | 46 |
| 780 | 21547 | M00055942B:F08 | MA179:F01 | 0 | 0 | 89.13043478 | 46 |
| 781 | 21550 | M00056910A:B07 | MA177:G01 | 73.91304348 | 8.695652174 | 0 | 46 |
| 782 | 21568 | M00056952B:C08 | MA177:H07 | 8.695652174 | 4.347826087 | 63.04347826 | 46 |
| 783 | 21569 | M00054728C:E03 | MA188:A01 | 63.04347826 | 10.86956522 | 0 | 46 |
| 784 | 21571 | M00054728D:E06 | MA188:B01 | 34.7826087 | 4.347826087 | 4.347826087 | 46 |

Table 4

| SEQ ID NO | SpotID | Clone ID | MAClone ID | >=2x | >=5x | <=halfx | Num Ratios |
|-----------|--------|----------------------|------------|-------------|-------------|-------------|------------|
| 785 | 21583 | M00054731C:H01 | MA188:H01 | 0 | 0 | 84.7826087 | 46 |
| 786 | 21591 | M00054778B:A12 | MA188:D07 | 43.47826087 | 4.347826087 | 0 | 46 |
| 787 | 21595 | M00054778C:D08 | MA188:F07 | 21.73913043 | 0 | 0 | 46 |
| 788 | 21599 | M00054780A:G06 | MA188:H07 | 39.13043478 | 0 | 0 | 46 |
| 789 | 21633 | M00042899D:D02 | MA168:A01 | 0 | 0 | 78.26086957 | 46 |
| 790 | 21638 | M00042831B:G10 | MA172:C01 | 34.7826087 | 0 | 0 | 46 |
| 791 | 21640 | M00042833A:G07 | MA172:D01 | 26.08695652 | 0 | 4.347826087 | 46 |
| 792 | 21641 | M00042906D:F05 | MA168:E01 | 2.173913043 | 0 | 28.26086957 | 46 |
| 793 | 21645 | M00042910C:A02 | MA168:G01 | 0 | 0 | 80.43478261 | 46 |
| 794 | 21648 | M00042838C:D06 | MA172:H01 | 54.34782609 | 4.347826087 | 0 | 46 |
| 795 | 21650 | M00042867B:F03 | MA172:A07 | 2.173913043 | 0 | 41.30434783 | 46 |
| 796 | 21651 | M00055439B:G05 | MA168:B07 | 0 | 0 | 32.60869565 | 46 |
| 797 | 21659 | M00055442D:E12 | MA168:F07 | 30.43478261 | 2.173913043 | 0 | 46 |
| 798 | 21667 | M00056711D:A02 | MA175:B01 | 54.34782609 | 4.347826087 | 0 | 46 |
| 799 | 21681 | M00056771C:A12 | MA175:A07 | 52.17391304 | 2.173913043 | 2.173913043 | 46 |
| 800 | 21685 | M00056772D:G07 | MA175:C07 | 47.82608696 | 0 | 0 | 46 |
| 801 | 21691 | M00056782D:E04 | MA175:F07 | 2.173913043 | 0 | 43.47826087 | 46 |
| 802 | 21693 | M00056785D:G01 | MA175:G07 | 73.91304348 | 10.86956522 | 0 | 46 |
| 803 | 21695 | M00056788C:A01 | MA175:H07 | 0 | 0 | 39.13043478 | 46 |
| 804 | 21723 | RG:1663880:10014:F07 | MA163:F07 | 0 | 0 | 30.43478261 | 46 |
| 805 | 21733 | M00043310B:D08 | MA183:C01 | 36.95652174 | 0 | 0 | 46 |
| 806 | 21734 | M00054538C:G03 | MA185:C01 | 71.73913043 | 2.173913043 | 0 | 46 |
| 807 | 21743 | M00043315C:G05 | MA183:H01 | 28.26086957 | 0 | 0 | 46 |
| 808 | 21764 | M00055397B:E08 | MA199:B01 | 43.47826087 | 0 | 0 | 46 |
| 809 | 21765 | M00056624B:H11 | MA186:C01 | 45.65217391 | 2.173913043 | 2.173913043 | 46 |
| 810 | 21786 | M00055423C:C03 | MA199:E07 | 34.7826087 | 2.173913043 | 0 | 46 |
| 811 | 21787 | M00056668D:C06 | MA186:F07 | 54.34782609 | 6.52173913 | 0 | 46 |
| 812 | 21789 | M00056669B:A10 | MA186:G07 | 52.17391304 | 6.52173913 | 0 | 46 |
| 813 | 21790 | M00055424A:D01 | MA199:G07 | 32.60869565 | 6.52173913 | 0 | 46 |
| 814 | 21791 | M00056669B:E07 | MA186:H07 | 34.7826087 | 6.52173913 | 0 | 46 |
| 815 | 21792 | M00055424D:F01 | MA199:H07 | 39.13043478 | 2.173913043 | 2.173913043 | 46 |
| 816 | 21798 | M00056243A:H07 | MA181:C02 | 2.173913043 | 0 | 23.91304348 | 46 |
| 817 | 21800 | M00056243C:G10 | MA181:D02 | 2.173913043 | 0 | 23.91304348 | 46 |
| 818 | 21803 | M00055528D:H03 | MA169:F02 | 2.173913043 | 0 | 21.73913043 | 46 |
| 819 | 21811 | M00055607B:A11 | MA169:B08 | 0 | 0 | 26.08695652 | 46 |
| 820 | 21842 | M00055363C:E02 | MA197:A08 | 2.173913043 | 0 | 21.73913043 | 46 |
| 821 | 21852 | M00055373D:H02 | MA197:F08 | 43.47826087 | 2.173913043 | 2.173913043 | 46 |
| 822 | 21856 | M00055374D:E01 | MA197:H08 | 36.95652174 | 2.173913043 | 0 | 46 |
| 823 | 21889 | M00056401D:D09 | MA173:A02 | 43.47826087 | 4.347826087 | 0 | 46 |
| 824 | 21892 | M00056139D:A10 | MA180:B02 | 2.173913043 | 0 | 47.82608696 | 46 |
| 825 | 21896 | M00056140A:E11 | MA180:D02 | 0 | 0 | 71.73913043 | 46 |
| 826 | 21898 | M00056142D:A08 | MA180:E02 | 65.2173913 | 2.173913043 | 0 | 46 |
| 827 | 21899 | M00056412D:A09 | MA173:F02 | 2.173913043 | 0 | 23.91304348 | 46 |
| 828 | 21900 | M00056142D:H11 | MA180:F02 | 0 | 0 | 52.17391304 | 46 |
| 829 | 21901 | M00056414C:F03 | MA173:G02 | 36.95652174 | 2.173913043 | 2.173913043 | 46 |
| 830 | 21908 | M00056196A:H09 | MA180:B08 | 0 | 0 | 91.30434783 | 46 |
| 831 | 21912 | M00056200A:E11 | MA180:D08 | 0 | 0 | 84.7826087 | 46 |
| 832 | 21913 | M00056488C:G01 | MA173:E08 | 50 | 4.347826087 | 0 | 46 |
| 833 | 21914 | M00056200B:B01 | MA180:E08 | 0 | 0 | 86.95652174 | 46 |

Table 4

| SEQ ID NO | SpotID | Clone ID | MAClone ID | >=2x | >=5x | <=halfx | Num Ratios |
|--------------|--------|----------------------|------------|-------------|-------------|-------------|---------------|
| 834 | 21916 | M00056203B:G08 | MA180:F08 | 0 | 0 | 21.73913043 | 46 |
| 835 | 21919 | M00056493A:F09 | MA173:H08 | 0 | 0 | 50 | 46 |
| 836 | 21923 | M00054640D:D12 | MA187:B02 | 2.173913043 | 0 | 21.73913043 | 46 |
| 837 | 21927 | M00054643B:F04 | MA187:D02 | 2.173913043 | 0 | 23.91304348 | 46 |
| 838 | 21929 | M00054643C:D08 | MA187:E02 | 58.69565217 | 2.173913043 | 0 | 46 |
| 839 | 21932 | M00054854D:B06 | MA189:F02 | 60.86956522 | 2.173913043 | 0 | 46 |
| 840 | 21933 | M00054644B:F02 | MA187:G02 | 26.08695652 | 0 | 2.173913043 | 46 |
| 841 | 21934 | M00054857A:E08 | MA189:G02 | 52.17391304 | 2.173913043 | 0 | 46 |
| 842 | 21939 | M00054681D:G03 | MA187:B08 | 36.95652174 | 0 | 0 | 46 |
| 843 | 21943 | M00054682D:F11 | MA187:D08 | 0 | 0 | 45.65217391 | 46 |
| 844 | 21947 | M00054684B:C07 | MA187:F08 | 56.52173913 | 2.173913043 | 0 | 46 |
| 845 | 21960 | M00057191B:E11 | MA193:D02 | 58.69565217 | 2.173913043 | 0 | 46 |
| 846 | 21966 | M00057194B:G12 | MA193:G02 | 0 | 0 | 84.7826087 | 46 |
| 847 | 21972 | M00057222D:G09 | MA193:B08 | 26.08695652 | 2.173913043 | 0 | 46 |
| 848 | 21985 | M00042531B:H03 | MA167:A02 | 13.04347826 | 0 | 21.73913043 | 46 |
| 849 | 21986 | M00042440C:G04 | MA171:A02 | 2.173913043 | 0 | 26.08695652 | 46 |
| 850 | 21989 | M00042533C:D02 | MA167:C02 | 45.65217391 | 0 | 0 | 46 |
| 851 | 21993 | M00042536D:H05 | MA167:E02 | 0 | 0 | 95.65217391 | 46 |
| 852 | 21994 | M00042465B:E04 | MA171:E02 | 21.73913043 | 0 | 4.347826087 | 46 |
| 853 | 21995 | M00042537D:F10 | MA167:F02 | 39.13043478 | 0 | 0 | 46 |
| 854 | 21996 | M00042467B:B04 | MA171:F02 | 54.34782609 | 4.347826087 | 0 | 46 |
| 855 | 21997 | M00042538D:D12 | MA167:G02 | 0 | 0 | 23.91304348 | 46 |
| 856 | 21998 | M00042467B:B08 | MA171:G02 | 26.08695652 | 0 | 0 | 46 |
| 857 | 22003 | M00042711B:G09 | MA167:B08 | 4.347826087 | 0 | 52.17391304 | 46 |
| 858 | 22004 | M00042790B:E12 | MA171:B08 | 4.347826087 | 0 | 67.39130435 | 46 |
| 859 | 22006 | M00042791A:C10 | MA171:C08 | 0 | 0 | 45.65217391 | 46 |
| 860 | 22007 | M00042711C:H05 | MA167:D08 | 0 | 0 | 65.2173913 | 46 |
| 861 | 22016 | M00042801D:B02 | MA171:H08 | 39.13043478 | 0 | 0 | 46 |
| 862 | 22016 | M00042801D:B02 | MA171:H08 | 39.13043478 | 0 | 0 | 46 |
| 863 | 22021 | M00056532A:D09 | MA174:C02 | 2.173913043 | 0 | 21.73913043 | 46 |
| 864 | 22025 | M00056533D:H04 | MA174:E02 | 2.173913043 | 0 | 50 | 46 |
| 865 | 22035 | M00056575B:C04 | MA174:B08 | 2.173913043 | 0 | 54.34782609 | 46 |
| 866 | 22037 | M00056578C:A09 | MA174:C08 | 58.69565217 | 2.173913043 | 0 | 46 |
| 867 | 22040 | RG:1862072:20001:D08 | MA139:D08 | 39.13043478 | 4.347826087 | 2.173913043 | 46 |
| 868 | 22044 | RG:1862465:20001:F08 | MA139:F08 | 2.173913043 | 0 | 23.91304348 | 46 |
| 869 | 22049 | RG:347381:10009:A02 | MA158:A02 | 60.86956522 | 6.52173913 | 0 | 46 |
| 870 | 22071 | RG:417093:10009:D08 | MA158:D08 | 47.82608696 | 6.52173913 | 0 | 46 |
| 871 | 22082 | M00043413B:C04 | MA184:A02 | 67.39130435 | 0 | 0 | 46 |
| 872 | 22092 | M00043502D:C12 | MA184:F02 | 39.13043478 | 0 | 0 | 46 |
| 873 | 22105 | M00057341B:B11 | MA182:E08 | 47.82608696 | 2.173913043 | 0 | 46 |
| 874 | 22110 | M00054512A:F11 | MA184:G08 | 41.30434783 | 0 | 0 | 46 |
| 875 | 22111 | M00042353A:D05 | MA182:H08 | 26.08695652 | 0 | 0 | 46 |
| 876 | 22116 | M00054937B:D09 | MA198:B02 | 36.95652174 | 0 | 0 | 46 |
| 877 | 22167 | M00055797C:H09 | MA170:D08 | 0 | 0 | 93.47826087 | 46 |
| 878 | 22169 | M00055799B:C01 | MA170:E08 | 2.173913043 | 0 | 41.30434783 | 46 |
| 879 | 22183 | M00055194C:G12 | MA196:D02 | 34.7826087 | 0 | 0 | 46 |
| 880 | 22195 | M00055233B:D08 | MA196:B08 | 0 | 0 | 21.73913043 | 46 |
| 881 | 22255 | M00055966C:D06 | MA179:H02 | 0 | 0 | 91.30434783 | 46 |
| 882 | 22263 | M00056024B:B06 | MA179:D08 | 0 | 0 | 82.60869565 | 46 |

Table 4

| SEQ ID NO | SpotID | Clone ID | MAClone ID | >=2x | >=5x | <=halfx | Num Ratios |
|--------------|--------|----------------------|------------|-------------|-------------|-------------|---------------|
| 883 | 22265 | M00056024C:G04 | MA179:E08 | 0 | 0 | 93.47826087 | 46 |
| 884 | 22279 | M00054737D:F10 | MA188:D02 | 65.2173913 | 17.39130435 | 0 | 46 |
| 885 | 22289 | M00054780D:C09 | MA188:A08 | 34.7826087 | 4.347826087 | 0 | 46 |
| 886 | 22295 | M00054787A:E09 | MA188:D08 | 54.34782609 | 13.04347826 | 0 | 46 |
| 887 | 22297 | M00054806B:E11 | MA188:E08 | 43.47826087 | 8.695652174 | 2.173913043 | 46 |
| 888 | 22339 | M00042913B:C11 | MA168:B02 | 52.17391304 | 0 | 0 | 46 |
| 889 | 22343 | M00042915B:B10 | MA168:D02 | 0 | 0 | 26.08695652 | 46 |
| 890 | 22345 | M00054792C:E12 | MA168:E02 | 47.82608696 | 4.347826087 | 0 | 46 |
| 891 | 22350 | M00042842A:C01 | MA172:G02 | 2.173913043 | 0 | 21.73913043 | 46 |
| 892 | 22367 | M00055450A:C09 | MA168:H08 | 2.173913043 | 0 | 23.91304348 | 46 |
| 893 | 22399 | M00056804C:D01 | MA175:H08 | 21.73913043 | 0 | 0 | 46 |
| 894 | 22423 | RG:1647954:10014:D08 | MA163:D08 | 41.30434783 | 0 | 0 | 46 |
| 895 | 22427 | RG:1664311:10014:F08 | MA163:F08 | 39.13043478 | 8.695652174 | 2.173913043 | 46 |
| 896 | 22429 | RG:1671377:10014:G08 | MA163:G08 | 47.82608696 | 4.347826087 | 0 | 46 |
| 897 | 22437 | M00043316B:F10 | MA183:C02 | 26.08695652 | 0 | 2.173913043 | 46 |
| 898 | 22440 | M00054545B:A03 | MA185:D02 | 26.08695652 | 0 | 0 | 46 |
| 899 | 22442 | M00054545B:B09 | MA185:E02 | 45.65217391 | 0 | 0 | 46 |
| 900 | 22456 | M00054575A:B09 | MA185:D08 | 30.43478261 | 2.173913043 | 2.173913043 | 46 |
| 901 | 22459 | M00043374B:H05 | MA183:F08 | 34.7826087 | 0 | 0 | 46 |
| 902 | 22475 | M00056641A:G11 | MA186:F02 | 39.13043478 | 6.52173913 | 4.347826087 | 46 |
| 903 | 22479 | M00056642A:D08 | MA186:H02 | 2.173913043 | 0 | 23.91304348 | 46 |
| 904 | 22480 | M00055403B:B11 | MA199:H02 | 43.47826087 | 0 | 0 | 46 |
| 905 | 22495 | M00056676B:C11 | MA186:H08 | 0 | 0 | 43.47826087 | 46 |
| 906 | 22499 | M00055530D:B02 | MA169:B03 | 45.65217391 | 4.347826087 | 0 | 46 |
| 907 | 22502 | M00056253A:D06 | MA181:C03 | 2.173913043 | 0 | 67.39130435 | 46 |
| 908 | 22504 | M00056253B:B06 | MA181:D03 | 0 | 0 | 36.95652174 | 46 |
| 909 | 22519 | M00055642D:F09 | MA169:D09 | 0 | 0 | 56.52173913 | 46 |
| 910 | 22521 | M00055643A:E09 | MA169:E09 | 0 | 0 | 93.47826087 | 46 |
| 911 | 22523 | M00055643D:E02 | MA169:F09 | 0 | 0 | 82.60869565 | 46 |
| 912 | 22548 | M00055376D:D08 | MA197:B09 | 2.173913043 | 0 | 34.7826087 | 46 |
| 913 | 22595 | M00056415C:D02 | MA173:B03 | 2.173913043 | 0 | 23.91304348 | 46 |
| 914 | 22596 | M00056146D:F05 | MA180:B03 | 0 | 0 | 23.91304348 | 46 |
| 915 | 22597 | M00056417A:F02 | MA173:C03 | 8.695652174 | 6.52173913 | 65.2173913 | 46 |
| 916 | 22598 | M00056148A:B07 | MA180:C03 | 0 | 0 | 30.43478261 | 46 |
| 917 | 22599 | M00056420C:E07 | MA173:D03 | 43.47826087 | 6.52173913 | 2.173913043 | 46 |
| 918 | 22600 | M00056150A:E04 | MA180:D03 | 2.173913043 | 0 | 23.91304348 | 46 |
| 919 | 22603 | M00056421C:H11 | MA173:F03 | 58.69565217 | 6.52173913 | 0 | 46 |
| 920 | 22604 | M00056150C:A10 | MA180:F03 | 69.56521739 | 26.08695652 | 0 | 46 |
| 921 | 22605 | M00056421D:H05 | MA173:G03 | 0 | 0 | 52.17391304 | 46 |
| 922 | 22606 | M00056150C:C04 | MA180:G03 | 39.13043478 | 0 | 0 | 46 |
| 923 | 22607 | M00056422B:D11 | MA173:H03 | 36.95652174 | 0 | 0 | 46 |
| 924 | 22608 | M00056151C:A12 | MA180:H03 | 10.86956522 | 8.695652174 | 67.39130435 | 46 |
| 925 | 22609 | M00056493C:E06 | MA173:A09 | 34.7826087 | 2.173913043 | 0 | 46 |
| 926 | 22610 | M00056205D:E03 | MA180:A09 | 0 | 0 | 23.91304348 | 46 |
| 927 | 22611 | M00056495A:G10 | MA173:B09 | 34.7826087 | 0 | 0 | 46 |
| 928 | 22618 | M00056206D:B10 | MA180:E09 | 6.52173913 | 0 | 28.26086957 | 46 |
| 929 | 22623 | M00056501D:C08 | MA173:H09 | 2.173913043 | 0 | 50 | 46 |
| 930 | 22624 | M00056209D:H10 | MA180:H09 | 0 | 0 | 63.04347826 | 46 |
| 931 | 22627 | M00054645B:C12 | MA187:B03 | 52.17391304 | 10.86956522 | 0 | 46 |

Table 4

| SEQ ID NO | SpotID | Clone ID | MAClone ID | >=2x | >=5x | <=halfx | Num Ratios |
|--------------|--------|----------------------|------------|-------------|-------------|-------------|---------------|
| 932 | 22629 | M00054646A:B10 | MA187:C03 | 89.13043478 | 36.95652174 | 0 | 46 |
| 933 | 22637 | M00054647D:E01 | MA187:G03 | 47.82608696 | 4.347826087 | 2.173913043 | 46 |
| 934 | 22666 | M00057202C:G06 | MA193:E03 | 32.60869565 | 0 | 0 | 46 |
| 935 | 22668 | M00057202D:C11 | MA193:F03 | 32.60869565 | 2.173913043 | 0 | 46 |
| 936 | 22693 | M00042549A:G12 | MA167:C03 | 0 | 0 | 36.95652174 | 46 |
| 937 | 22695 | M00042549D:F03 | MA167:D03 | 0 | 0 | 54.34782609 | 46 |
| 938 | 22697 | M00042551B:D12 | MA167:E03 | 45.65217391 | 6.52173913 | 0 | 46 |
| 939 | 22698 | M00042513A:D03 | MA171:E03 | 34.7826087 | 2.173913043 | 0 | 46 |
| 940 | 22700 | M00042513D:A12 | MA171:F03 | 2.173913043 | 0 | 2.173913043 | 46 |
| 941 | 22703 | M00042551D:D12 | MA167:H03 | 28.26086957 | 2.173913043 | 2.173913043 | 46 |
| 942 | 22705 | M00042717B:D05 | MA167:A09 | 0 | 0 | 89.13043478 | 46 |
| 943 | 22707 | M00042719D:C09 | MA167:B09 | 0 | 0 | 78.26086957 | 46 |
| 944 | 22710 | M00042803C:F11 | MA171:C09 | 41.30434783 | 0 | 2.173913043 | 46 |
| 945 | 22714 | M00042805D:D12 | MA171:E09 | 67.39130435 | 15.2173913 | 0 | 46 |
| 946 | 22715 | M00042731A:G04 | MA167:F09 | 6.52173913 | 6.52173913 | 60.86956522 | 46 |
| 947 | 22718 | M00042806C:E09 | MA171:G09 | 52.17391304 | 4.347826087 | 0 | 46 |
| 948 | 22720 | M00042806D:F08 | MA171:H09 | 47.82608696 | 2.173913043 | 0 | 46 |
| 949 | 22725 | M00056537A:F05 | MA174:C03 | 58.69565217 | 0 | 2.173913043 | 46 |
| 950 | 22727 | M00056537D:A07 | MA174:D03 | 47.82608696 | 4.347826087 | 0 | 46 |
| 951 | 22734 | RG:1862584:20001:G03 | MA139:G03 | 2.173913043 | 0 | 23.91304348 | 46 |
| 952 | 22737 | M00056585D:D05 | MA174:A09 | 45.65217391 | 0 | 0 | 46 |
| 953 | 22739 | M00056586C:B08 | MA174:B09 | 36.95652174 | 0 | 0 | 46 |
| 954 | 22745 | M00056592A:B08 | MA174:E09 | 4.347826087 | 0 | 43.47826087 | 46 |
| 955 | 22757 | RG:378550:10009:C03 | MA158:C03 | 0 | 0 | 63.04347826 | 46 |
| 956 | 22780 | RG:789040:10011:F09 | MA160:F09 | 28.26086957 | 4.347826087 | 0 | 46 |
| 957 | 22787 | M00057283A:D01 | MA182:B03 | 36.95652174 | 4.347826087 | 0 | 46 |
| 958 | 22792 | M00043505A:E07 | MA184:D03 | 32.60869565 | 0 | 0 | 46 |
| 959 | 22798 | M00043506B:G10 | MA184:G03 | 34.7826087 | 0 | 0 | 46 |
| 960 | 22800 | M00043507A:B02 | MA184:H03 | 28.26086957 | 0 | 0 | 46 |
| 961 | 22801 | M00042353C:F02 | MA182:A09 | 54.34782609 | 2.173913043 | 0 | 46 |
| 962 | 22812 | M00054516B:A08 | MA184:F09 | 43.47826087 | 0 | 0 | 46 |
| 963 | 22834 | M00054986D:B04 | MA198:A09 | 34.7826087 | 0 | 0 | 46 |
| 964 | 22836 | M00054987C:B10 | MA198:B09 | 21.73913043 | 4.347826087 | 0 | 46 |
| 965 | 22838 | M00054988D:B11 | MA198:C09 | 28.26086957 | 0 | 0 | 46 |
| 966 | 22857 | M00055743C:G08 | MA170:E03 | 47.82608696 | 4.347826087 | 0 | 46 |
| 967 | 22887 | M00055196B:C09 | MA196:D03 | 0 | 0 | 28.26086957 | 46 |
| 968 | 22899 | M00055238B:G05 | MA196:B09 | 32.60869565 | 0 | 0 | 46 |
| 969 | 22910 | M00056207B:H06 | MA180:G09 | 2.173913043 | 0 | 26.08695652 | 46 |
| 970 | 22945 | M00055966C:G04 | MA179:A03 | 50 | 8.695652174 | 4.347826087 | 46 |
| 971 | 22946 | M00056920D:C08 | MA177:A03 | 26.08695652 | 0 | 0 | 46 |
| 972 | 22949 | M00055969D:D01 | MA179:C03 | 0 | 0 | 82.60869565 | 46 |
| 973 | 22969 | M00056055D:F06 | MA179:E09 | 0 | 0 | 41.30434783 | 46 |
| 974 | 22970 | M00056956B:G12 | MA177:E09 | 0 | 0 | 23.91304348 | 46 |
| 975 | 22971 | M00056060D:C04 | MA179:F09 | 0 | 0 | 32.60869565 | 46 |
| 976 | 22973 | M00056061C:H04 | MA179:G09 | 0 | 0 | 30.43478261 | 46 |
| 977 | 22977 | M00054743C:E05 | MA188:A03 | 60.86956522 | 10.86956522 | 0 | 46 |
| 978 | 22979 | M00054744C:B02 | MA188:B03 | 43.47826087 | 0 | 0 | 46 |
| 979 | 22997 | M00054808A:E02 | MA188:C09 | 23.91304348 | 0 | 0 | 46 |
| 980 | 23005 | M00054811A:G01 | MA188:G09 | 45.65217391 | 2.173913043 | 0 | 46 |

Table 4

| SEQ ID NO | SpotID | Clone ID | MAClone ID | >=2x | >=5x | <=halfx | Num Ratios |
|-----------|--------|----------------------|------------|-------------|-------------|-------------|------------|
| 981 | 23041 | M00054797C:G10 | MA168:A03 | 0 | 0 | 28.26086957 | 46 |
| 982 | 23042 | M00042843B:H01 | MA172:A03 | 30.43478261 | 0 | 0 | 46 |
| 983 | 23048 | M00042844D:D10 | MA172:D03 | 32.60869565 | 0 | 0 | 46 |
| 984 | 23050 | M00042845D:A12 | MA172:E03 | 58.69565217 | 6.52173913 | 0 | 46 |
| 985 | 23053 | M00054800C:H10 | MA168:G03 | 8.695652174 | 8.695652174 | 58.69565217 | 46 |
| 986 | 23055 | M00054911D:E09 | MA168:H03 | 36.95652174 | 2.173913043 | 0 | 46 |
| 987 | 23057 | M00055450A:G03 | MA168:A09 | 0 | 0 | 89.13043478 | 46 |
| 988 | 23063 | M00055456B:H05 | MA168:D09 | 2.173913043 | 0 | 21.73913043 | 46 |
| 989 | 23079 | M00056733C:D03 | MA175:D03 | 0 | 0 | 36.95652174 | 46 |
| 990 | 23087 | M00056737D:E08 | MA175:H03 | 26.08695652 | 0 | 0 | 46 |
| 991 | 23097 | M00056809B:A12 | MA175:E09 | 4.347826087 | 2.173913043 | 28.26086957 | 46 |
| 992 | 23101 | M00056809D:C07 | MA175:G09 | 4.347826087 | 0 | 23.91304348 | 46 |
| 993 | 23131 | RG:1664308:10014:F09 | MA163:F09 | 0 | 0 | 23.91304348 | 46 |
| 994 | 23139 | M00043321A:G07 | MA183:B03 | 21.73913043 | 0 | 0 | 46 |
| 995 | 23142 | M00054549A:F03 | MA185:C03 | 2.173913043 | 0 | 26.08695652 | 46 |
| 996 | 23159 | M00043381A:C08 | MA183:D09 | 39.13043478 | 0 | 0 | 46 |
| 997 | 23169 | M00056642B:G03 | MA186:A03 | 23.91304348 | 6.52173913 | 15.2173913 | 46 |
| 998 | 23199 | M00056688C:A07 | MA186:H09 | 36.95652174 | 0 | 0 | 46 |
| 999 | 23202 | M00056257C:G03 | MA181:A04 | 0 | 0 | 30.43478261 | 46 |
| 1000 | 23213 | M00055545C:F11 | MA169:G04 | 0 | 0 | 23.91304348 | 46 |
| 1001 | 23221 | M00055653C:F04 | MA169:C10 | 0 | 0 | 84.7826087 | 46 |
| 1002 | 23223 | M00055653D:F01 | MA169:D10 | 0 | 0 | 60.86956522 | 46 |
| 1003 | 23252 | M00055385A:C11 | MA197:B10 | 34.7826087 | 0 | 0 | 46 |
| 1004 | 23304 | M00056157A:F11 | MA180:D04 | 30.43478261 | 0 | 0 | 46 |
| 1005 | 23306 | M00056160A:F03 | MA180:E04 | 2.173913043 | 0 | 23.91304348 | 46 |
| 1006 | 23307 | M00056426A:H07 | MA173:F04 | 8.695652174 | 0 | 23.91304348 | 46 |
| 1007 | 23318 | M00056214C:B04 | MA180:C10 | 0 | 0 | 89.13043478 | 46 |
| 1008 | 23320 | M00056216A:F10 | MA180:D10 | 2.173913043 | 0 | 21.73913043 | 46 |
| 1009 | 23325 | M00056507A:G11 | MA173:G10 | 2.173913043 | 0 | 21.73913043 | 46 |
| 1010 | 23329 | M00054648C:C10 | MA187:A04 | 34.7826087 | 0 | 0 | 46 |
| 1011 | 23330 | M00054862A:H11 | MA189:A04 | 0 | 0 | 21.73913043 | 46 |
| 1012 | 23331 | M00054648D:F12 | MA187:B04 | 50 | 0 | 0 | 46 |
| 1013 | 23335 | M00054650C:H08 | MA187:D04 | 43.47826087 | 0 | 0 | 46 |
| 1014 | 23344 | M00054868C:C11 | MA189:H04 | 0 | 0 | 21.73913043 | 46 |
| 1015 | 23351 | M00054700C:E02 | MA187:D10 | 56.52173913 | 4.347826087 | 2.173913043 | 46 |
| 1016 | 23356 | M00054902D:G11 | MA189:F10 | 0 | 0 | 26.08695652 | 46 |
| 1017 | 23358 | M00054903B:G06 | MA189:G10 | 28.26086957 | 0 | 0 | 46 |
| 1018 | 23359 | M00054706A:D05 | MA187:H10 | 2.173913043 | 0 | 45.65217391 | 46 |
| 1019 | 23366 | M00057207A:D05 | MA193:C04 | 39.13043478 | 0 | 8.695652174 | 46 |
| 1020 | 23368 | M00057207C:F06 | MA193:D04 | 54.34782609 | 8.695652174 | 4.347826087 | 46 |
| 1021 | 23372 | M00057208B:F11 | MA193:F04 | 52.17391304 | 2.173913043 | 0 | 46 |
| 1022 | 23382 | M00057242B:B10 | MA193:C10 | 32.60869565 | 0 | 0 | 46 |
| 1023 | 23397 | M00042555A:E06 | MA167:C04 | 2.173913043 | 0 | 21.73913043 | 46 |
| 1024 | 23399 | M00042561A:H03 | MA167:D04 | 0 | 0 | 30.43478261 | 46 |
| 1025 | 23402 | M00042756C:E10 | MA171:E04 | 52.17391304 | 2.173913043 | 0 | 46 |
| 1026 | 23404 | M00042758D:F01 | MA171:F04 | 52.17391304 | 2.173913043 | 0 | 46 |
| 1027 | 23408 | M00042759B:E02 | MA171:H04 | 52.17391304 | 4.347826087 | 0 | 46 |
| 1028 | 23412 | M00042808D:D03 | MA171:B10 | 39.13043478 | 2.173913043 | 0 | 46 |
| 1029 | 23414 | M00042808D:D10 | MA171:C10 | 34.7826087 | 0 | 0 | 46 |

Table 4

| SEQ ID NO | SpotID | Clone ID | MAClone ID | >=2x | >=5x | <=halfx | Num Ratios |
|--------------|--------|----------------------|------------|-------------|-------------|-------------|---------------|
| 1030 | 23416 | M00042811B:A05 | MA171:D10 | 2.173913043 | 0 | 50 | 46 |
| 1031 | 23417 | M00042746B:F05 | MA167:E10 | 73.91304348 | 8.695652174 | 0 | 46 |
| 1032 | 23421 | M00042746C:D01 | MA167:G10 | 0 | 0 | 63.04347826 | 46 |
| 1033 | 23422 | M00042812D:B04 | MA171:G10 | 58.69565217 | 0 | 0 | 46 |
| 1034 | 23425 | M00056546B:F12 | MA174:A04 | 60.86956522 | 6.52173913 | 2.173913043 | 46 |
| 1035 | 23439 | M00056550A:G09 | MA174:H04 | 21.73913043 | 0 | 0 | 46 |
| 1036 | 23453 | M00056610C:B08 | MA174:G10 | 2.173913043 | 0 | 39.13043478 | 46 |
| 1037 | 23460 | RG:745556:10011:B04 | MA160:B04 | 0 | 0 | 36.95652174 | 46 |
| 1038 | 23469 | RG:446537:10009:G04 | MA158:G04 | 30.43478261 | 0 | 0 | 46 |
| 1039 | 23475 | RG:375937:10009:B10 | MA158:B10 | 67.39130435 | 8.695652174 | 0 | 46 |
| 1040 | 23476 | RG:755120:10011:B10 | MA160:B10 | 43.47826087 | 0 | 0 | 46 |
| 1041 | 23480 | RG:781108:10011:D10 | MA160:D10 | 23.91304348 | 8.695652174 | 0 | 46 |
| 1042 | 23505 | M00042450C:H10 | MA182:A10 | 43.47826087 | 2.173913043 | 2.173913043 | 46 |
| 1043 | 23507 | M00042451B:B05 | MA182:B10 | 45.65217391 | 6.52173913 | 0 | 46 |
| 1044 | 23508 | M00054517D:D12 | MA184:B10 | 32.60869565 | 0 | 0 | 46 |
| 1045 | 23544 | M00055002B:G06 | MA198:D10 | 71.73913043 | 26.08695652 | 0 | 46 |
| 1046 | 23555 | M00055749A:C09 | MA170:B04 | 0 | 0 | 84.7826087 | 46 |
| 1047 | 23559 | M00055750A:F10 | MA170:D04 | 8.695652174 | 2.173913043 | 63.04347826 | 46 |
| 1048 | 23565 | M00055757A:H06 | MA170:G04 | 2.173913043 | 2.173913043 | 65.2173913 | 46 |
| 1049 | 23591 | M00055200B:F03 | MA196:D04 | 36.95652174 | 2.173913043 | 0 | 46 |
| 1050 | 23595 | M00055203B:F05 | MA196:F04 | 36.95652174 | 4.347826087 | 0 | 46 |
| 1051 | 23657 | M00055980B:F12 | MA179:E04 | 0 | 0 | 84.7826087 | 46 |
| 1052 | 23667 | M00056066C:H10 | MA179:B10 | 0 | 0 | 23.91304348 | 46 |
| 1053 | 23669 | M00056067B:F12 | MA179:C10 | 0 | 0 | 21.73913043 | 46 |
| 1054 | 23671 | M00056075D:H10 | MA179:D10 | 0 | 0 | 43.47826087 | 46 |
| 1055 | 23672 | M00056962D:A05 | MA177:D10 | 0 | 0 | 21.73913043 | 46 |
| 1056 | 23673 | M00056081D:B09 | MA179:E10 | 0 | 0 | 34.7826087 | 46 |
| 1057 | 23674 | M00056963A:E01 | MA177:E10 | 0 | 0 | 23.91304348 | 46 |
| 1058 | 23675 | M00056081D:C02 | MA179:F10 | 0 | 0 | 28.26086957 | 46 |
| 1059 | 23678 | M00056964D:C08 | MA177:G10 | 60.86956522 | 4.347826087 | 0 | 46 |
| 1060 | 23679 | M00056084A:B08 | MA179:H10 | 0 | 0 | 67.39130435 | 46 |
| 1061 | 23683 | M00054750C:G08 | MA188:B04 | 28.26086957 | 0 | 0 | 46 |
| 1062 | 23685 | M00054750D:F04 | MA188:C04 | 30.43478261 | 4.347826087 | 2.173913043 | 46 |
| 1063 | 23693 | M00054757A:F05 | MA188:G04 | 32.60869565 | 2.173913043 | 0 | 46 |
| 1064 | 23695 | M00054760D:B10 | MA188:H04 | 67.39130435 | 4.347826087 | 4.347826087 | 46 |
| 1065 | 23746 | M00042847A:A04 | MA172:A04 | 63.04347826 | 13.04347826 | 0 | 46 |
| 1066 | 23748 | M00042847A:D10 | MA172:B04 | 2.173913043 | 0 | 21.73913043 | 46 |
| 1067 | 23755 | M00054917B:G02 | MA168:F04 | 80.43478261 | 41.30434783 | 0 | 46 |
| 1068 | 23765 | M00055468D:D05 | MA168:C10 | 65.2173913 | 13.04347826 | 0 | 46 |
| 1069 | 23767 | M00055469B:E11 | MA168:D10 | 0 | 0 | 23.91304348 | 46 |
| 1070 | 23773 | M00055492C:C01 | MA168:G10 | 43.47826087 | 2.173913043 | 0 | 46 |
| 1071 | 23775 | M00055496A:E06 | MA168:H10 | 0 | 0 | 41.30434783 | 46 |
| 1072 | 23787 | M00056742D:D01 | MA175:F04 | 45.65217391 | 4.347826087 | 0 | 46 |
| 1073 | 23805 | M00056814D:C08 | MA175:G10 | 50 | 10.86956522 | 0 | 46 |
| 1074 | 23827 | RG:1636303:10014:B10 | MA163:B10 | 0 | 0 | 26.08695652 | 46 |
| 1075 | 23829 | RG:1643142:10014:C10 | MA163:C10 | 0 | 0 | 80.43478261 | 46 |
| 1076 | 23831 | RG:1650444:10014:D10 | MA163:D10 | 23.91304348 | 4.347826087 | 0 | 46 |
| 1077 | 23840 | RG:1418984:10003:H10 | MA152:H10 | 67.39130435 | 13.04347826 | 0 | 46 |
| 1078 | 23841 | M00043339C:C12 | MA183:A04 | 41.30434783 | 0 | 0 | 46 |

Table 4

| SEQ ID NO | SpotID | Clone ID | MAClone ID | >=2x | >=5x | <=halfx | Num Ratios |
|-----------|--------|----------------|------------|-------------|-------------|-------------|------------|
| 1079 | 23843 | M00043342C:H03 | MA183:B04 | 36.95652174 | 0 | 0 | 46 |
| 1080 | 23847 | M00043350A:C04 | MA183:D04 | 50 | 2.173913043 | 0 | 46 |
| 1081 | 23875 | M00056646D:G05 | MA186:B04 | 0 | 0 | 78.26086957 | 46 |
| 1082 | 23880 | M00055406C:H08 | MA199:D04 | 34.7826087 | 0 | 2.173913043 | 46 |
| 1083 | 23887 | M00056653C:F06 | MA186:H04 | 34.7826087 | 2.173913043 | 0 | 46 |
| 1084 | 23888 | M00055408A:H06 | MA199:H04 | 54.34782609 | 8.695652174 | 0 | 46 |
| 1085 | 23905 | M00055545D:E02 | MA169:A05 | 0 | 0 | 86.95652174 | 46 |
| 1086 | 23909 | M00055548B:H07 | MA169:C05 | 39.13043478 | 0 | 2.173913043 | 46 |
| 1087 | 23912 | M00056271C:F02 | MA181:D05 | 4.347826087 | 0 | 63.04347826 | 46 |
| 1088 | 23915 | M00055550D:A05 | MA169:F05 | 0 | 0 | 47.82608696 | 46 |
| 1089 | 23929 | M00055661A:F09 | MA169:E11 | 0 | 0 | 78.26086957 | 46 |
| 1090 | 24003 | M00056427D:A09 | MA173:B05 | 41.30434783 | 0 | 0 | 46 |
| 1091 | 24004 | M00056163C:H09 | MA180:B05 | 0 | 0 | 36.95652174 | 46 |
| 1092 | 24005 | M00056428B:F07 | MA173:C05 | 41.30434783 | 6.52173913 | 2.173913043 | 46 |
| 1093 | 24006 | M00056163D:E01 | MA180:C05 | 50 | 0 | 2.173913043 | 46 |
| 1094 | 24009 | M00056428C:A12 | MA173:E05 | 50 | 6.52173913 | 2.173913043 | 46 |
| 1095 | 24011 | M00056429D:D07 | MA173:F05 | 2.173913043 | 0 | 2.173913043 | 46 |
| 1096 | 24014 | M00056175D:B05 | MA180:G05 | 41.30434783 | 2.173913043 | 2.173913043 | 46 |
| 1097 | 24017 | M00056507D:D04 | MA173:A11 | 2.173913043 | 0 | 23.91304348 | 46 |
| 1098 | 24027 | M00056511D:H07 | MA173:F11 | 52.17391304 | 0 | 0 | 46 |
| 1099 | 24033 | M00054654A:F12 | MA187:A05 | 76.08695652 | 6.52173913 | 0 | 46 |
| 1100 | 24034 | M00054868D:F12 | MA189:A05 | 32.60869565 | 0 | 0 | 46 |
| 1101 | 24039 | M00054661B:H10 | MA187:D05 | 43.47826087 | 4.347826087 | 0 | 46 |
| 1102 | 24043 | M00054666B:C07 | MA187:F05 | 21.73913043 | 0 | 0 | 46 |
| 1103 | 24044 | M00054870B:H05 | MA189:F05 | 34.7826087 | 0 | 4.347826087 | 46 |
| 1104 | 24045 | M00054669B:B03 | MA187:G05 | 41.30434783 | 0 | 0 | 46 |
| 1105 | 24049 | M00054706B:G04 | MA187:A11 | 0 | 0 | 26.08695652 | 46 |
| 1106 | 24055 | M00054720C:F01 | MA187:D11 | 34.7826087 | 0 | 0 | 46 |
| 1107 | 24057 | M00054722B:E08 | MA187:E11 | 30.43478261 | 0 | 2.173913043 | 46 |
| 1108 | 24058 | M00054908A:H08 | MA189:E11 | 26.08695652 | 2.173913043 | 0 | 46 |
| 1109 | 24061 | M00054723B:H12 | MA187:G11 | 0 | 0 | 65.2173913 | 46 |
| 1110 | 24070 | M00057210B:G10 | MA193:C05 | 50 | 8.695652174 | 0 | 46 |
| 1111 | 24084 | M00057248D:B05 | MA193:B11 | 36.95652174 | 0 | 0 | 46 |
| 1112 | 24092 | M00057252A:F06 | MA193:F11 | 21.73913043 | 0 | 0 | 46 |
| 1113 | 24099 | M00042573B:A02 | MA167:B05 | 67.39130435 | 10.86956522 | 0 | 46 |
| 1114 | 24108 | M00042766A:E10 | MA171:F05 | 0 | 0 | 21.73913043 | 46 |
| 1115 | 24113 | M00042882D:G08 | MA167:A11 | 4.347826087 | 0 | 21.73913043 | 46 |
| 1116 | 24115 | M00042885C:A12 | MA167:B11 | 60.86956522 | 4.347826087 | 0 | 46 |
| 1117 | 24116 | M00042815A:E07 | MA171:B11 | 2.173913043 | 0 | 21.73913043 | 46 |
| 1118 | 24118 | M00042817B:E11 | MA171:C11 | 0 | 0 | 60.86956522 | 46 |
| 1119 | 24121 | M00042887C:A07 | MA167:E11 | 0 | 0 | 76.08695652 | 46 |
| 1120 | 24126 | M00042818D:A08 | MA171:G11 | 47.82608696 | 4.347826087 | 0 | 46 |
| 1121 | 24133 | M00056552A:G08 | MA174:C05 | 32.60869565 | 0 | 0 | 46 |
| 1122 | 24135 | M00056552C:D08 | MA174:D05 | 34.7826087 | 2.173913043 | 0 | 46 |
| 1123 | 24137 | M00056553C:E10 | MA174:E05 | 50 | 21.73913043 | 2.173913043 | 46 |
| 1124 | 24143 | M00056555B:C11 | MA174:H05 | 50 | 10.86956522 | 0 | 46 |
| 1125 | 24151 | M00056611C:D03 | MA174:D11 | 21.73913043 | 0 | 0 | 46 |
| 1126 | 24155 | M00056611D:B03 | MA174:F11 | 71.73913043 | 6.52173913 | 0 | 46 |
| 1127 | 24157 | M00056611D:F08 | MA174:G11 | 65.2173913 | 0 | 0 | 46 |

Table 4

| SEQ ID NO | SpotID | Clone ID | MAClone ID | >=2x | >=5x | <=halfx | Num Ratios |
|--------------|--------|---------------------|------------|-------------|-------------|-------------|---------------|
| 1128 | 24159 | M00056614C:F06 | MA174:H11 | 71.73913043 | 4.347826087 | 0 | 46 |
| 1129 | 24161 | RG:358387:10009:A05 | MA158:A05 | 32.60869565 | 6.52173913 | 0 | 46 |
| 1130 | 24193 | M00057302A:F08 | MA182:A05 | 67.39130435 | 30.43478261 | 0 | 46 |
| 1131 | 24197 | M00057302C:H09 | MA182:C05 | 32.60869565 | 0 | 0 | 46 |
| 1132 | 24204 | M00054496A:B09 | MA184:F05 | 2.173913043 | 0 | 21.73913043 | 46 |
| 1133 | 24208 | M00054496A:H05 | MA184:H05 | 28.26086957 | 0 | 0 | 46 |
| 1134 | 24209 | M00042460B:A08 | MA182:A11 | 30.43478261 | 0 | 0 | 46 |
| 1135 | 24210 | M00054524B:B09 | MA184:A11 | 52.17391304 | 0 | 0 | 46 |
| 1136 | 24212 | M00054526C:E05 | MA184:B11 | 54.34782609 | 0 | 0 | 46 |
| 1137 | 24213 | M00042516B:A08 | MA182:C11 | 47.82608696 | 0 | 0 | 46 |
| 1138 | 24215 | M00042517D:H10 | MA182:D11 | 43.47826087 | 0 | 0 | 46 |
| 1139 | 24216 | M00054527B:H11 | MA184:D11 | 32.60869565 | 0 | 0 | 46 |
| 1140 | 24217 | M00042517D:H11 | MA182:E11 | 43.47826087 | 2.173913043 | 4.347826087 | 46 |
| 1141 | 24222 | M00054529C:G04 | MA184:G11 | 39.13043478 | 0 | 0 | 46 |
| 1142 | 24223 | M00043300D:A06 | MA182:H11 | 32.60869565 | 0 | 0 | 46 |
| 1143 | 24230 | M00054958A:G10 | MA198:C05 | 0 | 0 | 26.08695652 | 46 |
| 1144 | 24232 | M00054958B:B07 | MA198:D05 | 0 | 0 | 28.26086957 | 46 |
| 1145 | 24240 | M00054961D:E08 | MA198:H05 | 32.60869565 | 0 | 2.173913043 | 46 |
| 1146 | 24246 | M00055015C:H02 | MA198:C11 | 36.95652174 | 0 | 0 | 46 |
| 1147 | 24250 | M00055016B:D03 | MA198:E11 | 43.47826087 | 2.173913043 | 2.173913043 | 46 |
| 1148 | 24265 | M00055764D:D05 | MA170:E05 | 50 | 6.52173913 | 0 | 46 |
| 1149 | 24275 | M00055815C:E08 | MA170:B11 | 34.7826087 | 0 | 0 | 46 |
| 1150 | 24283 | M00055819B:B12 | MA170:F11 | 0 | 0 | 86.95652174 | 46 |
| 1151 | 24287 | M00055820C:H11 | MA170:H11 | 47.82608696 | 10.86956522 | 4.347826087 | 46 |
| 1152 | 24289 | M00055204B:C04 | MA196:A05 | 60.86956522 | 23.91304348 | 0 | 46 |
| 1153 | 24295 | M00055209A:C09 | MA196:D05 | 36.95652174 | 2.173913043 | 0 | 46 |
| 1154 | 24311 | M00055252C:G12 | MA196:D11 | 23.91304348 | 0 | 0 | 46 |
| 1155 | 24354 | M00056934C:D08 | MA177:A05 | 39.13043478 | 8.695652174 | 0 | 46 |
| 1156 | 24355 | M00055989C:D03 | MA179:B05 | 0 | 0 | 21.73913043 | 46 |
| 1157 | 24360 | M00056937C:G12 | MA177:D05 | 41.30434783 | 2.173913043 | 0 | 46 |
| 1158 | 24367 | M00055997B:A02 | MA179:H05 | 0 | 0 | 21.73913043 | 46 |
| 1159 | 24373 | M00056087A:G01 | MA179:C11 | 0 | 0 | 26.08695652 | 46 |
| 1160 | 24375 | M00056091A:H05 | MA179:D11 | 6.52173913 | 0 | 26.08695652 | 46 |
| 1161 | 24378 | M00056966B:A05 | MA177:E11 | 0 | 0 | 36.95652174 | 46 |
| 1162 | 24379 | M00056093A:F08 | MA179:F11 | 2.173913043 | 0 | 32.60869565 | 46 |
| 1163 | 24383 | M00056096C:H10 | MA179:H11 | 0 | 0 | 23.91304348 | 46 |
| 1164 | 24399 | M00054766B:E10 | MA188:H05 | 56.52173913 | 4.347826087 | 0 | 46 |
| 1165 | 24403 | M00054817B:H09 | MA188:B11 | 32.60869565 | 0 | 0 | 46 |
| 1166 | 24407 | M00054818D:G04 | MA188:D11 | 63.04347826 | 4.347826087 | 0 | 46 |
| 1167 | 24450 | M00042851D:H04 | MA172:A05 | 60.86956522 | 13.04347826 | 0 | 46 |
| 1168 | 24452 | M00042853A:F01 | MA172:B05 | 54.34782609 | 2.173913043 | 0 | 46 |
| 1169 | 24457 | M00055426A:G06 | MA168:E05 | 0 | 0 | 84.7826087 | 46 |
| 1170 | 24467 | M00055496A:G12 | MA168:B11 | 0 | 0 | 41.30434783 | 46 |
| 1171 | 24475 | M00055509C:C02 | MA168:F11 | 2.173913043 | 0 | 23.91304348 | 46 |
| 1172 | 24477 | M00055510B:F08 | MA168:G11 | 0 | 0 | 73.91304348 | 46 |
| 1173 | 24479 | M00055510D:A08 | MA168:H11 | 28.26086957 | 2.173913043 | 2.173913043 | 46 |
| 1174 | 24483 | M00056748C:B08 | MA175:B05 | 76.08695652 | 19.56521739 | 0 | 46 |
| 1175 | 24485 | M00056749A:F01 | MA175:C05 | 13.04347826 | 6.52173913 | 69.56521739 | 46 |
| 1176 | 24493 | M00056754B:A10 | MA175:G05 | 2.173913043 | 0 | 41.30434783 | 46 |

Table 4

| SEQ ID NO | SpotID | Clone ID | MAClone ID | >=2x | >=5x | <=halfx | Num Ratios |
|-----------|--------|----------------------|------------|-------------|-------------|-------------|------------|
| 1177 | 24495 | M00056754B:H06 | MA175:H05 | 2.173913043 | 0 | 41.30434783 | 46 |
| 1178 | 24521 | RG:1653390:10014:E05 | MA163:E05 | 4.347826087 | 0 | 34.7826087 | 46 |
| 1179 | 24525 | RG:1669553:10014:G05 | MA163:G05 | 43.47826087 | 6.52173913 | 0 | 46 |
| 1180 | 24547 | M00043355A:H12 | MA183:B05 | 52.17391304 | 2.173913043 | 0 | 46 |
| 1181 | 24549 | M00043355B:F10 | MA183:C05 | 56.52173913 | 4.347826087 | 0 | 46 |
| 1182 | 24557 | M00043357B:B10 | MA183:G05 | 56.52173913 | 6.52173913 | 0 | 46 |
| 1183 | 24558 | M00054557C:D09 | MA185:G05 | 36.95652174 | 0 | 0 | 46 |
| 1184 | 24559 | M00043358B:G11 | MA183:H05 | 47.82608696 | 6.52173913 | 0 | 46 |
| 1185 | 24561 | M00043396D:B04 | MA183:A11 | 45.65217391 | 2.173913043 | 0 | 46 |
| 1186 | 24576 | M00054612D:D11 | MA185:H11 | 41.30434783 | 8.695652174 | 0 | 46 |
| 1187 | 24578 | M00055409B:D08 | MA199:A05 | 58.69565217 | 0 | 0 | 46 |
| 1188 | 24580 | M00055409D:F06 | MA199:B05 | 36.95652174 | 0 | 0 | 46 |
| 1189 | 24582 | M00055410A:A06 | MA199:C05 | 0 | 0 | 21.73913043 | 46 |
| 1190 | 24587 | M00056659A:D08 | MA186:F05 | 6.52173913 | 2.173913043 | 30.43478261 | 46 |
| 1191 | 24599 | M00056704C:H08 | MA186:D11 | 30.43478261 | 0 | 0 | 46 |
| 1192 | 24609 | M00055553C:B06 | MA169:A06 | 0 | 0 | 91.30434783 | 46 |
| 1193 | 24610 | M00056280B:D10 | MA181:A06 | 2.173913043 | 0 | 21.73913043 | 46 |
| 1194 | 24614 | M00056282D:G10 | MA181:C06 | 0 | 0 | 54.34782609 | 46 |
| 1195 | 24622 | M00056288B:A12 | MA181:G06 | 54.34782609 | 8.695652174 | 0 | 46 |
| 1196 | 24627 | M00055686D:E11 | MA169:B12 | 0 | 0 | 30.43478261 | 46 |
| 1197 | 24630 | M00042346B:F09 | MA181:C12 | 2.173913043 | 0 | 34.7826087 | 46 |
| 1198 | 24633 | M00055698C:E05 | MA169:E12 | 0 | 0 | 34.7826087 | 46 |
| 1199 | 24634 | M00042347C:D07 | MA181:E12 | 2.173913043 | 2.173913043 | 63.04347826 | 46 |
| 1200 | 24635 | M00055702C:C04 | MA169:F12 | 0 | 0 | 26.08695652 | 46 |
| 1201 | 24638 | M00042348C:F03 | MA181:G12 | 56.52173913 | 6.52173913 | 0 | 46 |
| 1202 | 24648 | M00055335D:E01 | MA197:D06 | 28.26086957 | 0 | 0 | 46 |
| 1203 | 24708 | M00056180C:E06 | MA180:B06 | 0 | 0 | 73.91304348 | 46 |
| 1204 | 24712 | M00056184B:G11 | MA180:D06 | 65.2173913 | 4.347826087 | 0 | 46 |
| 1205 | 24721 | M00056514A:F06 | MA173:A12 | 23.91304348 | 0 | 0 | 46 |
| 1206 | 24727 | M00056514C:H11 | MA173:D12 | 56.52173913 | 0 | 0 | 46 |
| 1207 | 24741 | M00054674D:C05 | MA187:C06 | 54.34782609 | 6.52173913 | 2.173913043 | 46 |
| 1208 | 24743 | M00054675A:H07 | MA187:D06 | 34.7826087 | 6.52173913 | 19.56521739 | 46 |
| 1209 | 24744 | M00054878A:G12 | MA189:D06 | 39.13043478 | 0 | 0 | 46 |
| 1210 | 24751 | M00054676B:D07 | MA187:H06 | 45.65217391 | 0 | 2.173913043 | 46 |
| 1211 | 24755 | M00054725A:E09 | MA187:B12 | 54.34782609 | 8.695652174 | 0 | 46 |
| 1212 | 24758 | M00054924C:B09 | MA189:C12 | 0 | 0 | 21.73913043 | 46 |
| 1213 | 24759 | M00054726D:B04 | MA187:D12 | 32.60869565 | 4.347826087 | 4.347826087 | 46 |
| 1214 | 24762 | M00054927A:H09 | MA189:E12 | 60.86956522 | 4.347826087 | 0 | 46 |
| 1215 | 24763 | M00054727C:F11 | MA187:F12 | 2.173913043 | 0 | 21.73913043 | 46 |
| 1216 | 24767 | M00054728A:H05 | MA187:H12 | 36.95652174 | 4.347826087 | 4.347826087 | 46 |
| 1217 | 24768 | M00054930B:G05 | MA189:H12 | 36.95652174 | 2.173913043 | 0 | 46 |
| 1218 | 24772 | M00057214C:G11 | MA193:B06 | 43.47826087 | 2.173913043 | 0 | 46 |
| 1219 | 24776 | M00057216C:G01 | MA193:D06 | 0 | 0 | 95.65217391 | 46 |
| 1220 | 24780 | M00057217C:B07 | MA193:F06 | 26.08695652 | 0 | 0 | 46 |
| 1221 | 24803 | M00042695A:H04 | MA167:B06 | 45.65217391 | 4.347826087 | 6.52173913 | 46 |
| 1222 | 24805 | M00042695D:D09 | MA167:C06 | 10.86956522 | 6.52173913 | 67.39130435 | 46 |
| 1223 | 24808 | M00042771A:D01 | MA171:D06 | 58.69565217 | 13.04347826 | 0 | 46 |
| 1224 | 24810 | M00042772D:F02 | MA171:E06 | 43.47826087 | 6.52173913 | 0 | 46 |
| 1225 | 24812 | M00042773A:A12 | MA171:F06 | 45.65217391 | 6.52173913 | 2.173913043 | 46 |

Table 4

| SEQ ID NO | SpotID | Clone ID | MAClone ID | >=2x | >=5x | <=halfx | Num Ratios |
|--------------|--------|---------------------|------------|-------------|-------------|-------------|---------------|
| 1226 | 24813 | M00042699B:B10 | MA167:G06 | 0 | 0 | 84.7826087 | 46 |
| 1227 | 24817 | M00042889A:H07 | MA167:A12 | 0 | 0 | 76.08695652 | 46 |
| 1228 | 24818 | M00042819A:C09 | MA171:A12 | 47.82608696 | 2.173913043 | 0 | 46 |
| 1229 | 24820 | M00042819C:B03 | MA171:B12 | 32.60869565 | 0 | 0 | 46 |
| 1230 | 24821 | M00042895B:C02 | MA167:C12 | 60.86956522 | 2.173913043 | 0 | 46 |
| 1231 | 24822 | M00042823B:A02 | MA171:C12 | 23.91304348 | 0 | 0 | 46 |
| 1232 | 24825 | M00042895D:B04 | MA167:E12 | 0 | 0 | 63.04347826 | 46 |
| 1233 | 24843 | M00056564B:F11 | MA174:F06 | 47.82608696 | 6.52173913 | 0 | 46 |
| 1234 | 24845 | M00056564C:E08 | MA174:G06 | 56.52173913 | 30.43478261 | 0 | 46 |
| 1235 | 24849 | M00056615D:A01 | MA174:A12 | 32.60869565 | 2.173913043 | 4.347826087 | 46 |
| 1236 | 24861 | M00056620D:F02 | MA174:G12 | 0 | 0 | 54.34782609 | 46 |
| 1237 | 24865 | RG:359184:10009:A06 | MA158:A06 | 30.43478261 | 0 | 0 | 46 |
| 1238 | 24887 | RG:428530:10009:D12 | MA158:D12 | 0 | 0 | 36.95652174 | 46 |
| 1239 | 24897 | M00057310A:A07 | MA182:A06 | 47.82608696 | 6.52173913 | 2.173913043 | 46 |
| 1240 | 24908 | M00054503C:H10 | MA184:F06 | 39.13043478 | 2.173913043 | 0 | 46 |
| 1241 | 24917 | M00043302C:D03 | MA182:C12 | 47.82608696 | 8.695652174 | 0 | 46 |
| 1242 | 24924 | M00054535B:F10 | MA184:F12 | 28.26086957 | 2.173913043 | 0 | 46 |
| 1243 | 24926 | M00054535C:D10 | MA184:G12 | 34.7826087 | 0 | 0 | 46 |
| 1244 | 24928 | M00054535C:H09 | MA184:H12 | 36.95652174 | 6.52173913 | 0 | 46 |
| 1245 | 24934 | M00054964B:A08 | MA198:C06 | 30.43478261 | 4.347826087 | 2.173913043 | 46 |
| 1246 | 24936 | M00054966C:H01 | MA198:D06 | 47.82608696 | 6.52173913 | 0 | 46 |
| 1247 | 24952 | M00055022D:F01 | MA198:D12 | 23.91304348 | 0 | 0 | 46 |
| 1248 | 24958 | M00055026C:C12 | MA198:G12 | 36.95652174 | 0 | 0 | 46 |
| 1249 | 24960 | M00055027B:C11 | MA198:H12 | 39.13043478 | 4.347826087 | 2.173913043 | 46 |
| 1250 | 24985 | M00055826D:C11 | MA170:E12 | 2.173913043 | 0 | 21.73913043 | 46 |
| 1251 | 24989 | M00055828C:D10 | MA170:G12 | 0 | 0 | 45.65217391 | 46 |
| 1252 | 24991 | M00055828D:F12 | MA170:H12 | 0 | 0 | 47.82608696 | 46 |
| 1253 | 24995 | M00055215C:E11 | MA196:B06 | 28.26086957 | 0 | 0 | 46 |
| 1254 | 24999 | M00055217C:E09 | MA196:D06 | 32.60869565 | 2.173913043 | 0 | 46 |
| 1255 | 25001 | M00055221B:C01 | MA196:E06 | 32.60869565 | 2.173913043 | 0 | 46 |
| 1256 | 25005 | M00055222A:E02 | MA196:G06 | 36.95652174 | 0 | 2.173913043 | 46 |
| 1257 | 25012 | M00056226D:F03 | MA180:B12 | 0 | 0 | 26.08695652 | 46 |
| 1258 | 25019 | M00055258A:G02 | MA196:F12 | 26.08695652 | 0 | 0 | 46 |
| 1259 | 25057 | M00055998A:A02 | MA179:A06 | 0 | 0 | 50 | 46 |
| 1260 | 25058 | M00056945A:B11 | MA177:A06 | 0 | 0 | 21.73913043 | 46 |
| 1261 | 25062 | M00056945D:H03 | MA177:C06 | 0 | 0 | 23.91304348 | 46 |
| 1262 | 25063 | M00056001A:F11 | MA179:D06 | 39.13043478 | 0 | 0 | 46 |
| 1263 | 25068 | M00056946D:B04 | MA177:F06 | 41.30434783 | 0 | 0 | 46 |
| 1264 | 25073 | M00056101B:B02 | MA179:A12 | 0 | 0 | 36.95652174 | 46 |
| 1265 | 25081 | M00056110C:D09 | MA179:E12 | 0 | 0 | 28.26086957 | 46 |
| 1266 | 25083 | M00056111B:H03 | MA179:F12 | 0 | 0 | 32.60869565 | 46 |
| 1267 | 25101 | M00054772B:H06 | MA188:G06 | 30.43478261 | 2.173913043 | 4.347826087 | 46 |
| 1268 | 25109 | M00054825B:B05 | MA188:C12 | 43.47826087 | 2.173913043 | 0 | 46 |
| 1269 | 25111 | M00054831A:G04 | MA188:D12 | 69.56521739 | 19.56521739 | 0 | 46 |
| 1270 | 25115 | M00054831D:B07 | MA188:F12 | 58.69565217 | 4.347826087 | 2.173913043 | 46 |
| 1271 | 25156 | M00042862D:A12 | MA172:B06 | 76.08695652 | 47.82608696 | 0 | 46 |
| 1272 | 25162 | M00042864A:E05 | MA172:E06 | 2.173913043 | 0 | 34.7826087 | 46 |
| 1273 | 25164 | M00042864D:E06 | MA172:F06 | 41.30434783 | 0 | 0 | 46 |
| 1274 | 25177 | M00055514B:A05 | MA168:E12 | 6.52173913 | 0 | 58.69565217 | 46 |

Table 4

| SEQ ID NO | SpotID | Clone ID | MAClone ID | >=2x | >=5x | <=halfx | Num Ratios |
|--------------|--------|----------------------|------------|-------------|-------------|-------------|---------------|
| 1275 | 25191 | M00056763B:A12 | MA175:D06 | 2.173913043 | 0 | 30.43478261 | 46 |
| 1276 | 25195 | M00056767D:F06 | MA175:F06 | 0 | 0 | 39.13043478 | 46 |
| 1277 | 25201 | M00056821A:D08 | MA175:A12 | 47.82608696 | 2.173913043 | 0 | 46 |
| 1278 | 25205 | M00056822C:G03 | MA175:C12 | 52.17391304 | 2.173913043 | 0 | 46 |
| 1279 | 25209 | M00056823D:H02 | MA175:E12 | 54.34782609 | 13.04347826 | 0 | 46 |
| 1280 | 25217 | RG:1609994:10014:A06 | MA163:A06 | 2.173913043 | 0 | 34.7826087 | 46 |
| 1281 | 25243 | RG:1667183:10014:F12 | MA163:F12 | 34.7826087 | 4.347826087 | 0 | 46 |
| 1282 | 25249 | M00043358D:C06 | MA183:A06 | 73.91304348 | 6.52173913 | 0 | 46 |
| 1283 | 25250 | M00054558B:E05 | MA185:A06 | 0 | 0 | 23.91304348 | 46 |
| 1284 | 25257 | M00043361B:G03 | MA183:E06 | 52.17391304 | 2.173913043 | 0 | 46 |
| 1285 | 25277 | M00043408C:D11 | MA183:G12 | 32.60869565 | 2.173913043 | 0 | 46 |
| 1286 | 25280 | M00054632A:E11 | MA185:H12 | 23.91304348 | 4.347826087 | 0 | 46 |
| 1287 | 25281 | M00056661A:G05 | MA186:A06 | 26.08695652 | 0 | 0 | 46 |
| 1288 | 25283 | M00056661C:C11 | MA186:B06 | 30.43478261 | 0 | 0 | 46 |
| 1289 | 25284 | M00055412D:E05 | MA199:B06 | 45.65217391 | 0 | 0 | 46 |
| 1290 | 25286 | M00055413A:G12 | MA199:C06 | 43.47826087 | 4.347826087 | 0 | 46 |
| 1291 | 25288 | M00055414D:A09 | MA199:D06 | 58.69565217 | 8.695652174 | 0 | 46 |
| 1292 | 25301 | M00056707B:C01 | MA186:C12 | 10.86956522 | 2.173913043 | 69.56521739 | 46 |
| 1293 | 25317 | M00056237D:C10 | MA181:D01 | 2.173913043 | 0 | 21.73913043 | 46 |
| 1294 | 25319 | M00056238B:D03 | MA181:E01 | 30.43478261 | 4.347826087 | 0 | 46 |
| 1295 | 25323 | M00056239B:D05 | MA181:G01 | 2.173913043 | 0 | 21.73913043 | 46 |
| 1296 | 25325 | M00056241B:H07 | MA181:H01 | 0 | 0 | 47.82608696 | 46 |
| 1297 | 25380 | I:2921194:04B02:C06 | MA118:C06 | 0 | 0 | 54.34782609 | 46 |
| 1298 | 25388 | I:1624865:04B02:G06 | MA118:G06 | 26.08695652 | 2.173913043 | 0 | 46 |
| 1299 | 25389 | I:1728607:04A02:H06 | MA116:H06 | 26.08695652 | 4.347826087 | 6.52173913 | 46 |
| 1300 | 25390 | I:2827453:04B02:H06 | MA118:H06 | 2.173913043 | 0 | 21.73913043 | 46 |
| 1301 | 25398 | I:2070593:04B02:D12 | MA118:D12 | 39.13043478 | 4.347826087 | 2.173913043 | 46 |
| 1302 | 25405 | I:2683114:04A02:H12 | MA116:H12 | 6.52173913 | 2.173913043 | 26.08695652 | 46 |
| 1303 | 25419 | I:1809336:02A02:G06 | MA108:G06 | 0 | 0 | 56.52173913 | 46 |

Table 4

| SEQ ID NO | Patient ID | | | | | | | |
|-----------|------------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|
| | 10 | 15 | 52 | 121 | 125 | 128 | 130 | 133 |
| 1 | | 2.128801 | 1 | 1 | 1 | 1.4205775 | 1 | 1000 |
| 2 | | 0.6825724 | 0.7069319 | 0.5065385 | 0.5136583 | 0.653875 | 1 | 0.3601765 |
| 3 | | 1 | 1 | 1 | 1 | 1.6486853 | 1 | 1 |
| 4 | | 0.2794264 | 0.5458162 | 0.2749892 | 0.3184148 | 1 | 0.5530271 | 0.5955789 |
| 5 | | 0.5904543 | 0.2721974 | 0.6867976 | 0.6329049 | 0.4980132 | 0.9139001 | 0.3071505 |
| 6 | | 0.6222916 | 0.300322 | 0.6511049 | 0.7847649 | 0.557357 | 1 | 0.371577 |
| 7 | | 1.8284428 | 2.5304701 | 0.7096727 | 1.4761251 | 1 | 1.6635898 | 1.8967177 |
| 8 | | 2.5110151 | 1 | 2.3108704 | 2.4245002 | 1.6127135 | 2.1201773 | 1.4131083 |
| 9 | | 1 | 0.4035251 | 0.7255718 | 1 | 0.6251442 | 0.4107112 | 0.725505 |
| 10 | | 1.078641 | 0.3154543 | 0.2304271 | 0.5293137 | 0.7338017 | 0.6638112 | 0.6031687 |
| 11 | | 1 | 0.7376916 | 0.3105158 | 1 | 0.5290522 | 0.7058015 | 0.4326032 |
| 12 | | 1.3749136 | 1 | 1 | 1.8724187 | 1.4275301 | 2.2010755 | 2.223963 |
| 13 | | 1 | 2.030784 | 0.511902 | 0.3810055 | 0.8079506 | 1 | 1.3139832 |
| 14 | | 1.3092284 | 1 | 1.9423807 | 1.5467323 | 2.4001706 | 1 | 1 |
| 15 | | 0.5326345 | 0.3818144 | 0.6079308 | 0.4668647 | 0.4344923 | 1 | 0.1902738 |
| 16 | | 1.9756354 | 4.4565549 | 1.6177057 | 1.9947428 | 2.3599668 | 2.2977243 | 2.527358 |
| 17 | | 1 | 1 | 1 | 2.2435514 | 2.0981131 | 1 | 1.6320844 |
| 18 | | 1 | 2.6193568 | 1.7717377 | 1.376408 | 1.5811797 | 2.0123087 | 1 |
| 19 | | 0.7097665 | 1 | 0.2216074 | 1 | 1 | 1 | 0.3897705 |
| 20 | | 1 | 1 | 1 | 1.9675142 | 3.1171405 | 1 | 1 |
| 21 | | 1 | 1 | 0.3979005 | 1 | 0.1533749 | 1 | 2.6820023 |
| 22 | | 1.9711102 | 1 | 3.4511454 | 1.5172672 | 2.233715 | 1 | 3.1314971 |
| 23 | | 2.7722496 | 1 | 1.90164 | 1.7023399 | 2.3569783 | 1 | 2.9169944 |
| 24 | | 1.5255324 | 2.5717712 | 1.4550554 | 1.3387965 | 1.4608706 | 1 | 2.0688454 |
| 25 | | 0.7543324 | 0.3426939 | 0.7255379 | 0.7552914 | 0.6658152 | 1 | 0.4347491 |
| 26 | | 1.5828589 | 1 | 1 | 1 | 2.4717913 | 1 | 3.2757587 |
| 27 | | 0.6106194 | 0.2804768 | 0.696815 | 0.7148743 | 0.4848432 | 0.9253698 | 0.361502 |
| 28 | | 0.3050711 | 1 | 1 | 0.2595219 | 2.4893375 | 1 | 2.2476082 |
| 29 | | 2.1077137 | 1 | 3.128655 | 1.7836162 | 1.4723574 | 1 | 4.5326684 |
| 30 | | 3.3500504 | 4.6085126 | 2.8873698 | 3.1891107 | 4.2573014 | 3.2306517 | 6.8094918 |
| 31 | | 2.9727261 | 1 | 3.766358 | 6.0948703 | 3.8799752 | 4.7812335 | 4.9631492 |
| 32 | | 1.8072214 | 2.1864045 | 1.5323531 | 1.8802969 | 1.4158509 | 2.1113331 | 4.7064844 |
| 33 | | 1.7197573 | 2.0665186 | 1.3591788 | 1.4150681 | 1.8361427 | 2.0096454 | 2.0756384 |
| 34 | | 1.780097 | 2.3516946 | 1.636413 | 2.3798241 | 1.7154145 | 2.1218847 | 3.2189456 |
| 35 | | 1.8770405 | 2.7402185 | 1.844494 | 2.9582193 | 2.1951738 | 2.1843311 | 4.7256641 |
| 36 | | 2.2345161 | 2.6281385 | 1.3920569 | 1.9115258 | 1.6482662 | 1.627386 | 2.794879 |
| 37 | | 2.4456194 | 1 | 1.5231536 | 2.0282669 | 1.8309764 | 1.6095216 | 4.2361452 |
| 38 | | 2.2292617 | 2.7777225 | 2.0173304 | 1.1731178 | 2.2598077 | 1.0971816 | 2.7534506 |
| 39 | | 1 | 0.6133625 | 0.5012187 | 0.5629959 | 0.8259502 | 0.5659861 | 1 |
| 40 | | 2.8453017 | 2.4846529 | 2.54578 | 1.89804 | 2.0281 | 2.2843075 | 3.7353995 |
| 41 | | 5.2427952 | 1.62607 | 2.2819307 | 3.2862529 | 0.851981 | 1 | 3.7360149 |
| 42 | | 2.1412668 | 1.9706703 | 2.5521997 | 2.4141428 | 2.5818433 | 1.2849025 | 3.1865666 |
| 43 | | 0.6827279 | 0.3117736 | 0.684873 | 0.7373492 | 0.524463 | 1 | 0.4154985 |
| 44 | | 0.6045286 | 1 | 0.4831435 | 1 | 0.4851317 | 1 | 0.6165179 |
| 45 | | 1.9907659 | 1.2378146 | 1 | 2.8833893 | 2.4827628 | 1.6111716 | 4.080641 |
| 46 | | 1.8357721 | 1 | 1.3219175 | 1 | 1.3362128 | 3.0627683 | 1.4800437 |
| 47 | | 3.239483 | 3.1121354 | 2.1128662 | 2.1776359 | 1.9845024 | 2.3831127 | 3.4227816 |
| 48 | | 0.8421343 | 0.3464825 | 0.7022384 | 1 | 0.5435894 | 0.3088469 | 0.6176619 |
| 49 | | 1 | 1 | 3.3414161 | 1 | 3.568279 | 2.6053795 | 1.8156678 |

Table 4

| SEQ ID NO | Patient ID | | | | | | | |
|--------------|------------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|
| | 10 | 15 | 52 | 121 | 125 | 128 | 130 | 133 |
| 50 | | 0.0921771 | 0.4331462 | 0.6008421 | 0.0873679 | 0.1872788 | 0.1370323 | 0.1107307 |
| 51 | | 3.1797706 | 1 | 2.9695083 | 2.9865921 | 2.3700796 | 1.7498969 | 3.1757342 |
| 52 | | 0.7105976 | 0.2881723 | 0.6895186 | 0.7220852 | 0.5232127 | 1 | 0.3499753 |
| 53 | | 1 | 1 | 1 | 1 | 1000 | 1 | 1 |
| 54 | | 1.5218114 | 1 | 3.414695 | 1 | 1.7020041 | 1 | 1 |
| 55 | | 0.5046522 | 1 | 1 | 1 | 0.4190277 | 0.001 | 0.2902667 |
| 56 | | 1.9188076 | 3.3332965 | 1.7719063 | 2.1291465 | 2.0991162 | 2.1965422 | 2.9530183 |
| 57 | | 0.4132848 | 1 | 0.4373751 | 0.2061158 | 0.858542 | 1 | 1 |
| 58 | | 1 | 0.5551412 | 0.7273004 | 1 | 0.615162 | 1 | 0.4545442 |
| 59 | | 1.7802471 | 3.1293733 | 1.4475003 | 1.5854896 | 1.7151191 | 1.1830904 | 3.0794257 |
| 60 | | 1.7003803 | 1 | 2.3967644 | 1 | 3.3606304 | 1 | 1 |
| 61 | | 2.9304121 | 1.9331291 | 2.5327613 | 1.7199115 | 2.0439768 | 1.9261658 | 3.8425878 |
| 62 | | 0.8313307 | 1.6036167 | 1.4830278 | 1.3504597 | 1.6411076 | 1.4883863 | 1.7423812 |
| 63 | | 1.9339863 | 2.2409376 | 1.6814183 | 1.600673 | 1.6280132 | 1.5994068 | 2.8131119 |
| 64 | | 2.0982451 | 2.1810058 | 2.2504387 | 1.8863409 | 1 | 1.8562809 | 4.0629131 |
| 65 | | 2.3659778 | 3.2940771 | 1.8848563 | 1.5505271 | 1.8876546 | 1.7352879 | 2.8327175 |
| 66 | | 0.6935208 | 0.2873036 | 0.7305243 | 0.7130416 | 0.4663832 | 0.837573 | 0.3711273 |
| 67 | | 2.3259479 | 3.1761276 | 1.9241574 | 2.2166384 | 1.8492783 | 2.3536854 | 3.5472954 |
| 68 | | 2.1851141 | 1 | 3.0579626 | 2.3118291 | 1.6585782 | 1 | 5.5503178 |
| 69 | | 2.5195616 | 2.6188099 | 1.7235604 | 2.326483 | 1.5174527 | 1.8841958 | 3.7556048 |
| 70 | | 1 | 1 | 1 | 1 | 1 | 1 | 1 |
| 71 | | 0.5564723 | 1 | 2.9072939 | 1 | 1.4285125 | 1 | 1 |
| 72 | | 0.7401616 | 0.5589312 | 0.5114914 | 0.2810505 | 1.0672761 | 0.6061379 | 1 |
| 73 | | 1 | 1 | 1.3660583 | 1 | 2.1396772 | 1 | 1 |
| 74 | | 1.9813456 | 1 | 1.7165383 | 1.6403254 | 2.3522379 | 2.3032181 | 3.3513332 |
| 75 | | 1 | 1 | 2.1417344 | 1 | 2.6900267 | 1 | 1000 |
| 76 | | 1.4266855 | 2.790453 | 1 | 1.7339563 | 1.604332 | 1 | 2.4249824 |
| 77 | | 0.8110959 | 0.3056499 | 0.7410064 | 0.7172458 | 0.5489412 | 0.9101861 | 0.3773285 |
| 78 | | 0.6448319 | 0.2531379 | 0.7203681 | 0.7045098 | 0.4573353 | 0.8889967 | 0.3363183 |
| 79 | | 0.5751844 | 0.3552057 | 0.7571428 | 0.7296723 | 0.4719137 | 0.9150763 | 0.3555769 |
| 80 | | 2.5438336 | 3.1700268 | 3.4085698 | 3.0803053 | 1.4809588 | 1.9207147 | 4.662129 |
| 81 | | 3.9129781 | 6.8575878 | 3.1407914 | 2.8455177 | 3.4137294 | 2.3441393 | 6.8900842 |
| 82 | | 0.8445685 | 4.3285919 | 1.3383339 | 2.0624989 | 1.6535218 | 1.9765245 | 2.8030132 |
| 83 | | 2.4342313 | 2.6760247 | 1.805684 | 2.0401999 | 2.2814553 | 2.2595332 | 2.7812615 |
| 84 | | 1.6254034 | 1 | 3.3677627 | 2.3267364 | 3.2623674 | 1 | 4.0667474 |
| 85 | | 1.926523 | 0.5682655 | 0.3929336 | 0.4780718 | 0.3565442 | 0.3647118 | 0.3486735 |
| 86 | | 1.9044652 | 3.4763104 | 1.7120879 | 2.2080234 | 1.8051242 | 1.9977248 | 3.1360731 |
| 87 | | 3.1078926 | 1 | 3.5940828 | 1 | 3.3055048 | 2.0396142 | 3.8089623 |
| 88 | | 1.6217682 | 1 | 1.3979297 | 1.2840098 | 1.8035029 | 1.800108 | 2.1162935 |
| 89 | | 1.7349253 | 3.8368088 | 1.4031118 | 3.100424 | 1.4453992 | 2.1956808 | 3.20233 |
| 90 | | 2.1036121 | 3.2537429 | 2.0193429 | 1.5337389 | 1.6332001 | 1.952998 | 4.3839571 |
| 91 | | 1.6404052 | 1 | 1.6675066 | 1.3257678 | 1.536847 | 1.8972442 | 2.3213918 |
| 92 | | 3.2164656 | 4.9677313 | 3.1439729 | 1.3224192 | 3.4047364 | 2.1059232 | 5.2950494 |
| 93 | | 0.7109354 | 0.2889371 | 1 | 0.7065558 | 0.4452165 | 1 | 0.3419752 |
| 94 | | 1.3995396 | 1 | 3.1679335 | 1.4458516 | 1.9305859 | 1 | 1 |
| 95 | | 1.8730407 | 1 | 7.6096684 | 5.8262332 | 1.92915 | 2.7869334 | 3.2208154 |
| 96 | | 2.7456184 | 2.809832 | 1.7379405 | 1.7501804 | 1.8046708 | 1.863928 | 3.4930307 |
| 97 | | 1 | 1 | 1 | 1 | 2.1859885 | 1 | 1 |
| 98 | | 2.5857937 | 2.4077647 | 3.0653115 | 1.5920597 | 1.5856796 | 1.830564 | 1.9071399 |

Table 4

| SEQ ID NO | Patient ID | | | | | | | |
|--------------|------------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|
| | 10 | 15 | 52 | 121 | 125 | 128 | 130 | 133 |
| 99 | | 0.7498822 | 0.2909559 | 0.802938 | 0.7583427 | 0.5782421 | 1 | 0.3639793 |
| 100 | | 0.6599463 | 0.2920548 | 0.7029595 | 0.8254746 | 0.4878454 | 1 | 0.3840663 |
| 101 | | 1.9760376 | 1 | 2.548079 | 1.9512671 | 2.6027628 | 2.147006 | 1 |
| 102 | | 1.6287008 | 1 | 2.3636062 | 1.3272341 | 1.5453247 | 1.4531618 | 2.0019336 |
| 103 | | 0.5464085 | 0.5452372 | 0.4632433 | 0.6637985 | 0.4699832 | 0.6268567 | 0.3801057 |
| 104 | | 0.7207096 | 0.2773607 | 1 | 0.7429863 | 0.5682324 | 1 | 0.3448865 |
| 105 | | 2.5086614 | 2.1645948 | 1 | 2.070937 | 1.6942684 | 2.4316922 | 3.1887915 |
| 106 | | 2.6920986 | 1.4907799 | 2.829289 | 2.011119 | 1.3613092 | 1.2840001 | 3.2379595 |
| 107 | | 3.6747236 | 1 | 1.6291976 | 0.8420503 | 2.1718567 | 1 | 1.6686133 |
| 108 | | 1.5291783 | 3.2852763 | 1.6258976 | 2.2946934 | 1.6463769 | 2.939751 | 3.1147238 |
| 109 | | 2.6079908 | 1 | 1 | 2.1270688 | 1.8274657 | 1 | 1 |
| 110 | | 0.9156744 | 1.9137795 | 4.797357 | 1.9653058 | 1.5349646 | 2.2131469 | 5.6071782 |
| 111 | | 1.5008743 | 2.1373723 | 1.6035805 | 1.873897 | 1.5414637 | 1.7030259 | 3.1024476 |
| 112 | | 1 | 1 | 1 | 0.2075226 | 2.0079706 | 0.001 | 1 |
| 113 | | 0.6000516 | 0.3291657 | 0.6983777 | 0.7675252 | 0.5328239 | 0.88196 | 0.3908592 |
| 114 | | 0.6065177 | 0.2960322 | 1 | 0.7697933 | 0.4550407 | 0.8825943 | 0.3499674 |
| 115 | | 1.510922 | 1 | 2.2748504 | 1 | 2.164066 | 1.3723552 | 1 |
| 116 | | 0.6479631 | 0.3010226 | 0.691218 | 0.788397 | 0.5391719 | 0.8854644 | 0.3760189 |
| 117 | | 0.5604721 | 0.4462612 | 0.7497898 | 1 | 0.4346846 | 1 | 0.4192303 |
| 118 | | 0.5572122 | 0.236498 | 0.4744918 | 0.63304 | 0.4449211 | 0.817726 | 0.2715999 |
| 119 | | 0.6542255 | 0.2739704 | 0.7167471 | 0.7244311 | 0.5409512 | 0.8524691 | 0.3372099 |
| 120 | | 0.6568151 | 0.2857497 | 0.6464982 | 0.7470501 | 0.5020115 | 0.8073936 | 0.3512613 |
| 121 | | 1 | 2.9624753 | 1.5613371 | 1.95059 | 1.2510442 | 1 | 1.7913599 |
| 122 | | 0.3384043 | 0.2957418 | 0.4464749 | 0.1757079 | 0.2980453 | 0.2388997 | 0.2738721 |
| 123 | | 2.8662549 | 1 | 6.9605967 | 3.8013491 | 1.3435706 | 1.6583853 | 2.7360856 |
| 124 | | 2.0530787 | 1 | 3.2430742 | 5.4357223 | 3.1639052 | 1 | 1 |
| 125 | | 2.7141242 | 1 | 2.6554843 | 2.7974465 | 1.9681584 | 1.9947446 | 2.9356454 |
| 126 | | 3.5768472 | 1 | 1.4714968 | 0.7677238 | 2.4981862 | 1 | 1.5562021 |
| 127 | | 0.7835264 | 0.2895695 | 0.8284051 | 0.7278176 | 0.5657454 | 0.8383804 | 0.4285558 |
| 128 | | 0.7476625 | 0.2813967 | 0.8040335 | 0.6823258 | 0.4813532 | 1 | 0.359569 |
| 129 | | 1 | 1 | 2.1292941 | 1 | 1.3906789 | 1 | 1 |
| 130 | | 1 | 1 | 1 | 1 | 2.8682026 | 1 | 1 |
| 131 | | 1 | 1000 | 1 | 1 | 2.101136 | 1 | 1 |
| 132 | | 2.3592329 | 1 | 1 | 1.2446715 | 1.4822092 | 1.8171966 | 1 |
| 133 | | 3.2121012 | 2.4922561 | 2.394053 | 1.8018812 | 2.2953741 | 2.109742 | 4.1922396 |
| 134 | | 0.7253528 | 0.3509185 | 0.7046565 | 0.7200698 | 0.5597616 | 0.9427225 | 0.4835069 |
| 135 | | 1 | 0.2974122 | 0.8609515 | 0.7286269 | 0.5682461 | 0.8509791 | 0.4150251 |
| 136 | | 0.3757051 | 0.1981924 | 0.6750419 | 0.6743985 | 0.4194674 | 1 | 0.5863165 |
| 137 | | 1.5323953 | 1 | 2.9988696 | 1 | 1.6415953 | 1 | 1 |
| 138 | | 0.4413046 | 0.4564106 | 0.5556664 | 0.2310934 | 0.5147693 | 0.4454465 | 0.8541135 |
| 139 | | 3.5254131 | 3.6833455 | 2.9217077 | 2.9483384 | 3.1548436 | 4.0815515 | 4.9578711 |
| 140 | | 1.2965106 | 1 | 2.0168061 | 1.4122241 | 0.8281349 | 0.873081 | 2.1103211 |
| 141 | | 2.6894125 | 3.7340065 | 1.8106702 | 2.5584848 | 1.9848527 | 1.6040173 | 3.4527858 |
| 142 | | 3.1597128 | 3.0205491 | 1.5744585 | 2.8635988 | 1.9356629 | 1.6682055 | 4.2267251 |
| 143 | | 1 | 2.3212289 | 1.7710637 | 2.1946843 | 2.4266754 | 1.9617223 | 4.9916702 |
| 144 | | 1.3940814 | 2.4792504 | 1 | 1.7104093 | 1.3019791 | 1 | 2.4762412 |
| 145 | | 2.3266771 | 1 | 2.9360799 | 1.3879447 | 2.6291371 | 1.7637117 | 2.864134 |
| 146 | | 1.8604892 | 2.4062865 | 1.8510945 | 1.4955753 | 1.8146462 | 1.9255862 | 2.6996593 |
| 147 | | 2.451737 | 1.8519517 | 1.4901242 | 1.4160436 | 1.5551627 | 1.6377392 | 1.5831925 |

Table 4

| SEQ ID | Patient ID | | | | | | | |
|--------|------------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|
| NO | 10 | 15 | 52 | 121 | 125 | 128 | 130 | 133 |
| 148 | | 2.1681607 | 2.0226622 | 1.9051808 | 1.7817714 | 1.8538675 | 1.2955873 | 2.7930249 |
| 149 | | 0.5715224 | 0.2731208 | 0.6138342 | 0.6984378 | 0.417001 | 0.8928241 | 0.323979 |
| 150 | | 0.4322649 | 1 | 1.1163694 | 0.8896316 | 0.5700049 | 0.7267695 | 0.3904647 |
| 151 | | 1.886166 | 1 | 2.1842897 | 1.9415482 | 2.9239122 | 2.5620881 | 1 |
| 152 | | 2.2130267 | 2.4239579 | 1.8672797 | 1.9627415 | 1.503321 | 1.9331486 | 3.6760933 |
| 153 | | 1.4170238 | 1 | 2.8197784 | 1 | 1.8284688 | 1 | 1 |
| 154 | | 2.9907143 | 2.8112175 | 1.8568161 | 1.8631425 | 1.8796304 | 1.9053548 | 2.6879195 |
| 155 | | 1.5341271 | 1 | 3.8170002 | 2.2515443 | 2.2888132 | 1 | 1 |
| 156 | | 2.061459 | 1 | 1.9171846 | 1.2179315 | 1.4732505 | 1.7416302 | 1 |
| 157 | | 2.3259104 | 3.7404652 | 1.5759241 | 1.1759723 | 1.7645082 | 1 | 1 |
| 158 | | 2.6490341 | 3.724692 | 1.4182645 | 4.8414173 | 3.7181913 | 3.556269 | 2.322307 |
| 159 | | 0.6934082 | 0.3525678 | 0.8470185 | 0.7378739 | 0.6148116 | 0.8920684 | 0.4422443 |
| 160 | | 0.7873332 | 0.2647097 | 1 | 0.6298705 | 0.439954 | 0.8019943 | 0.3121682 |
| 161 | | 0.6748087 | 0.2968856 | 0.7093754 | 0.7035399 | 0.5096099 | 1 | 0.3675218 |
| 162 | | 1 | 0.4564172 | 1.3935361 | 1 | 1 | 0.7843008 | 1.4817558 |
| 163 | | 1.7151302 | 2.4530663 | 1.9699969 | 1.3690334 | 1.2533182 | 2.0120828 | 2.3446189 |
| 164 | | 2.6521599 | 2.5634663 | 3.5974154 | 1.6111766 | 1.5217122 | 1 | 2.9533339 |
| 165 | | 0.4701877 | 1 | 1.3369311 | 0.3508098 | 1 | 1 | 1.5998238 |
| 166 | | 1.9558135 | 3.2046931 | 2.7167713 | 3.008973 | 1.4670262 | 1 | 1 |
| 167 | | 0.4225443 | 2.0099561 | 0.4584557 | 0.2019076 | 0.3995029 | 1 | 1 |
| 168 | | 1.3637239 | 0.3044717 | 5.9534464 | 1.2662301 | 0.6694151 | 0.1695956 | 1.3857708 |
| 169 | | 1.2739971 | 4.1479357 | 1.5671711 | 1.6819922 | 1.5052721 | 1.7562778 | 2.4040434 |
| 170 | | 1 | 3.389506 | 1.8166758 | 1.2615935 | 1.2726987 | 1.6617999 | 2.1378164 |
| 171 | | 2.427926 | 1 | 1.9139531 | 1.2856017 | 2.2065163 | 1.4747633 | 2.6022462 |
| 172 | | 2.2183776 | 1.9085958 | 2.513481 | 1.3399722 | 2.2629267 | 2.2597042 | 2.1714656 |
| 173 | | 2.0947868 | 2.1173827 | 1.9808514 | 1.7989676 | 1.5649045 | 1.9460827 | 2.3416445 |
| 174 | | 1.9460017 | 2.5007034 | 1.6678949 | 1.7992101 | 1.5081918 | 1.8326986 | 3.7221844 |
| 175 | | 1.7083584 | 3.704888 | 1.6472985 | 1.543023 | 1.96416 | 2.2669663 | 2.5289123 |
| 176 | | 1.615731 | 1 | 2.4413189 | 1.9584228 | 2.9144452 | 2.8148675 | 1 |
| 177 | | 0.575994 | 0.4819971 | 0.6905925 | 0.4007012 | 0.441115 | 0.2459025 | 0.4628204 |
| 178 | | 1.682376 | 1 | 1.6880636 | 1.4416752 | 2.1061305 | 1.2073419 | 1 |
| 179 | | 2.4637578 | 2.7549042 | 2.3457425 | 3.1350976 | 3.0043885 | 3.2159232 | 4.1455173 |
| 180 | | 1.5694012 | 2.1670631 | 1.4638625 | 1.9464664 | 1.4058687 | 1.822483 | 2.3238929 |
| 181 | | 1.3810581 | 1 | 1 | 1.7444632 | 2.0538628 | 1.557421 | 1 |
| 182 | | 2.3028447 | 1.269718 | 1.6524438 | 1.3918878 | 2.30559 | 1.3332635 | 1.9642292 |
| 183 | | 2.4161144 | 2.7597536 | 3.06622 | 1.713565 | 1.5672678 | 1 | 2.0153381 |
| 184 | | 2.3794462 | 2.7168323 | 2.9647807 | 1 | 4.9553236 | 1 | 4.023891 |
| 185 | | 1.4646833 | 1 | 1.4024989 | 1.4184508 | 1.9990738 | 2.2386419 | 1 |
| 186 | | 2.2789372 | 1.7749028 | 2.757074 | 1.4713261 | 4.0246594 | 2.1181221 | 3.638665 |
| 187 | | 2.2403603 | 2.6853062 | 1.2630309 | 1.5938177 | 1.4127456 | 1.1667575 | 3.4160123 |
| 188 | | 3.6811093 | 3.662052 | 2.2219759 | 2.5202696 | 2.1693148 | 1.767156 | 4.4224505 |
| 189 | | 2.303027 | 2.3770995 | 2.9903941 | 1.8577306 | 2.5755229 | 1.517172 | 2.8028948 |
| 190 | | 1 | 1 | 0.2956487 | 0.4181832 | 1.1055287 | 0.4341394 | 1 |
| 191 | | 1.7306628 | 1 | 2.7420532 | 2.378923 | 2.9792371 | 1 | 1 |
| 192 | | 0.8283657 | 0.280176 | 0.8284493 | 0.7000767 | 0.5024306 | 0.842013 | 0.3347562 |
| 193 | | 1.6420137 | 3.5422865 | 1.6890129 | 2.3277506 | 1.925186 | 2.3916379 | 5.6470523 |
| 194 | | 1 | 0.7068841 | 0.3827434 | 0.5265918 | 1 | 0.6043836 | 0.6518002 |
| 195 | | 0.7159699 | 0.2686134 | 1 | 0.7098193 | 0.4708213 | 0.8545834 | 0.3156555 |
| 196 | | 2.6164783 | 2.4080421 | 3.5317821 | 1.6584089 | 2.7630833 | 1.318255 | 3.4018583 |

Table 4

| SEQ ID | Patient ID | | | | | | | |
|--------|------------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|
| NO | 10 | 15 | 52 | 121 | 125 | 128 | 130 | 133 |
| 197 | | 0.6513784 | 0.3198237 | 0.838189 | 0.7168655 | 0.7678292 | 0.9529308 | 0.4569584 |
| 198 | | 4.3102263 | 3.1273445 | 2.3592344 | 1.4306103 | 2.3126456 | 1.7286247 | 4.3222446 |
| 199 | | 2.1875483 | 1 | 2.412163 | 1.349061 | 2.007895 | 1 | 2.6658128 |
| 200 | | 1 | 1 | 3.2072162 | 1 | 2.1781566 | 1 | 1 |
| 201 | | 2.4574686 | 2.0475591 | 3.1904027 | 1.9109102 | 1.6536867 | 1.9281558 | 2.3141492 |
| 202 | | 2.3172621 | 1 | 1.8758946 | 1.6239396 | 3.7579692 | 1 | 1 |
| 203 | | 1.8994575 | 1 | 2.0694753 | 1.9775687 | 3.0046015 | 1.848353 | 1 |
| 204 | | 3.7539148 | 1 | 1.3444209 | 1.2391552 | 2.0122713 | 2.1771647 | 1 |
| 205 | | 1.7543612 | 1 | 1 | 1 | 1.7820132 | 1.3201588 | 1.3037109 |
| 206 | | 1.6067449 | 3.4836485 | 1.7990205 | 2.4481183 | 1.4793787 | 1 | 3.052672 |
| 207 | | 2.2707339 | 2.1975135 | 2.0523243 | 1.3658994 | 2.5986888 | 1.7552798 | 2.9632906 |
| 208 | | 1 | 1 | 1 | 1 | 1.8865348 | 1 | 1 |
| 209 | | 0.3488648 | 1 | 0.3895863 | 0.1271932 | 0.6732418 | 0.7011174 | 0.8991474 |
| 210 | | 0.7899443 | 0.4346653 | 0.8421844 | 0.6943513 | 0.4859218 | 0.7944836 | 0.3687999 |
| 211 | | 2.9085474 | 1 | 4.3626436 | 2.4765003 | 1.5645335 | 1 | 1 |
| 212 | | 4.6968799 | 2.0605435 | 1 | 1 | 1 | 1 | 0.6035395 |
| 213 | | 0.6371433 | 0.256266 | 0.7190719 | 0.6681378 | 0.4972368 | 0.8540294 | 0.3055489 |
| 214 | | 2.0175633 | 2.8588913 | 2.159417 | 1.3957256 | 2.3816831 | 2.0831041 | 3.0095237 |
| 215 | | 3.2062517 | 1 | 2.9932781 | 1.4301506 | 2.1366063 | 1.3707173 | 1 |
| 216 | | 0.5635497 | 0.2942335 | 0.7843909 | 0.6935082 | 0.5445993 | 1 | 0.3120657 |
| 217 | | 1.2295171 | 2.9937292 | 2.7187544 | 1.4594642 | 1.4903777 | 1.8767356 | 1.9303827 |
| 218 | | 2.1585741 | 1 | 1.6086782 | 1 | 1.1703 | 1.9847569 | 1.9069742 |
| 219 | | 2.1621235 | 1 | 1.5685175 | 1.396693 | 1.2223135 | 1.9702649 | 2.4114439 |
| 220 | | 1.6876518 | 2.3215726 | 1.6845515 | 1.7242708 | 1.984997 | 1 | 2.5641789 |
| 221 | | 0.4968028 | 0.2947535 | 0.6825485 | 0.7197689 | 0.5371589 | 0.868342 | 0.3350166 |
| 222 | | 0.61263 | 0.2999643 | 0.7185281 | 0.7748473 | 0.5706644 | 0.8589341 | 0.3523106 |
| 223 | | 0.5360445 | 0.3390991 | 0.6984877 | 0.7694217 | 0.494846 | 0.8092096 | 0.305967 |
| 224 | | 0.677377 | 0.2962559 | 0.7919632 | 0.7770289 | 0.5015719 | 0.8469485 | 0.3437661 |
| 225 | | 0.6612438 | 0.3422619 | 0.8190198 | 1 | 0.7012305 | 0.8606836 | 0.5230812 |
| 226 | | 2.0445538 | 1 | 6.1683936 | 2.7084878 | 1.5631045 | 1 | 2.6827597 |
| 227 | | 1.1976851 | 2.0822312 | 1.8324425 | 1.7082208 | 2.155128 | 1.7980125 | 3.4062055 |
| 228 | | 1.3314469 | 1 | 2.0493882 | 1.6213265 | 1.4892304 | 1.3779278 | 1 |
| 229 | | 1 | 1 | 1.8807826 | 1 | 2.7433661 | 1 | 1 |
| 230 | | 1.9597758 | 1 | 2.2314545 | 2.8232536 | 2.3326101 | 2.9753885 | 4.4885339 |
| 231 | | 0.7583107 | 0.2722765 | 0.7716499 | 0.6884657 | 0.547045 | 0.8390321 | 0.3443657 |
| 232 | | 1 | 0.2889171 | 2.302926 | 1 | 7.2663203 | 1 | 1 |
| 233 | | 1 | 1 | 20.127951 | 1 | 1.7587442 | 1 | 1 |
| 234 | | 1 | 1 | 1 | 1 | 1 | 1 | 1 |
| 235 | | 1 | 1 | 0.2501569 | 0.5970379 | 0.5738109 | 0.1850908 | 0.2228578 |
| 236 | | 2.9614399 | 1.7572965 | 2.635342 | 1.9550531 | 2.367359 | 1.1873555 | 3.3692584 |
| 237 | | 2.5993425 | 1 | 1 | 1 | 2.365243 | 1 | 3.3394042 |
| 238 | | 0.6567508 | 0.1280736 | 0.1524233 | 0.2599495 | 0.1750637 | 0.2035966 | 0.2783928 |
| 239 | | 0.6530566 | 0.2890436 | 0.8304591 | 0.656479 | 0.4825211 | 0.8715776 | 0.3311112 |
| 240 | | 0.5757742 | 2.2335948 | 0.341273 | 0.7184133 | 1.3059912 | 0.7870293 | 0.6021115 |
| 241 | | 0.7007483 | 2.1860234 | 0.4111754 | 0.780561 | 1 | 0.822667 | 0.6969682 |
| 242 | | 2.921351 | 1.3047465 | 6.0352542 | 2.8365248 | 8.2384593 | 2.2129282 | 2.94961 |
| 243 | | 2.4623584 | 2.7470603 | 1.8964114 | 2.8562472 | 1.8897432 | 1.5125867 | 3.997161 |
| 244 | | 1.7507099 | 1 | 1.6321677 | 1.3735405 | 2.2725036 | 1 | 2.8302718 |
| 245 | | 2.4312717 | 3.2813227 | 3.2902895 | 1 | 3.4594292 | 1.6881037 | 2.5495673 |

Table 4

| SEQ ID | Patient ID | | | | | | | |
|--------|------------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|
| | 10 | 15 | 52 | 121 | 125 | 128 | 130 | 133 |
| 246 | | 1.3079255 | 2.1449752 | 1 | 1 | 1.5182222 | 1.3165695 | 3.5997219 |
| 247 | | 2.5467504 | 3.1867798 | 2.4927557 | 4.1788218 | 3.4161888 | 2.2187377 | 5.9504315 |
| 248 | | 1.3638848 | 1 | 2.612714 | 1.5998578 | 2.3399611 | 1 | 1 |
| 249 | | 0.8337059 | 1 | 0.4808481 | 0.8791383 | 0.3749698 | 1 | 0.3784646 |
| 250 | | 2.6837828 | 1.8478046 | 2.0837396 | 2.2411504 | 2.0467386 | 1 | 3.2960981 |
| 251 | | 1.3453228 | 1 | 1.8601547 | 1.4704349 | 1.9010651 | 1 | 2.4158778 |
| 252 | | 5.6583801 | 1 | 6.9689321 | 1 | 6.0412794 | 3.8887864 | 3.0518909 |
| 253 | | 1 | 1 | 2.3205458 | 0.6839687 | 1.7408888 | 1.433582 | 2.6466647 |
| 254 | | 1 | 0.2570591 | 0.8126933 | 0.7178918 | 0.5484671 | 0.8471246 | 0.3225194 |
| 255 | | 1 | 1 | 1 | 0.6734247 | 1 | 1 | 1 |
| 256 | | 1 | 1 | 2.2893367 | 1 | 1.2602639 | 1 | 1 |
| 257 | | 0.6579143 | 0.2627731 | 0.7588273 | 0.6716081 | 0.5201211 | 0.8705189 | 0.2980064 |
| 258 | | 1 | 2.8905162 | 3.715114 | 1.7617568 | 1.3112125 | 1.2304244 | 2.1411063 |
| 259 | | 1 | 1.9215197 | 3.9324226 | 2.1377976 | 2.5807991 | 2.1468002 | 3.0441749 |
| 260 | | 1 | 0.558349 | 0.2448676 | 0.19916 | 1 | 0.4224817 | 0.3110006 |
| 261 | | 1 | 2.1973595 | 2.1040336 | 1.5853955 | 1.8946484 | 1.2792879 | 2.7987607 |
| 262 | | 1 | 1 | 3.6310846 | 1 | 3.7921616 | 1 | 1 |
| 263 | | 1 | 1 | 3.387612 | 2.2612687 | 6.2909455 | 2.9002549 | 3.8426667 |
| 264 | | 3.6864924 | 1 | 1.3687894 | 1 | 2.1015207 | 1 | 1 |
| 265 | | 0.6953867 | 0.2828283 | 0.8679173 | 0.7854517 | 0.5797673 | 1 | 0.3579122 |
| 266 | | 0.2261426 | 1 | 0.0195719 | 0.020125 | 0.0143448 | 0.0540226 | 1 |
| 267 | | 3.32988 | 1.5427084 | 2.7641948 | 1.9660655 | 2.1022352 | 1.2184258 | 3.1737933 |
| 268 | | 1 | 2.756115 | 2.142375 | 1.6065961 | 2.7594216 | 2.5873952 | 3.7642676 |
| 269 | | 1.8234672 | 2.4188159 | 2.6119078 | 2.7204918 | 2.5802976 | 2.6618919 | 5.2123821 |
| 270 | | 1.3257475 | 3.5267484 | 1.909596 | 2.1410546 | 1.7131749 | 1.8450031 | 3.1165463 |
| 271 | | 0.5704233 | 0.2705673 | 0.7280112 | 0.6862628 | 0.5088748 | 0.8118863 | 0.3145272 |
| 272 | | 0.5686003 | 0.3795246 | 0.8248751 | 1 | 0.7120853 | 0.815686 | 0.4855898 |
| 273 | | 2.0224478 | 3.1885621 | 2.4241578 | 2.0209367 | 1 | 1 | 5.1615572 |
| 274 | | 0.5620645 | 1 | 0.4442743 | 0.47328 | 0.5716606 | 0.2917321 | 0.4587257 |
| 275 | | 0.7242536 | 0.3455566 | 0.8053061 | 0.7218363 | 0.5668927 | 0.8587365 | 0.345991 |
| 276 | | 5.1293324 | 1 | 2.9082928 | 1.3236647 | 3.9846411 | 1.5769124 | 0.6859701 |
| 277 | | 1 | 1000 | 4.7574035 | 1.2408252 | 6.05368 | 1 | 1 |
| 278 | | 1.4513275 | 2.4956282 | 3.3303016 | 2.0794445 | 2.3992568 | 1.6143071 | 1.9784226 |
| 279 | | 2.2131018 | 3.4120044 | 2.2570941 | 1.3599688 | 3.4963285 | 1.8743404 | 2.5448493 |
| 280 | | 1.6494074 | 1 | 1 | 0.5551822 | 2.6969174 | 1 | 2.1081514 |
| 281 | | 0.7607127 | 0.3038742 | 1 | 0.6439868 | 0.5565464 | 0.8419101 | 0.3251861 |
| 282 | | 0.851544 | 2.7603609 | 1.8877988 | 1.4237451 | 1.4564669 | 1 | 2.1466527 |
| 283 | | 1.3175121 | 0.747264 | 1.9021062 | 1.3346142 | 1.5662098 | 1 | 1.3120897 |
| 284 | | 2.0063629 | 2.7096716 | 1.8131383 | 1.1664556 | 2.4848445 | 1.2659823 | 2.3733213 |
| 285 | | 1 | 0.6136086 | 0.4948497 | 0.5008441 | 1 | 0.4996318 | 1 |
| 286 | | 1.463241 | 3.1649074 | 1.5414602 | 1.2983226 | 2.4236182 | 1.2299346 | 1.6510589 |
| 287 | | 5.5326928 | 1 | 3.8934519 | 3.4574164 | 1.838135 | 1.5940565 | 2.6261123 |
| 288 | | 2.686678 | 1 | 4.4489418 | 2.5649362 | 1.9590487 | 1 | 2.8405914 |
| 289 | | 2.3579354 | 2.3332331 | 2.4366551 | 1.9739504 | 1.5939512 | 1.7212514 | 3.0527825 |
| 290 | | 2.2531853 | 2.4139744 | 2.2419316 | 1.8652574 | 1.6282193 | 1.5667361 | 3.2983308 |
| 291 | | 3.0001615 | 1 | 1.6197882 | 2.893074 | 2.0188872 | 1.8567811 | 3.7476994 |
| 292 | | 2.0054246 | 2.2366218 | 1.7339597 | 1 | 1.9900465 | 1 | 2.0247267 |
| 293 | | 0.7764812 | 0.6944229 | 1 | 1 | 1 | 1 | 1 |
| 294 | | 1.6681409 | 1 | 1 | 2.1931521 | 2.1731964 | 2.3562235 | 2.0495237 |

Table 4

| SEQ ID | Patient ID | | | | | | | |
|--------|------------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|
| | 10 | 15 | 52 | 121 | 125 | 128 | 130 | 133 |
| 295 | | 2.5545622 | 3.6714853 | 2.1376533 | 2.7531708 | 2.5089585 | 2.7526801 | 4.6268546 |
| 296 | | 0.7292131 | 0.283611 | 0.8477126 | 0.6778568 | 0.5265309 | 0.7384514 | 0.3380462 |
| 297 | 0.5974434 | 0.5663728 | 0.3031837 | 0.6397729 | 0.6483574 | 0.4805356 | 0.8606919 | 0.3738887 |
| 298 | 1.2999719 | 2.2684146 | 2.8818823 | 1.4887424 | 1.4702325 | 1.6510555 | 1.697926 | 3.4356259 |
| 299 | 0.6937975 | 0.4958224 | 0.2943357 | 0.556224 | 0.6221291 | 0.3508832 | 0.8486413 | 0.3355373 |
| 300 | 1 | 1 | 3.2539117 | 2.3201411 | 1.8888428 | 1.1944621 | 1.8001803 | 2.3027881 |
| 301 | 1 | 1 | 1 | 1 | 0.3291955 | 0.6456858 | 1 | 0.2709371 |
| 302 | 2.0868425 | 1 | 1 | 1.9321831 | 1.7013095 | 1.7418781 | 1.9856367 | 2.7909263 |
| 303 | 1 | 1 | 1 | 0.3715648 | 0.4610963 | 0.4686778 | 0.2922613 | 0.4884695 |
| 304 | 0.1864112 | 1 | 1 | 0.2267935 | 0.3728054 | 0.4437051 | 1 | 0.7806297 |
| 305 | 1 | 1 | 1.7896421 | 1.9836789 | 2.4499715 | 1.6090105 | 1 | 2.8614594 |
| 306 | 0.5941257 | 0.4176859 | 0.2963329 | 0.4283587 | 0.5978333 | 0.3271951 | 0.4045737 | 0.1359143 |
| 307 | 1.9092242 | 1 | 1.8351517 | 3.4663056 | 2.5766931 | 2.2218092 | 2.4873937 | 1 |
| 308 | 2.8753767 | 1 | 0.1560925 | 1 | 0.4400998 | 0.7244927 | 1 | 0.5552156 |
| 309 | 0.2356817 | 0.3617294 | 0.4677569 | 0.1249358 | 0.1653047 | 0.172192 | 0.2512198 | 0.7322033 |
| 310 | 0.5960041 | 2.5451556 | 9.7927295 | 0.3549838 | 1.9585665 | 0.4927163 | 2.0081138 | 0.2256823 |
| 311 | 0.8591281 | 1 | 1 | 0.4506083 | 0.5808616 | 0.2819349 | 0.477265 | 0.4614002 |
| 312 | 3.243386 | 2.2516483 | 4.0241684 | 3.1029026 | 2.9733723 | 2.1861122 | 2.8962231 | 7.4869096 |
| 313 | 2.9248598 | 1 | 1 | 1 | 2.7019785 | 1.9868932 | 3.2045347 | 1 |
| 314 | 1 | 1 | 1 | 1.7539162 | 0.4661597 | 1 | 0.4689481 | 1.2416986 |
| 315 | 0.3120861 | 0.6257805 | 0.0461577 | 0.0618521 | 0.2490394 | 0.0765947 | 0.1617148 | 0.2171221 |
| 316 | 1.4537867 | 1.2888831 | 2.387325 | 1 | 1.2480603 | 2.7299214 | 1.5180718 | 3.3880673 |
| 317 | 1.3398345 | 1 | 1.9532997 | 1 | 1 | 2.0496515 | 2.8022764 | 2.1069364 |
| 318 | 1000 | 1 | 1 | 1 | 1 | 2.7807875 | 1 | 1.5056218 |
| 319 | 2.1229146 | 1.7435044 | 2.9398387 | 2.172669 | 2.1333142 | 1.6619446 | 2.1833197 | 3.9556932 |
| 320 | 0.047724 | 0.352829 | 1 | 0.0302746 | 0.0930339 | 0.2801762 | 0.2072723 | 0.2281518 |
| 321 | 0.4826478 | 1 | 0.4490669 | 0.7079784 | 0.686757 | 0.4882439 | 1 | 0.4410056 |
| 322 | 1.2923056 | 1 | 2.7491075 | 2.4972349 | 1 | 1 | 1.6451679 | 3.0021469 |
| 323 | 0.5455478 | 0.698492 | 0.3117612 | 0.6817439 | 0.640734 | 0.4480607 | 0.8804432 | 0.3949776 |
| 324 | 1 | 1 | 1 | 1 | 0.5228437 | 1 | 1 | 1 |
| 325 | 0.5437714 | 1 | 1 | 0.3104672 | 0.4378859 | 0.4275947 | 0.2517966 | 1 |
| 326 | 0.5783652 | 0.6239599 | 0.3161907 | 0.6002456 | 0.7359013 | 0.3615456 | 1 | 0.4003425 |
| 327 | 2.0322216 | 1 | 1 | 1 | 1 | 1.8572407 | 1 | 1.9303117 |
| 328 | 1.955759 | 0.3736636 | 1 | 0.3519873 | 0.2576836 | 0.3589899 | 0.401148 | 1 |
| 329 | 0.5799269 | 1 | 0.3668779 | 0.4643082 | 0.6571293 | 0.382094 | 1 | 0.4114432 |
| 330 | 2.7155733 | 2.4243194 | 1.8701768 | 1.1769631 | 1.9527298 | 0.7571256 | 1.8812678 | 2.9726004 |
| 331 | 1.7834938 | 1 | 1 | 2.7907895 | 1.71417 | 2.6867222 | 2.8444506 | 3.343057 |
| 332 | 1 | 1 | 2.5728263 | 2.1702888 | 0.7344288 | 1.500037 | 1 | 2.8552661 |
| 333 | 1000 | 1 | 2.7777225 | 2.7134461 | 1.8480233 | 1 | 1 | 2.7994786 |
| 334 | 0.5539803 | 0.6184112 | 0.3329085 | 0.6089327 | 0.6151138 | 0.4034051 | 0.8513026 | 0.3644369 |
| 335 | 0.7135508 | 1 | 0.6347497 | 0.5759523 | 0.4656211 | 0.507542 | 0.57131 | 0.4529662 |
| 336 | 1 | 1 | 1 | 0.5270773 | 0.6176143 | 1 | 5.5279509 | 2.7659399 |
| 337 | 0.5482046 | 0.6859368 | 0.3149949 | 0.6062881 | 0.6527797 | 0.4955262 | 0.8421634 | 0.3680504 |
| 338 | 0.6045213 | 1 | 9.4290543 | 0.358958 | 2.0041376 | 0.4391777 | 1.9967008 | 0.2152759 |
| 339 | 1.2949416 | 1 | 2.9833329 | 2.9750112 | 1.6380361 | 1 | 1.53377 | 2.2224482 |
| 340 | 1 | 1 | 1 | 3.1585841 | 1 | 1 | 1 | 1000 |
| 341 | 0.9129826 | 1 | 1 | 1.6431415 | 1 | 1 | 1 | 1.0696183 |
| 342 | 1 | 1 | 1 | 1.4889804 | 1 | 1 | 1 | 1 |
| 343 | 2.2176856 | 1 | 2.512425 | 2.5855799 | 2.1580996 | 1 | 2.3298737 | 1.593094 |

Table 4

| SEQ ID | Patient ID | | | | | | | | |
|--------|------------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|--|
| NO | 10 | 15 | 52 | 121 | 125 | 128 | 130 | 133 | |
| 344 | 0.4442926 | 0.5692713 | 1 | 0.2376455 | 0.3545633 | 0.6695045 | 1 | 1 | |
| 345 | 0.8113647 | 1 | 1 | 0.18838 | 0.9021887 | 1 | 1 | 1 | |
| 346 | 1 | 0.5370217 | 0.3707231 | 0.6652894 | 0.5378865 | 0.3425223 | 0.7381168 | 0.3077185 | |
| 347 | 0.6606392 | 0.5732764 | 0.2674427 | 0.6387108 | 0.6028544 | 0.367763 | 0.8602043 | 0.3256121 | |
| 348 | 2.8784443 | 2.6578223 | 2.486229 | 1.4587711 | 2.3554197 | 1.8737496 | 3.2001848 | 3.633087 | |
| 349 | 3.7245562 | 1 | 1.8897318 | 2.8041531 | 2.5630896 | 2.2354807 | 1.2763535 | 2.4292271 | |
| 350 | 0.2603503 | 1 | 1 | 0.4524696 | 0.4934648 | 0.7654041 | 0.727094 | 1.2567125 | |
| 351 | 1 | 1.6651526 | 1 | 2.8744452 | 1.8213934 | 1.6733352 | 2.3007929 | 3.656819 | |
| 352 | 1.2453869 | 1 | 1 | 2.4601538 | 1.9040629 | 1 | 2.7437436 | 1 | |
| 353 | 1.7546068 | 1 | 5.8874052 | 2.6141077 | 1 | 1.9162068 | 1.555069 | 2.7514309 | |
| 354 | 0.8379492 | 1 | 1 | 0.6020971 | 0.4853099 | 1.2599135 | 1 | 1.5453855 | |
| 355 | 0.303759 | 0.5563121 | 1 | 0.5662329 | 1 | 1 | 0.3210737 | 1 | |
| 356 | 1 | 1 | 1 | 3.5866069 | 2.4247754 | 3.2985797 | 1 | 3.3074118 | |
| 357 | 0.3276881 | 0.6926358 | 0.5270546 | 0.5151704 | 0.6544597 | 0.5053642 | 0.6354246 | 0.8052532 | |
| 358 | 1.152169 | 1 | 1 | 0.8213244 | 1.4166822 | 1.4626775 | 2.0077988 | 1 | |
| 359 | 0.5229462 | 0.6668522 | 0.3205479 | 0.6826186 | 0.6572182 | 0.4274298 | 0.8425198 | 0.3437188 | |
| 360 | 0.1628232 | 0.522968 | 1 | 0.7147993 | 0.5138362 | 1 | 0.761779 | 0.7149092 | |
| 361 | 2.4719118 | 1 | 1 | 0.4879976 | 0.4620638 | 0.5616783 | 0.4513966 | 1 | |
| 362 | 1 | 1 | 1 | 1 | 3.4819882 | 1 | 1 | 1 | |
| 363 | 1.9723344 | 1 | 2.6362033 | 2.8643647 | 2.0116872 | 1 | 1.5233637 | 2.7543816 | |
| 364 | 1.760941 | 2.0479068 | 4.6234621 | 2.0540901 | 1.2029114 | 1.7211648 | 1.6619849 | 3.0351019 | |
| 365 | 1.9496644 | 1 | 1 | 1 | 0.3710195 | 2.0171216 | 0.2402065 | 1 | |
| 366 | 1.3087011 | 3.6771311 | 3.0353148 | 1.9031559 | 1.6447205 | 1.6179004 | 1.6149473 | 5.8262411 | |
| 367 | 1 | 2.1148725 | 0.2679718 | 2.8094835 | 2.3922973 | 0.4128446 | 1 | 0.6806131 | |
| 368 | 8.1061813 | 1 | 1 | 4.2924535 | 1.4715086 | 4.1988575 | 1 | 2.2525787 | |
| 369 | 1 | 1 | 4.1528799 | 1.2911228 | 0.8602536 | 0.792541 | 1.0887411 | 0.5059529 | |
| 370 | 1 | 0.5294386 | 0.5102737 | 0.6625295 | 1 | 0.4739472 | 0.6602059 | 0.6968894 | |
| 371 | 1.6311601 | 1 | 3.2035472 | 1.512367 | 1.763473 | 1 | 2.3055892 | 1.8123305 | |
| 372 | 0.7175657 | 0.1204822 | 1 | 1.8712199 | 0.0746514 | 0.0987439 | 0.1318715 | 0.1195276 | |
| 373 | 0.5909133 | 2.3876135 | 3.0546829 | 1.8063145 | 1 | 2.2499079 | 0.9172218 | 2.7904135 | |
| 374 | 5.2858416 | 1 | 1 | 1.9459529 | 1 | 1.5585909 | 1 | 1.5100716 | |
| 375 | 1.5512404 | 2.0296116 | 3.1222065 | 1.5956387 | 2.4930327 | 1.3620375 | 1.7626013 | 4.2934791 | |
| 376 | 2.005923 | 2.2294585 | 1.3472682 | 1.2360698 | 2.7294602 | 2.1964585 | 1.4601727 | 4.2006657 | |
| 377 | 0.9252914 | 1.2824093 | 1 | 0.1577876 | 1 | 0.4948186 | 0.5629806 | 0.5085328 | |
| 378 | 0.6172049 | 1 | 1 | 1 | 0.1915413 | 0.7207485 | 0.681542 | 1 | |
| 379 | 0.7121089 | 0.5875174 | 0.3071905 | 0.8233288 | 0.5979571 | 0.4382433 | 0.93824 | 0.4517355 | |
| 380 | 1 | 0.6454423 | 1 | 0.5002117 | 0.5996357 | 1 | 0.5944814 | 1 | |
| 381 | 0.5513236 | 0.583502 | 0.2901603 | 0.5856205 | 0.6182184 | 0.4110652 | 0.9013943 | 0.3662121 | |
| 382 | 1.4296419 | 1 | 1 | 2.07081 | 2.5665387 | 3.1748493 | 1 | 2.3995227 | |
| 383 | 1 | 1 | 1 | 0.4376979 | 0.5410938 | 0.6324884 | 1 | 1 | |
| 384 | 2.2865184 | 1.4289664 | 1 | 1.6169752 | 3.0261087 | 1.9112053 | 2.5708375 | 1.7739554 | |
| 385 | 2.6709648 | 1 | 1 | 2.6162378 | 1.8560196 | 2.1238348 | 1 | 2.0398353 | |
| 386 | 0.5112171 | 0.7472544 | 0.3245374 | 0.5666119 | 0.6480073 | 0.4059264 | 0.8017288 | 0.3613836 | |
| 387 | 0.5258029 | 0.4250636 | 0.2876542 | 0.6025178 | 0.6055031 | 0.3699821 | 0.8895616 | 0.2982983 | |
| 388 | 0.8109684 | 0.4745893 | 0.333679 | 0.5274834 | 1 | 0.4618078 | 1 | 1 | |
| 389 | 1.3401465 | 1 | 3.0891404 | 1 | 1.6973081 | 1.577305 | 2.0815068 | 2.4293059 | |
| 390 | 0.4677057 | 0.5273297 | 0.4281925 | 0.4398897 | 0.533787 | 0.438367 | 0.6238708 | 0.432903 | |
| 391 | 0.2412336 | 0.6198195 | 1.265235 | 0.4688556 | 0.7909308 | 1 | 0.8782422 | 1.1940059 | |
| 392 | 2.7681608 | 1.6459829 | 4.5312601 | 1.8837505 | 2.8944853 | 1 | 2.3860324 | 3.8240077 | |

Table 4

| SEQ ID | Patient ID | | | | | | | |
|--------|------------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|
| | 10 | 15 | 52 | 121 | 125 | 128 | 130 | 133 |
| 393 | 0.6951101 | 0.4671504 | 1 | 0.6855789 | 0.5040801 | 0.781487 | 0.519348 | 1 |
| 394 | 0.5540372 | 0.4896461 | 0.3136589 | 0.623143 | 0.6365221 | 0.4050264 | 0.8967206 | 0.3218015 |
| 395 | 0.880695 | 2.3344907 | 2.6791114 | 1.4048265 | 1.2322501 | 1.8568835 | 1.5927811 | 2.1551104 |
| 396 | 1 | 1 | 1 | 1 | 0.1520867 | 0.2692871 | 0.1440525 | 0.20584 |
| 397 | 1.4655328 | 1 | 1 | 3.054151 | 1.5940556 | 2.7345655 | 1 | 3.4636498 |
| 398 | 1.8384851 | 1.6178223 | 2.0194056 | 1.6597783 | 1 | 1.6559951 | 1 | 2.078021 |
| 399 | 0.2495937 | 1 | 1 | 0.3357659 | 0.8123218 | 0.6062034 | 0.683711 | 0.3047757 |
| 400 | 1 | 1 | 1 | 0.2674269 | 0.1752196 | 0.4541682 | 1 | 1 |
| 401 | 0.2158921 | 0.7385362 | 0.6441712 | 0.1236799 | 0.2992835 | 0.5422153 | 0.5861575 | 0.5395705 |
| 402 | 0.2599787 | 1 | 1 | 0.6316226 | 1 | 1 | 0.001 | 1 |
| 403 | 1.7231601 | 1 | 1 | 1.9764365 | 0.1957956 | 0.185946 | 0.1266768 | 0.2748188 |
| 404 | 0.7211498 | 0.6470001 | 1 | 0.4624495 | 0.5736056 | 0.5918724 | 0.5317653 | 0.66911 |
| 405 | 0.2351368 | 0.342885 | 1 | 0.1924181 | 0.242257 | 0.5132991 | 0.1623002 | 0.4462127 |
| 406 | 2.4879387 | 2.0826697 | 5.7073753 | 2.3498272 | 1.8943706 | 3.68944 | 3.4379451 | 4.2506069 |
| 407 | 0.3056018 | 4.2848436 | 1 | 0.4497921 | 0.4079558 | 0.3027032 | 0.3019759 | 0.5301424 |
| 408 | 1.8208819 | 2.0777465 | 3.4301067 | 1.7718051 | 2.2830684 | 1.676626 | 1.9527852 | 3.5135831 |
| 409 | 0.2857268 | 0.3572892 | 1 | 0.4860388 | 0.2663444 | 1 | 0.001 | 1 |
| 410 | 2.6829165 | 3.3420338 | 3.6813995 | 4.5569374 | 1.9631384 | 2.3533371 | 1.8131142 | 3.883385 |
| 411 | 0.2335164 | 0.3361267 | 1 | 0.1492862 | 0.4832086 | 0.2898768 | 0.4020229 | 1 |
| 412 | 0.5637578 | 0.4262328 | 0.3706443 | 0.6454719 | 0.6042357 | 0.4207521 | 0.7390119 | 0.4427176 |
| 413 | 1.2717475 | 1 | 1 | 2.9320119 | 2.67063 | 3.3157275 | 1 | 2.5573149 |
| 414 | 0.5041101 | 0.0494624 | 0.2739381 | 0.1632485 | 0.1474648 | 0.1198144 | 0.0846609 | 0.1699659 |
| 415 | 0.5629307 | 0.0428303 | 1 | 0.082723 | 0.0153272 | 0.0514501 | 0.0389858 | 0.062825 |
| 416 | 2.1341442 | 1 | 1 | 1.6082892 | 1 | 2.1005383 | 1 | 2.7515177 |
| 417 | 1.8803671 | 1 | 2.8203202 | 1.5221576 | 1.7033987 | 2.2212046 | 1 | 2.7826343 |
| 418 | 3.0497682 | 1 | 1 | 1 | 1 | 3.374192 | 2.7399674 | 1 |
| 419 | 1.1834385 | 1 | 2.7744045 | 2.3146618 | 0.6942249 | 1.439697 | 1 | 2.9426198 |
| 420 | 2.3394282 | 2.3674769 | 1 | 1 | 2.4095679 | 0.6439133 | 1 | 1 |
| 421 | 1 | 1 | 1 | 1.3832678 | 0.2939583 | 0.4437257 | 1 | 0.3405551 |
| 422 | 1.1531693 | 1 | 1 | 1 | 1 | 1 | 1 | 1.1392756 |
| 423 | 1.2660968 | 1 | 1 | 1.762048 | 1.4231949 | 2.7002426 | 1.3982951 | 3.4558075 |
| 424 | 0.6008193 | 0.5843478 | 1 | 0.3587657 | 0.5632868 | 0.534514 | 1 | 0.540604 |
| 425 | 1.3122017 | 1 | 1 | 1.6986264 | 1.8380373 | 1.9456795 | 1 | 2.612195 |
| 426 | 0.4046423 | 1 | 1 | 0.5985479 | 1 | 1 | 0.4381954 | 0.4262284 |
| 427 | 2.4644327 | 2.7955706 | 5.3862956 | 2.9757719 | 2.1844948 | 2.1181738 | 2.8554208 | 4.4961237 |
| 428 | 0.5258669 | 0.6785149 | 0.2817722 | 0.6834202 | 0.5769458 | 0.4700244 | 1 | 0.3223774 |
| 429 | 2.0695351 | 1.5450478 | 1 | 1.380008 | 2.5564639 | 1.3372433 | 2.0387323 | 2.115544 |
| 430 | 1.4437466 | 1 | 1 | 1 | 2.3031549 | 1.5216091 | 2.4213734 | 1 |
| 431 | 1 | 1 | 0.4722586 | 1.77002 | 1 | 0.1934069 | 0.305773 | 0.5164066 |
| 432 | 0.0556664 | 0.3205927 | 1 | 0.2088465 | 0.14018 | 0.0980362 | 0.1385489 | 0.4741183 |
| 433 | 2.4697199 | 1.7649116 | 2.2276442 | 1.9431914 | 1.4920652 | 2.3923043 | 1.2767718 | 3.7435495 |
| 434 | 0.5718492 | 0.6322894 | 0.2795341 | 0.7906787 | 0.6727164 | 0.512564 | 0.8044501 | 0.3406655 |
| 435 | 1 | 1 | 1 | 1000 | 1 | 1 | 1000 | 1 |
| 436 | 1 | 1 | 0.001 | 0.3948163 | 0.3851117 | 0.2698092 | 1 | 1 |
| 437 | 0.7775271 | 0.5920849 | 0.3736966 | 0.6212472 | 0.6118788 | 0.4948666 | 0.876944 | 0.4388833 |
| 438 | 2.2668873 | 1 | 1 | 3.2267779 | 2.1918019 | 2.3954439 | 1 | 3.439192 |
| 439 | 2.6744397 | 2.0968419 | 3.84198 | 1.8752901 | 1.6350771 | 2.3303498 | 1.6703517 | 3.7616719 |
| 440 | 1.958021 | 1.3693334 | 2.6493448 | 1.4615418 | 1.4561413 | 1.3777975 | 1.8537074 | 2.36555 |
| 441 | 1.1088571 | 1.6189458 | 2.0011692 | 2.8533924 | 1 | 1.8209873 | 1.966459 | 2.4944426 |

Table 4

| SEQ ID NO | Patient ID | | | | | | | |
|--------------|------------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|
| | 10 | 15 | 52 | 121 | 125 | 128 | 130 | 133 |
| 442 | 0.6375218 | 1 | 1 | 0.4666234 | 1 | 0.4180453 | 1 | 0.3355373 |
| 443 | 0.5384405 | 0.7428337 | 0.3326066 | 0.6743428 | 0.5786399 | 0.4785227 | 0.7554005 | 0.3571232 |
| 444 | 0.6290312 | 0.5801808 | 0.323954 | 0.7293856 | 0.6600083 | 0.4843004 | 0.8475975 | 0.3600582 |
| 445 | 1 | 1.2858847 | 2.5882229 | 1.4410038 | 1.2313977 | 1.3539788 | 1.4556884 | 3.7954079 |
| 446 | 1 | 0.6314926 | 1 | 0.5540759 | 0.4335806 | 1 | 0.6612292 | 1 |
| 447 | 1.5557686 | 1 | 1 | 3.2629626 | 1 | 1.631352 | 1 | 1 |
| 448 | 1.9853052 | 1.5883002 | 2.1962821 | 1.8021193 | 1 | 1.7471956 | 1.7744364 | 1.6829251 |
| 449 | 2.6744397 | 2.0867225 | 3.0485946 | 1.7944439 | 1.2830381 | 2.20923 | 1.3985134 | 2.416651 |
| 450 | 0.713209 | 1 | 1 | 0.3398071 | 0.4791055 | 0.6067736 | 0.4977883 | 0.4655028 |
| 451 | 1.6375642 | 1 | 1 | 1.534702 | 1.435012 | 1.7452788 | 1 | 3.0794888 |
| 452 | 1 | 1 | 1 | 4.1143521 | 1 | 1 | 1 | 2.5238314 |
| 453 | 0.4491276 | 1 | 1 | 0.3946607 | 0.5742285 | 0.7740261 | 0.5417305 | 0.5446751 |
| 454 | 1.3672041 | 1 | 0.425609 | 1 | 1.7717223 | 2.0924522 | 1 | 2.5695911 |
| 455 | 0.6031108 | 0.6284725 | 0.3349641 | 0.673348 | 0.6554436 | 0.5168647 | 0.8749143 | 0.3879164 |
| 456 | 0.5627876 | 1 | 1 | 0.4791827 | 0.4269425 | 0.5176685 | 1 | 0.626656 |
| 457 | 0.3313998 | 1 | 1 | 0.4755508 | 0.3995037 | 0.5392131 | 0.5509118 | 1 |
| 458 | 1 | 1 | 1 | 9.5853307 | 1 | 3.8690861 | 2.1040437 | 4.7333328 |
| 459 | 1.7141965 | 1 | 1 | 1.6472985 | 1 | 1.3830599 | 1.2214992 | 1.4017314 |
| 460 | 1000 | 1 | 1 | 1 | 1 | 1 | 1 | 7.8998755 |
| 461 | 0.6104323 | 0.7337354 | 0.3239323 | 0.6866052 | 0.6991281 | 0.5832367 | 1 | 0.3730997 |
| 462 | 4.7112811 | 1 | 1 | 4.9789798 | 1 | 1.5365928 | 1.6835038 | 4.8866121 |
| 463 | 2.6926224 | 2.06042 | 5.6340526 | 1.6400159 | 3.2443275 | 2.4100704 | 3.0296237 | 5.4706643 |
| 464 | 2.0191047 | 1.6731027 | 3.3685685 | 1.2095597 | 2.733162 | 1 | 2.1800256 | 3.4686833 |
| 465 | 1.6226683 | 1 | 1 | 1.3561697 | 1.7218802 | 1.7498406 | 2.0737974 | 2.4362804 |
| 466 | 1 | 0.1111372 | 1 | 1 | 0.481427 | 0.4979513 | 0.3257198 | 0.1622972 |
| 467 | 1.7951749 | 1.7668308 | 1.8209774 | 1.7301578 | 2.137926 | 2.0207078 | 2.3457966 | 2.4446276 |
| 468 | 2.8482478 | 2.203166 | 2.7201319 | 2.0143191 | 1.6893349 | 3.0436305 | 1.3378229 | 3.8240393 |
| 469 | 1.6758009 | 1 | 1.5633994 | 1 | 1 | 3.5697629 | 1.6304367 | 1.7267124 |
| 470 | 0.7651109 | 0.6673585 | 0.2985534 | 0.6814795 | 0.6470533 | 0.5143296 | 0.8484404 | 0.3433322 |
| 471 | 0.2916413 | 1 | 1 | 0.2084743 | 0.2462472 | 0.4312427 | 1 | 0.3277029 |
| 472 | 0.5741041 | 0.4468952 | 0.3083657 | 0.6420226 | 0.6351519 | 0.4619245 | 0.8544774 | 0.3158211 |
| 473 | 2.5437947 | 1 | 4.502954 | 1.6773897 | 2.1712611 | 2.0370655 | 2.0818938 | 5.5784364 |
| 474 | 0.8383235 | 1 | 1 | 0.6039952 | 1 | 0.9079448 | 0.7659081 | 1 |
| 475 | 1.8783626 | 1 | 1 | 5.3790816 | 2.1302506 | 4.7622946 | 3.2532946 | 4.1575884 |
| 476 | 2.2233966 | 1 | 3.2814944 | 2.547591 | 1.5458592 | 2.303577 | 2.5658305 | 5.6301764 |
| 477 | 1.4694238 | 1.714184 | 1.7790315 | 1.97715 | 1.5004286 | 3.1725203 | 1.6412196 | 3.3841461 |
| 478 | 3.1966728 | 3.0908081 | 5.9709264 | 1 | 1 | 1 | 1 | 0.409242 |
| 479 | 2.2100788 | 1 | 1 | 1.8495501 | 1.9875045 | 1.8176759 | 1.2792148 | 2.2874665 |
| 480 | 22.373396 | 0.1022477 | 1 | 1 | 0.4085332 | 1.72607 | 0.2488209 | 1 |
| 481 | 0.514213 | 1 | 1 | 0.3862923 | 0.4179345 | 0.6455141 | 1 | 1 |
| 482 | 1 | 1 | 1 | 1.8428512 | 1.4794374 | 2.9125972 | 1.5009294 | 5.0563413 |
| 483 | 0.6242783 | 0.5235195 | 0.311484 | 0.6617291 | 0.6789427 | 0.4133736 | 0.8569212 | 0.3736914 |
| 484 | 0.4822461 | 1 | 1 | 0.4226807 | 0.6236803 | 0.64076 | 0.6281225 | 1 |
| 485 | 1 | 1 | 1 | 1.7906824 | 1.4590256 | 2.1828832 | 1 | 3.7613169 |
| 486 | 0.0458707 | 0.0623714 | 0.2433231 | 0.0426479 | 0.0692868 | 0.0701643 | 0.2046931 | 0.155591 |
| 487 | 1.1404353 | 1.8223802 | 1 | 1.9174609 | 2.2773728 | 3.0626194 | 2.2578817 | 2.8046936 |
| 488 | 1 | 0.5362429 | 0.3099186 | 0.6928381 | 0.6798675 | 0.5123167 | 0.9402982 | 0.3820939 |
| 489 | 2.8267995 | 1 | 3.8922939 | 3.0291129 | 2.05121 | 2.1302514 | 1.9281558 | 4.2604295 |
| 490 | 1.8903301 | 1 | 1 | 2.4172353 | 1.6237174 | 1.7626052 | 1.6762274 | 2.1916235 |

Table 4

| SEQ ID NO | Patient ID | | | | | | | |
|--------------|------------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|
| | 10 | 15 | 52 | 121 | 125 | 128 | 130 | 133 |
| 491 | 0.4999533 | 1 | 1 | 0.5556034 | 0.5077706 | 0.4560163 | 0.6066305 | 0.6696071 |
| 492 | 2.8316204 | 2.6504646 | 2.8797649 | 2.6817944 | 1.9273586 | 1.821001 | 2.2373002 | 3.9629201 |
| 493 | 1.0736938 | 0.6141609 | 0.3961357 | 1.2898887 | 0.5590442 | 0.4848432 | 0.3716782 | 0.6051016 |
| 494 | 1.5022783 | 1.950391 | 3.0484464 | 2.9537767 | 1.4467134 | 3.678702 | 1.7296927 | 4.9085768 |
| 495 | 0.1932506 | 1 | 1 | 0.0598356 | 0.1506836 | 0.1633708 | 1 | 0.2649884 |
| 496 | 0.4134927 | 1 | 1 | 0.4333911 | 0.7426918 | 0.5293614 | 0.7309083 | 1.2020059 |
| 497 | 0.6787866 | 0.4996203 | 1 | 0.2977085 | 0.4936883 | 0.2934561 | 1 | 1 |
| 498 | 1 | 1 | 1 | 5.7988355 | 1 | 2.4050689 | 1.6654454 | 1 |
| 499 | 2.0471591 | 1.7878638 | 3.9666439 | 2.6152825 | 1.3494019 | 2.2976962 | 1.7484966 | 2.2604288 |
| 500 | 0.7492813 | 0.1041731 | 1 | 0.0418922 | 1.7762303 | 1 | 0.2237205 | 0.4495422 |
| 501 | 1.6982148 | 1.2730008 | 2.8496678 | 1.4555103 | 2.0170439 | 1.7008156 | 1.7763364 | 2.8973098 |
| 502 | 0.352296 | 1 | 1 | 1 | 0.552023 | 0.3743652 | 1 | 1.4398383 |
| 503 | 1.4666282 | 1 | 2.664994 | 3.0287188 | 1.6096711 | 1.4935311 | 1.4649481 | 3.1668978 |
| 504 | 1.899354 | 1 | 3.0512645 | 1.7464157 | 1.1866467 | 1.5902276 | 1 | 2.7359672 |
| 505 | 0.3421261 | 1 | 1.6238805 | 0.5545577 | 1 | 1 | 1 | 1 |
| 506 | 2.4266825 | 1.5564401 | 3.7543487 | 1 | 2.2055612 | 0.4395143 | 1 | 2.0687349 |
| 507 | 1 | 2.071325 | 4.9124738 | 3.0261595 | 1.6274285 | 2.4906635 | 1.5159397 | 3.488147 |
| 508 | 1.6999869 | 1 | 1 | 1 | 1.4856728 | 1.3236336 | 2.0560445 | 3.4267106 |
| 509 | 1.6513453 | 1 | 1 | 2.5958879 | 1 | 3.4658047 | 1 | 1 |
| 510 | 1.5183943 | 1 | 1 | 0.5328322 | 0.3649334 | 0.5504732 | 1 | 0.5576929 |
| 511 | 5.5512722 | 6.7340176 | 23.158287 | 1.6085948 | 7.1658173 | 4.7224961 | 6.8443711 | 13.768444 |
| 512 | 1 | 1 | 0.001 | 2.657379 | 0.3753616 | 1.581908 | 1 | 2.6598719 |
| 513 | 0.3312994 | 0.7150168 | 0.299433 | 0.6302502 | 0.6040716 | 0.6550429 | 0.8118569 | 0.3473875 |
| 514 | 1.7820214 | 2.6904982 | 4.3747918 | 3.4868148 | 3.2875679 | 4.9114993 | 4.2245578 | 6.9744005 |
| 515 | 1.678864 | 1 | 1 | 2.1690249 | 0.6996686 | 1.0716317 | 0.5650721 | 1 |
| 516 | 1.4765355 | 1 | 1 | 1.384646 | 2.0548802 | 2.2630778 | 1 | 2.5990825 |
| 517 | 0.2839163 | 1.2781903 | 0.2155274 | 0.3674793 | 0.2871073 | 0.3104871 | 0.1353606 | 0.2959314 |
| 518 | 1 | 1 | 1 | 1 | 3.0688879 | 1.8267032 | 1 | 1 |
| 519 | 0.4851429 | 1 | 1 | 0.4704213 | 1 | 0.5112656 | 1 | 1.2299667 |
| 520 | 0.1256607 | 1 | 1 | 0.5037841 | 0.1681476 | 0.236874 | 1 | 0.4016128 |
| 521 | 2.6446208 | 1.3761871 | 2.2270114 | 2.1577156 | 1.3467306 | 1.8476844 | 1.502087 | 2.4008008 |
| 522 | 2.5102906 | 1.5554918 | 3.4453708 | 1.6784177 | 2.2366918 | 1.7502802 | 2.6947202 | 1.1293189 |
| 523 | 1.8706707 | 1 | 4.777014 | 1.9729606 | 2.2785388 | 3.1545001 | 2.2301156 | 3.3401458 |
| 524 | 0.5457685 | 0.6254082 | 0.3126643 | 0.6107461 | 0.7272576 | 0.4027181 | 0.7757167 | 0.3834824 |
| 525 | 1 | 1 | 2.8392177 | 2.5839296 | 1.4431947 | 2.1147937 | 1 | 2.6230669 |
| 526 | 1.8223039 | 1.7402788 | 1.7102825 | 1.7097615 | 1.4636642 | 1.7305768 | 1.6442017 | 2.5794768 |
| 527 | 1.9763978 | 1 | 1 | 1.7167282 | 1.2470403 | 2.6314317 | 0.7928032 | 1.8277547 |
| 528 | 1 | 1 | 1 | 1.8752145 | 1.4867482 | 2.6893054 | 1 | 2.1987084 |
| 529 | 1 | 1 | 0.001 | 1 | 1 | 1 | 1 | 0.4096917 |
| 530 | 1 | 1 | 1 | 0.3748119 | 0.5385754 | 0.3985342 | 1 | 1 |
| 531 | 1 | 1 | 2.1783542 | 1.38372 | 1.3388301 | 2.7846279 | 1 | 2.8714555 |
| 532 | 1.8640472 | 1 | 1 | 1 | 2.5490205 | 5.278328 | 3.2040763 | 3.9927034 |
| 533 | 0.3270786 | 0.6193541 | 0.2452078 | 0.2511142 | 0.2257588 | 0.3530061 | 0.2157736 | 0.2620692 |
| 534 | 1.3090186 | 1.3732967 | 2.9258487 | 1.7844366 | 1 | 1.6268865 | 1.9473941 | 2.3445163 |
| 535 | 2.5606945 | 1 | 6.0691609 | 2.4041286 | 1 | 0.3045444 | 1 | 1 |
| 536 | 0.5799503 | 0.5738102 | 0.2959847 | 0.6604946 | 0.6398818 | 0.5870015 | 0.8498247 | 0.3598531 |
| 537 | 1.8771783 | 1 | 6.0744518 | 1.9333064 | 1.9276717 | 2.0440798 | 1.5256986 | 2.3907652 |
| 538 | 1.8597109 | 1 | 1 | 1.8524202 | 2.8264662 | 2.6236341 | 2.8458964 | 3.7462793 |
| 539 | 1.5470432 | 1 | 4.0264937 | 2.0606817 | 1.6005531 | 2.0161598 | 1 | 2.6752804 |

Table 4

| SEQ ID NO | Patient ID | | | | | | | |
|--------------|------------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|
| | 10 | 15 | 52 | 121 | 125 | 128 | 130 | 133 |
| 540 | 1.4276798 | 1 | 2.8315261 | 1.8537111 | 1 | 2.5665436 | 1 | 2.9030771 |
| 541 | 1 | 1 | 1.7728957 | 2.2515271 | 1.2132553 | 2.8574921 | 1 | 3.0785184 |
| 542 | 1.4472558 | 1.9373531 | 3.2266228 | 2.067683 | 1.1863303 | 2.5694703 | 1.3597118 | 3.796118 |
| 543 | 0.5545247 | 0.51392 | 0.291817 | 0.6500775 | 0.6522216 | 0.5408551 | 0.8333579 | 0.3279396 |
| 544 | 0.487606 | 0.8353522 | 0.3062709 | 0.174906 | 0.5475544 | 0.5883549 | 0.643767 | 0.4622444 |
| 545 | 2.0659202 | 1 | 4.333677 | 1.5166287 | 1 | 1.961625 | 1 | 3.8735703 |
| 546 | 2.5939293 | 1 | 1 | 2.2910829 | 1 | 2.7149033 | 1 | 2.3143464 |
| 547 | 1.4179494 | 1 | 2.2817042 | 2.2546893 | 1.3727108 | 1.9139396 | 1.7915403 | 2.0640722 |
| 548 | 1.3511571 | 1 | 2.7208399 | 2.3463927 | 0.7809263 | 2.02461 | 1 | 2.839187 |
| 549 | 1 | 2.737059 | 2.0794695 | 2.2942442 | 1.3447298 | 1.5804103 | 1.7908598 | 1.7299314 |
| 550 | 2.0503678 | 1 | 2.2005207 | 1.6579459 | 1.406737 | 2.6447047 | 1.6323975 | 1.2999949 |
| 551 | 0.1961424 | 0.0570151 | 1 | 0.0691381 | 0.3765977 | 0.6199505 | 0.0733275 | 0.0670459 |
| 552 | 1 | 1 | 3.5107563 | 1 | 1 | 2.3684926 | 1 | 3.2523502 |
| 553 | 0.5828395 | 1 | 0.5391297 | 0.255944 | 0.426312 | 0.5772597 | 0.7831558 | 0.3219987 |
| 554 | 0.5201015 | 0.4504621 | 0.3175066 | 0.6218114 | 0.580508 | 0.5669958 | 0.763864 | 0.3437346 |
| 555 | | 0.0510751 | 0.7137075 | 0.3422263 | 0.0799665 | 0.0352161 | 0.1168537 | 0.4301022 |
| 556 | | 1 | 1 | 2.2887177 | 2.0361937 | 1.2178273 | 1.2616143 | 1.9270454 |
| 557 | | 1 | 1 | 0.6122802 | 1.2836703 | 1.2151686 | 1.3078435 | 1 |
| 558 | | 1 | 0.7099259 | 2.404439 | 0.7751623 | 2.1885098 | 1 | 2.6309802 |
| 559 | | 1 | 1 | 1 | 1 | 2.2852201 | 1 | 1.8552026 |
| 560 | | 1 | 1 | 5.0527405 | 1 | 5.4843896 | 1 | 1 |
| 561 | | 1 | 1 | 2.5698093 | 1 | 1 | 0.939805 | 1.3921219 |
| 562 | | 2.0732473 | 1.935588 | 0.7045126 | 2.529102 | 0.7241354 | 1.8743796 | 2.4806989 |
| 563 | | 0.5231007 | 0.4823919 | 0.7621378 | 0.6303761 | 0.4461302 | 1 | 0.281738 |
| 564 | | 1.4871921 | 1 | 2.3060058 | 2.0508162 | 1.9728163 | 2.2537352 | 3.8408521 |
| 565 | | 0.6709663 | 0.4294373 | 0.7860729 | 0.7179208 | 0.4685954 | 1 | 0.3150085 |
| 566 | | 3.0595896 | 2.3001491 | 1.6056821 | 3.3155307 | 1.5417797 | 1.7020875 | 3.6754464 |
| 567 | | 1 | 3.3029493 | 4.8397475 | 1.7621637 | 5.0220872 | 1.4660989 | 1.2974071 |
| 568 | | 1 | 0.4188264 | 1 | 0.7571332 | 0.5668378 | 0.7456115 | 0.3769262 |
| 569 | | 1 | 0.4129753 | 1 | 1 | 0.2831784 | 1 | 1 |
| 570 | | 0.3392918 | 0.3095057 | 0.2787957 | 0.6247091 | 0.3296065 | 0.6689514 | 0.217698 |
| 571 | | 1 | 0.3992726 | 0.5681816 | 1 | 0.4846302 | 0.8226293 | 1 |
| 572 | | 2.6508577 | 1 | 1.3438 | 2.1883889 | 1.7681562 | 1.6827765 | 2.5987827 |
| 573 | | 3.5701324 | 2.003719 | 2.9956857 | 2.9775168 | 1.4836313 | 1.876539 | 5.4402814 |
| 574 | | 0.2623913 | 0.7166926 | 1 | 0.5536253 | 0.5007612 | 1.201851 | 1.4029228 |
| 575 | | 0.5753248 | 0.3619272 | 0.5828711 | 0.7585528 | 1 | 0.7612806 | 0.4113328 |
| 576 | | 0.6804006 | 0.4574511 | 0.7532716 | 0.5408226 | 0.5138899 | 0.7990971 | 0.407672 |
| 577 | | 1 | 1 | 0.7853568 | 0.3980817 | 0.602047 | 0.4875427 | 0.6169124 |
| 578 | | 1.7636924 | 1 | 2.3963327 | 1.4356678 | 2.0500499 | 1.7676441 | 1.3606976 |
| 579 | | 0.7353556 | 0.3642225 | 0.7686242 | 0.6784682 | 0.4708282 | 0.8184507 | 0.3188507 |
| 580 | | 1 | 0.5052757 | 0.6780701 | 0.8566176 | 0.6818706 | 0.2766622 | 0.5310182 |
| 581 | | 3.1566823 | 1 | 2.1609706 | 3.42812 | 3.1234679 | 2.0770669 | 3.181391 |
| 582 | | 1.7794381 | 1 | 1.6243659 | 1.6669243 | 1.7023064 | 2.1858234 | 2.1422424 |
| 583 | | 1.6142179 | 1 | 2.0665816 | 3.1474777 | 1.3221566 | 2.2992576 | 2.2615255 |
| 584 | | 2.2215143 | 1 | 1.6544403 | 1.2865619 | 1.653405 | 1 | 1.7533872 |
| 585 | | 1 | 1 | 1.1355525 | 1.7218802 | 2.1416352 | 1.4847601 | 2.8195498 |
| 586 | | 1 | 1 | 1.8384122 | 1 | 1.9884458 | 1.4233551 | 1 |
| 587 | | 0.4757684 | 1 | 0.4325575 | 0.553178 | 0.7227889 | 1 | 0.3925949 |
| 588 | | 0.9034974 | 1 | 1 | 1 | 0.3076497 | 0.2734631 | 1 |

Table 4

| SEQ ID | Patient ID | | | | | | | |
|--------|------------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|
| | 10 | 15 | 52 | 121 | 125 | 128 | 130 | 133 |
| 589 | | 0.2242063 | 1 | 0.6206591 | 0.3616857 | 0.3151381 | 0.265628 | 0.542253 |
| 590 | | 0.5519482 | 0.329141 | 0.458833 | 1 | 0.4867325 | 0.7674303 | 0.324263 |
| 591 | | 1 | 0.5031686 | 0.6181211 | 0.6572182 | 0.4091691 | 1 | 1 |
| 592 | | 0.610434 | 0.3828732 | 0.6731338 | 0.8374879 | 0.4068539 | 1 | 0.3583935 |
| 593 | | 2.0350812 | 0.7142343 | 0.7237726 | 3.9427999 | 0.9035961 | 0.4240756 | 1 |
| 594 | | 0.7759562 | 0.6702288 | 0.5052878 | 0.599986 | 1 | 0.6726078 | 0.5747266 |
| 595 | | 1 | 2.4926205 | 1.7046593 | 1.2158795 | 1.6059052 | 1.472969 | 2.0927825 |
| 596 | | 1 | 0.3228259 | 1 | 0.7264414 | 0.5162258 | 0.8527449 | 0.3247916 |
| 597 | | 1 | 1 | 2.4495397 | 1 | 1 | 1 | 1 |
| 598 | | 2.5145975 | 1.8172304 | 1.6905769 | 1 | 1.6227026 | 1 | 1 |
| 599 | | 1 | 2.1703653 | 1 | 1 | 1.4617363 | 1 | 1 |
| 600 | | 1 | 1 | 26.988957 | 1 | 2.2936223 | 2.3885134 | 6.5723064 |
| 601 | | 0.3918772 | 0.5129141 | 0.5272743 | 0.7896268 | 0.6102842 | 0.5060783 | 0.6458909 |
| 602 | | 2.3442896 | 1 | 2.7083947 | 1.8109243 | 2.0451103 | 1 | 1.902919 |
| 603 | | 1.933929 | 1 | 1 | 2.2006533 | 1 | 1 | 2.4955392 |
| 604 | | 0.3171246 | 1 | 2.5142954 | 2.4964707 | 1.2899564 | 0.7087105 | 1 |
| 605 | | 0.6780516 | 0.4236615 | 0.6365973 | 0.7258293 | 1 | 0.7677854 | 0.3376675 |
| 606 | | 1.498079 | 1 | 2.2382669 | 2.5216382 | 1.6588324 | 2.3945145 | 2.6059701 |
| 607 | | 2.0419015 | 1 | 2.3879745 | 1.5019266 | 2.1525518 | 2.2167613 | 3.1528149 |
| 608 | | 1.7353221 | 1 | 1 | 1.7909437 | 1.2589173 | 2.711604 | 1 |
| 609 | | 1 | 1 | 0.688158 | 0.1523676 | 1 | 0.4226112 | 1 |
| 610 | | 1 | 0.4791308 | 0.9330224 | 0.2818188 | 0.7785603 | 0.493361 | 0.484075 |
| 611 | | 1 | 0.6530079 | 0.4745765 | 0.5677905 | 1.2778032 | 0.4687248 | 1 |
| 612 | | 0.7207938 | 0.3807598 | 0.8163844 | 0.7099844 | 0.5212272 | 1 | 0.3267246 |
| 613 | | 0.5726763 | 0.3600772 | 0.6584162 | 0.7213634 | 0.4693099 | 1 | 0.3044838 |
| 614 | | 0.6350905 | 0.3878714 | 0.6857001 | 0.5972583 | 0.3888611 | 0.7390179 | 0.2827321 |
| 615 | | 0.8170219 | 0.3643103 | 0.7872492 | 1 | 0.5452657 | 1 | 0.3551508 |
| 616 | | 2.1044135 | 1 | 1.3672619 | 2.1589721 | 1.5628434 | 1.7949144 | 2.2514899 |
| 617 | | 2.1602034 | 0.3588543 | 0.2889924 | 0.5524313 | 0.113068 | 0.3107689 | 0.6848735 |
| 618 | | 2.1459375 | 0.359287 | 0.3256504 | 0.506252 | 0.1765889 | 0.2278695 | 0.6444787 |
| 619 | | 0.7680421 | 0.7029397 | 1 | 0.4809522 | 0.5493946 | 0.5036683 | 1 |
| 620 | | 1 | 1 | 0.7148158 | 0.8310174 | 0.6365143 | 1.2318117 | 0.8246143 |
| 621 | | 1.5298821 | 0.7102144 | 1.5571333 | 1 | 1 | 1 | 1 |
| 622 | | 1.9474157 | 2.1819044 | 1 | 1 | 1.8713382 | 1.7812457 | 2.0924906 |
| 623 | | 1 | 1 | 1.3924316 | 2.06226 | 3.8278243 | 2.1081037 | 3.4752238 |
| 624 | | 1 | 0.5149837 | 1.8613074 | 5.5637082 | 2.7677275 | 1 | 1 |
| 625 | | 1 | 1 | 1.6526491 | 1.5453895 | 1.8102768 | 2.1106864 | 1 |
| 626 | | 1 | 1 | 0.6750566 | 0.398816 | 0.7232904 | 0.471272 | 0.4064175 |
| 627 | | 0.3621447 | 0.4648449 | 0.4820155 | 0.7461369 | 0.4519354 | 0.393411 | 0.6050148 |
| 628 | | 0.4650232 | 0.3598075 | 0.629024 | 0.5808869 | 1 | 0.7446819 | 1 |
| 629 | | 1 | 2.7530912 | 1.5786762 | 2.4168742 | 2.0220406 | 1.9306073 | 3.1814226 |
| 630 | | 1 | 1 | 7.3160919 | 4.2949375 | 5.7823181 | 5.9493939 | 6.4315006 |
| 631 | | 1 | 1 | 1.1885311 | 0.4209123 | 0.390771 | 0.2976852 | 1 |
| 632 | | 1 | 1 | 1 | 0.4229307 | 0.4416921 | 0.6670586 | 1 |
| 633 | | 2.9948192 | 1 | 1.3584055 | 2.5680197 | 1.1807357 | 1.8181185 | 2.0914334 |
| 634 | | 1 | 2.4612015 | 1 | 1.6627722 | 1.7263036 | 1 | 1.8847176 |
| 635 | | 0.4681742 | 0.4609755 | 0.5652189 | 0.8665631 | 0.5091221 | 0.4218689 | 0.4978345 |
| 636 | | 2.11204 | 1 | 2.0311483 | 1 | 1.5175833 | 1 | 1 |
| 637 | | 2.3045884 | 1.8443035 | 2.2784687 | 2.3272434 | 1.7144046 | 1.7337431 | 1.987614 |

Table 4

| SEQ ID NO | Patient ID | | | | | | | |
|--------------|------------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|
| | 10 | 15 | 52 | 121 | 125 | 128 | 130 | 133 |
| 638 | | 0.4434503 | 1 | 0.6136441 | 0.568416 | 1 | 0.541426 | 0.6457568 |
| 639 | | 1.8664711 | 1 | 1.8009691 | 1.4991439 | 2.1856519 | 1.804568 | 2.5683761 |
| 640 | | 1.9375632 | 2.494621 | 1.8412478 | 1.8599952 | 3.8448072 | 1.5301548 | 2.9958195 |
| 641 | | 0.5822094 | 0.7052726 | 0.1785994 | 0.6034573 | 0.4418501 | 0.4816631 | 0.4203743 |
| 642 | | 0.6116178 | 0.3097565 | 0.7124312 | 0.7361295 | 0.4598704 | 0.8576514 | 0.320121 |
| 643 | | 0.5977418 | 0.3785084 | 0.7027366 | 0.6653533 | 0.510187 | 1 | 0.3013516 |
| 644 | | 1 | 1 | 1.9751369 | 1.3683669 | 2.989714 | 1 | 1.903921 |
| 645 | | 1 | 2.2506689 | 1 | 1 | 2.1795787 | 1.5722354 | 2.2149689 |
| 646 | | 0.5601656 | 0.4104354 | 1 | 0.7473481 | 0.4857569 | 1 | 0.3795455 |
| 647 | | 0.8337804 | 0.3864666 | 0.7963523 | 0.7370643 | 0.4938293 | 1 | 0.3636716 |
| 648 | | 1 | 1 | 1 | 1.4225693 | 1.4905632 | 1.2027384 | 2.7442513 |
| 649 | | 3.4055036 | 6.3217978 | 1.8059642 | 1.5292152 | 1.9016215 | 2.1977816 | 2.8673845 |
| 650 | | 1.9316994 | 1.9486949 | 1.5697074 | 1.2374611 | 1 | 1.8424987 | 1.3819837 |
| 651 | | 1 | 2.0546793 | 5.2778541 | 1 | 2.5066502 | 1.8013748 | 2.8412304 |
| 652 | | 1 | 1 | 1 | 1 | 2.2475102 | 1 | 3.0807906 |
| 653 | | 1 | 1 | 0.7866972 | 0.5763387 | 0.6223344 | 1 | 1 |
| 654 | | 0.2713249 | 0.6445292 | 0.2372919 | 0.1174458 | 0.5733025 | 0.5518043 | 1 |
| 655 | | 2.4531592 | 1 | 1.5059828 | 1 | 2.5618514 | 1 | 1.251529 |
| 656 | | 1 | 0.612922 | 0.1819487 | 0.2506942 | 0.4216864 | 0.6800675 | 1 |
| 657 | | 1 | 0.4288416 | 0.6569853 | 0.4302984 | 0.5677446 | 0.6021291 | 1 |
| 658 | | 1.5741243 | 1 | 1.6628313 | 1.8944042 | 1.5897742 | 1.6839152 | 1.6979942 |
| 659 | | 0.572499 | 0.6896948 | 0.2726988 | 0.2193634 | 0.3578151 | 0.3582937 | 0.3772812 |
| 660 | | 1 | 1 | 3.7368825 | 1 | 2.0470889 | 2.0277495 | 1 |
| 661 | | 1 | 0.5865639 | 0.3575671 | 0.4834164 | 0.551222 | 1 | 1 |
| 662 | | 1 | 0.4191211 | 0.7964886 | 1 | 1 | 1 | 1 |
| 663 | | 0.2591271 | 0.5439067 | 0.0773793 | 0.549501 | 0.6479049 | 0.4382704 | 1 |
| 664 | | 2.496101 | 1 | 3.787192 | 4.0189083 | 1 | 1.9397201 | 3.5473664 |
| 665 | | 1 | 1 | 4.0395619 | 0.7596696 | 3.2462227 | 1 | 4.0167036 |
| 666 | | 1.4270267 | 1 | 2.0012875 | 1.8215487 | 2.279676 | 1.9609494 | 2.3376997 |
| 667 | | 1.1746615 | 1 | 6.049763 | 2.9596948 | 3.1482139 | 1.308665 | 1.4350572 |
| 668 | | 1.2916777 | 1 | 2.1700359 | 1.2470985 | 1.8265177 | 1.3112509 | 2.1932803 |
| 669 | | 1 | 1 | 2.4750639 | 1.7207983 | 1.476349 | 1 | 2.0711097 |
| 670 | | 1 | 1 | 1.7552387 | 1 | 2.967132 | 2.7575945 | 1 |
| 671 | | 0.5194467 | 2.9067559 | 0.4890126 | 1 | 1.3881369 | 1 | 2.4327695 |
| 672 | | 1 | 4.5462525 | 2.2337564 | 3.3337445 | 2.3406687 | 1 | 3.0315357 |
| 673 | | 1 | 1 | 1.8291308 | 1.6148061 | 1.835016 | 1.6382484 | 3.3159641 |
| 674 | | 0.6474689 | 0.7087657 | 1 | 1.973768 | 0.955534 | 2.6933429 | 3.3081771 |
| 675 | | 1 | 1 | 1.8717089 | 1 | 2.8266248 | 1 | 4.9209004 |
| 676 | | 1 | 1 | 1.5073968 | 0.6957671 | 1.8469081 | 1.8633077 | 3.4005723 |
| 677 | | 1 | 1 | 2.2007067 | 2.3135317 | 1.9038887 | 2.4811248 | 3.9892478 |
| 678 | | 0.5362268 | 0.3545083 | 0.7483917 | 0.6955903 | 0.4248879 | 1 | 0.3051228 |
| 679 | | 1 | 1 | 1 | 1.3405777 | 1 | 1 | 2.4052111 |
| 680 | | 1 | 1 | 4.1754216 | 1.2713849 | 3.6227176 | 1 | 1 |
| 681 | | 1 | 1 | 3.7839599 | 1 | 1.2993272 | 1 | 1 |
| 682 | | 0.1046559 | 1 | 0.6141541 | 0.2327294 | 0.3258142 | 0.2361167 | 0.5279412 |
| 683 | | 2.5346877 | 1 | 2.7094193 | 1.4516093 | 2.1814474 | 1 | 3.6363139 |
| 684 | | 1 | 0.7344089 | 0.793333 | 0.2985073 | 0.7318231 | 0.3846675 | 1 |
| 685 | | 0.5679747 | 1 | 0.7455573 | 1 | 0.8325661 | 0.5104178 | 0.5364304 |
| 686 | | 0.490394 | 0.802634 | 0.6380412 | 0.5821121 | 0.5041894 | 0.6768459 | 1 |

Table 4

| SEQ ID NO | Patient ID | | | | | | | |
|--------------|------------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|
| | 10 | 15 | 52 | 121 | 125 | 128 | 130 | 133 |
| 687 | | | 1 | 0.7380776 | 0.3589926 | 1 | 0.2231063 | 1 |
| 688 | | 0.6396975 | 0.504981 | 0.9499954 | 0.6696795 | 0.4820814 | 0.8032959 | 0.381297 |
| 689 | | 0.5731232 | 0.422771 | 0.5860222 | 1.1754675 | 1 | 0.367389 | 1 |
| 690 | | | 1 | 1 | 1 | 1.3825928 | 1 | 1 |
| 691 | | | 1 | 1 | 1.738265 | 1 | 2.1299011 | 1 |
| 692 | | | 1 | 1.5842216 | 2.6867469 | 1 | 1.5169169 | 1.6604755 |
| 693 | | 0.6590487 | 0.3719612 | 0.9090829 | 0.7671724 | 0.5484259 | 0.8993221 | 0.3895732 |
| 694 | | | 1 | 1 | 3.0898259 | 2.019943 | 2.5085944 | 1 |
| 695 | | | 1 | 1 | 2.3261111 | 1 | 0.780216 | 1 |
| 696 | | | 1 | 1 | 0.6280481 | 0.2345092 | 0.1950282 | 0.1691971 |
| 697 | | | 1 | 1 | 2.8878176 | 2.5215191 | 2.948514 | 3.119506 |
| 698 | | 1.9198714 | 1 | 1.8630205 | 1.4636442 | 3.4184079 | 1 | 2.3950256 |
| 699 | | 0.5074221 | 0.3895458 | 0.7945718 | 0.7398981 | 0.4917064 | 1 | 0.3792852 |
| 700 | | | 1 | 1 | 1.9609524 | 1 | 3.0244835 | 2.0122183 |
| 701 | | 0.4452252 | 0.3491464 | 0.7670728 | 0.6139928 | 0.448466 | 1 | 0.306827 |
| 702 | | | 1 | 1 | 2.8142387 | 1 | 2.5297268 | 1.7780639 |
| 703 | | 0.5924644 | 0.325811 | 0.710252 | 0.6979221 | 0.554183 | 1 | 1 |
| 704 | | | 1 | 2.3717419 | 1.7321856 | 2.5957301 | 1.9746919 | 2.0697727 |
| 705 | | 0.4877131 | 0.5357792 | 0.6306386 | 0.7981475 | 0.7565073 | 0.7585282 | 1 |
| 706 | | 0.4420828 | 0.3624853 | 0.7509751 | 0.6707561 | 0.4253894 | 1 | 0.342204 |
| 707 | | 0.4941817 | 0.4601728 | 0.7971773 | 0.5207686 | 0.4159567 | 0.8012053 | 0.312184 |
| 708 | | | 1 | 1 | 0.7160031 | 0.3444516 | 0.1706944 | 0.4906831 |
| 709 | | 2.7293957 | 1.9803335 | 3.402591 | 2.5643819 | 2.2321555 | 2.3797575 | 4.8251205 |
| 710 | | | 1 | 1 | 3.0278324 | 1.5415309 | 2.8247905 | 2.5453453 |
| 711 | | | 1 | 1 | 2.2424175 | 1 | 1.5063163 | 1 |
| 712 | | | 1 | 1 | 2.2346678 | 1.4759415 | 3.737036 | 1 |
| 713 | | | 1 | 1 | 1 | 1 | 2.3488578 | 1 |
| 714 | | | 1 | 1 | 1 | 1 | 4.8525951 | 1 |
| 715 | | 0.475874 | 0.3800449 | 0.7566444 | 0.677371 | 0.4737686 | 1 | 0.3502514 |
| 716 | | | 1 | 0.4655536 | 0.7970818 | 1 | 1 | 1 |
| 717 | 0.6095876 | 0.6287095 | 0.2435698 | 1 | 0.6002288 | 0.4253001 | 0.8035265 | 0.3367602 |
| 718 | 2.0255469 | 1.6581844 | 3.2226434 | 1 | 1.5450318 | 1.1086546 | 1 | 2.5486915 |
| 719 | 4.1944684 | 5.5199161 | 22.946447 | 1 | 5.9290833 | 3.9178775 | 7.3370985 | 8.9076708 |
| 720 | 3.8682319 | 3.7168821 | 21.558144 | 1 | 4.5366566 | 1 | 1 | 8.3860807 |
| 721 | 3.080453 | 2.7407554 | 4.1187863 | 1.978999 | 2.4717435 | 1.2857244 | 2.5283203 | 2.4782294 |
| 722 | 2.2556349 | 2.8439399 | 2.994444 | 1 | 2.0397324 | 1.6878379 | 2.0096454 | 2.9051915 |
| 723 | 1.7072141 | 1.4357252 | 1 | 3.0054518 | 1 | 2.0994047 | 1 | 1.4465839 |
| 724 | 1.5378397 | 1.3285034 | 2.6075942 | 1.7057836 | 1.4835061 | 1.2492992 | 2.0322574 | 2.5979622 |
| 725 | 0.6164381 | 0.4789379 | 0.3576569 | 1 | 0.629362 | 0.220585 | 0.3155102 | 0.3517268 |
| 726 | 5.4551675 | 1 | 5.3784425 | 2.4621705 | 3.0413607 | 1 | 1.1790886 | 1 |
| 727 | 1.2202348 | 1.3560407 | 3.3309948 | 1.6783572 | 1 | 1.4333216 | 2.0695815 | 2.1149207 |
| 728 | 0.5213074 | 1 | 0.1724211 | 1 | 0.4723423 | 0.2936004 | 0.5429091 | 0.1957649 |
| 729 | 0.5101267 | 1 | 0.246636 | 1 | 0.5617227 | 0.4987551 | 0.5781643 | 0.2834422 |
| 730 | 0.4047713 | 1.1125747 | 0.4258258 | 1 | 0.6131363 | 0.8431392 | 0.3251842 | 0.6972365 |
| 731 | 0.4397263 | 2.1075636 | 1 | 1 | 1 | 1 | 0.4160925 | 1 |
| 732 | 1.3347391 | 1.2800236 | 3.1520225 | 3.3720314 | 1.14747 | 1.7760568 | 1.9672363 | 2.9485055 |
| 733 | 1.8062539 | 1 | 1 | 1.3934318 | 0.3766044 | 2.073793 | 0.2842231 | 1 |
| 734 | 2.039085 | 2.6749629 | 3.205676 | 1.7025087 | 2.6315447 | 1.7740989 | 1.6990209 | 3.3788285 |
| 735 | 0.6135905 | 1 | 1.3758203 | 0.4380891 | 0.8393241 | 1.3151697 | 1 | 1 |

Table 4

| SEQ ID NO | Patient ID | | | | | | | |
|--------------|------------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|
| | 10 | 15 | 52 | 121 | 125 | 128 | 130 | 133 |
| 736 | 1.6788313 | 2.7248582 | 2.6966219 | 1.3874106 | 1 | 1 | 0.8020015 | 1.6335124 |
| 737 | 9.274781 | 2.2961373 | 3.6023114 | 1.6823601 | 0.7503091 | 0.4330633 | 0.2385956 | 3.4668214 |
| 738 | 2.6942188 | 2.7653063 | 3.5950837 | 7.5114474 | 1.7701367 | 3.0792038 | 2.0639551 | 4.790067 |
| 739 | 0.5018568 | 1 | 1 | 1 | 0.3240862 | 0.6423607 | 0.2857607 | 0.7323216 |
| 740 | 1 | 2.0210216 | 3.8831356 | 2.9044826 | 1 | 2.7203582 | 1 | 2.7142471 |
| 741 | 1 | 2.1687236 | 1 | 3.9185213 | 2.8012617 | 1 | 1.8089771 | 2.413582 |
| 742 | 1.6710654 | 1.6944129 | 4.2854066 | 1.8092277 | 3.2412754 | 1.3592276 | 2.4303728 | 2.8880789 |
| 743 | 0.0765229 | 0.6745031 | 1 | 0.0909296 | 0.0739966 | 0.1655899 | 0.215823 | 0.2059267 |
| 744 | 1.2145019 | 1.1617247 | 3.5221926 | 2.7752348 | 1.3327324 | 1.6354397 | 1.8984906 | 2.0615081 |
| 745 | 1.9512947 | 1.6670739 | 2.5842766 | 2.9240933 | 2.6897305 | 1.5112422 | 2.068769 | 2.5033342 |
| 746 | 0.5177033 | 0.0409253 | 1 | 0.5019266 | 0.0633551 | 0.0580042 | 0.1375896 | 0.3517425 |
| 747 | 1.35266 | 1.3590915 | 4.0095032 | 2.837134 | 1.899728 | 2.251804 | 2.4291207 | 2.9940838 |
| 748 | 0.6013256 | 0.7572008 | 1 | 0.4673542 | 0.2089521 | 0.4209376 | 0.4545527 | 0.4483429 |
| 749 | 0.0414488 | 0.3205769 | 1 | 0.0224109 | 0.0811839 | 0.0748772 | 0.0792774 | 0.1018549 |
| 750 | 0.5026983 | 0.1989002 | 1 | 0.2474169 | 0.1724856 | 0.1866192 | 0.2156993 | 0.3054779 |
| 751 | 1.1238244 | 1.9001223 | 2.9253027 | 2.6177824 | 2.5799919 | 1.9726034 | 2.0871321 | 2.8973414 |
| 752 | 10.619795 | 0.3036449 | 1 | 1 | 0.1056362 | 0.3496809 | 0.2663514 | 1.3951831 |
| 753 | 2.1323521 | 3.2108198 | 3.673636 | 5.3481851 | 2.0369704 | 2.4389866 | 1.9095787 | 3.6684641 |
| 754 | 0.576146 | 0.5982662 | 0.2673492 | 1 | 0.6442782 | 0.4137308 | 1 | 0.2941326 |
| 755 | 0.5317681 | 0.0526672 | 1 | 0.4058101 | 0.0969415 | 0.0797961 | 0.1799179 | 0.4250765 |
| 756 | 10.756065 | 0.2227004 | 1 | 1.8305692 | 0.0555039 | 0.3330484 | 0.2052695 | 1 |
| 757 | 0.9037793 | 1.9665207 | 2.7048799 | 1 | 1.8156961 | 0.5100015 | 0.6059739 | 0.6858676 |
| 758 | 1 | 1.5803818 | 4.6940599 | 2.9353394 | 1.6970384 | 1.7911779 | 1.5614113 | 3.889886 |
| 759 | 1 | 1.3921781 | 2.8360078 | 2.0379055 | 1 | 1.6842655 | 1 | 2.0183203 |
| 760 | 2.2221377 | 3.0813097 | 3.3046656 | 2.8572451 | 2.8179649 | 1.8284138 | 1 | 2.4461187 |
| 761 | 1.8524886 | 1.8991411 | 2.8545969 | 1.7530246 | 2.4002541 | 2.0074554 | 1.5575023 | 3.7050797 |
| 762 | 0.934303 | 1.2379402 | 1 | 1.7522329 | 1.2892174 | 1.8896264 | 1.3603106 | 1.2258168 |
| 763 | 0.3895968 | 0.5114454 | 2.4204029 | 0.3850622 | 0.3070291 | 0.4811814 | 0.5572515 | 0.7334814 |
| 764 | 1.2173959 | 1 | 1 | 3.3344758 | 0.7650731 | 1 | 1 | 2.7582159 |
| 765 | 1 | 1 | 1 | 1.8511313 | 2.3250143 | 1 | 2.5032406 | 2.0285847 |
| 766 | 1.9369363 | 1.7920748 | 2.2366218 | 2.4393362 | 1.936444 | 1.5184832 | 1.9692687 | 2.4438544 |
| 767 | 1.3165839 | 1.7371021 | 3.699206 | 1.5561964 | 2.237629 | 1.2376819 | 1.9506592 | 3.5231059 |
| 768 | 2.3822895 | 2.6498437 | 2.8763308 | 2.0788083 | 2.5640741 | 1 | 2.222977 | 3.376864 |
| 769 | 2.1046984 | 1.9558725 | 4.6737696 | 1.6467159 | 1.8629475 | 2.5063754 | 2.0462295 | 2.8488202 |
| 770 | 0.7634938 | 0.5370472 | 0.2725795 | 1 | 0.5315872 | 1 | 0.5681397 | 1 |
| 771 | 1 | 1 | 1 | 10.716067 | 1.2886264 | 1 | 1.6560248 | 3.6277773 |
| 772 | 2.3857785 | 2.2500059 | 3.4417782 | 1.7045657 | 3.4963502 | 2.2531712 | 2.8076336 | 3.8750851 |
| 773 | 1 | 0.3409028 | 0.535804 | 0.7296313 | 1 | 0.7453159 | 0.3129313 | 0.6316028 |
| 774 | 1 | 0.1720706 | 1 | 0.4203033 | 1 | 0.6199161 | 0.5326126 | 0.759951 |
| 775 | 1 | 2.5090206 | 4.4366919 | 9.2824147 | 1.7398313 | 1 | 0.5978736 | 3.2178095 |
| 776 | 2.5468713 | 2.9446687 | 2.6588926 | 2.6652899 | 1.8463621 | 2.2413271 | 2.365556 | 3.5225536 |
| 777 | 0.4545111 | 0.7874136 | 0.2926176 | 1 | 0.5877952 | 0.5790528 | 1 | 0.3097304 |
| 778 | 2.4363377 | 9.4950408 | 6.0236903 | 6.3066853 | 1.2067441 | 4.5229473 | 1.5086893 | 10.545641 |
| 779 | 1.4188115 | 1.7745423 | 2.2002891 | 1.8951762 | 2.2380979 | 1.4378352 | 2.3949626 | 2.737774 |
| 780 | 0.152949 | 0.7271918 | 1 | 0.1256513 | 0.215523 | 0.2126638 | 0.2346429 | 0.263868 |
| 781 | 2.6318834 | 3.8389663 | 4.4638508 | 3.1049721 | 2.1555734 | 2.4272044 | 2.8552388 | 4.5371497 |
| 782 | 0.3972474 | 0.0477238 | 1 | 0.3206454 | 0.092571 | 0.0793839 | 0.1690681 | 0.4360194 |
| 783 | 1.6142343 | 2.9895401 | 3.1598045 | 4.4495796 | 1.6343515 | 3.3453101 | 1.8364179 | 3.8121654 |
| 784 | 1.6451466 | 1.9602744 | 2.3699131 | 1 | 1.8556327 | 1.5461629 | 1.8132977 | 3.5979152 |

Table 4

| SEQ ID NO | Patient ID | | | | | | | |
|--------------|------------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|
| | 10 | 15 | 52 | 121 | 125 | 128 | 130 | 133 |
| 785 | 0.1043845 | 0.3238743 | 1 | 0.2961085 | 0.0930783 | 0.0891738 | 0.1658781 | 0.3231664 |
| 786 | 1.5566382 | 1.6617284 | 3.5131164 | 2.3888935 | 2.625916 | 1.9815757 | 2.0762004 | 2.2945119 |
| 787 | 1.2250828 | 2.1682679 | 2.7477825 | 2.4369102 | 1 | 1.8963591 | 1 | 1.9288679 |
| 788 | 1.7996277 | 1.602209 | 1 | 3.4064499 | 1.7403416 | 2.2837912 | 3.4895015 | 2.5447941 |
| 789 | 0.065808 | 0.0342769 | 1 | 0.0483838 | 0.0282375 | 0.0358482 | 0.1734828 | 1 |
| 790 | 1.9891014 | 2.2745836 | 1.4672369 | 2.9550891 | 1.5527135 | 1.8383755 | 1.3422326 | 2.2253122 |
| 791 | 1.692688 | 1.4573486 | 2.9538241 | 1.7509478 | 1 | 2.1069962 | 1.8636954 | 1.8229341 |
| 792 | 1 | 0.266194 | 0.7647044 | 0.6193916 | 1 | 0.4706633 | 0.721897 | 0.7500653 |
| 793 | 0.3944615 | 0.5614104 | 0.1587597 | 0.1102818 | 0.3886233 | 0.1469925 | 0.2429009 | 0.3268429 |
| 794 | 2.7655894 | 1.6460724 | 4.3650477 | 1.8578164 | 2.3930477 | 1.227837 | 2.7605686 | 2.6591934 |
| 795 | 0.5770741 | 0.6106462 | 0.2500803 | 1 | 0.4185798 | 0.258027 | 0.5603151 | 0.2489251 |
| 796 | 0.7473291 | 0.4429882 | 0.3410965 | 1 | 1 | 1 | 1 | 1 |
| 797 | 1.7924543 | 1.6145032 | 2.4162996 | 1.4341235 | 3.5656843 | 1.6794908 | 2.3855241 | 2.624558 |
| 798 | 1.8184658 | 1 | 5.191014 | 2.6819489 | 2.5644435 | 2.5505363 | 3.2737428 | 3.003504 |
| 799 | 0.5705568 | 2.4390621 | 3.2001143 | 2.8039842 | 1 | 2.4319448 | 1 | 2.7372454 |
| 800 | 2.6726184 | 2.9758197 | 3.5056538 | 2.3346263 | 2.5713582 | 1.8573369 | 1.836945 | 1.96703 |
| 801 | 1 | 0.4543387 | 0.4813755 | 0.7302322 | 1 | 0.4532888 | 0.3167742 | 0.6248809 |
| 802 | 2.2796361 | 3.2159669 | 4.4804344 | 2.1686713 | 4.3250256 | 1.9860001 | 3.025531 | 4.8304775 |
| 803 | 0.7427389 | 0.469362 | 0.2849124 | 0.7580119 | 0.6317781 | 0.7424374 | 0.5018204 | 1 |
| 804 | 0.6833045 | 1 | 1.637534 | 1 | 0.7753536 | 0.6847629 | 1 | 0.5840995 |
| 805 | 1.7212364 | 3.240743 | 2.4426517 | 1.6779338 | 2.1671639 | 1.2510717 | 2.4730427 | 3.7718495 |
| 806 | 2.3796631 | 2.8748925 | 2.7124844 | 3.4512733 | 2.1303781 | 2.2688899 | 2.4847032 | 2.5316105 |
| 807 | 2.1787357 | 1.8920852 | 2.82197 | 1 | 2.0451222 | 1 | 2.2355694 | 2.9354718 |
| 808 | 1.7316273 | 2.074032 | 3.3022295 | 2.561256 | 1.5394867 | 2.0036493 | 2.2794833 | 2.6233825 |
| 809 | 1 | 2.4893059 | 3.3845669 | 1 | 1.9553037 | 1 | 2.0328108 | 2.3535657 |
| 810 | 1.8336435 | 1.8048248 | 3.2897571 | 2.0505165 | 2.8079635 | 1.6860655 | 2.4641317 | 3.094053 |
| 811 | 3.0266752 | 2.5664758 | 3.8206799 | 2.1117641 | 2.6104487 | 1.3410768 | 2.5371275 | 2.655438 |
| 812 | 2.2665302 | 2.4331697 | 3.2727607 | 4.4277855 | 1.7906134 | 1.7952175 | 2.495153 | 3.7709501 |
| 813 | 1 | 2.097977 | 2.2948126 | 5.1146335 | 1.7274779 | 2.1424596 | 1.5809475 | 3.082976 |
| 814 | 2.6492463 | 3.1779852 | 3.2932122 | 1 | 2.3984754 | 1.3695671 | 1.8779945 | 3.0042693 |
| 815 | 2.2933816 | 2.5035088 | 3.5813283 | 1.6101804 | 2.7789589 | 1 | 2.3477023 | 3.7529381 |
| 816 | 0.7727255 | 0.5061213 | 0.2978628 | 1 | 0.6310987 | 0.4427295 | 0.9308601 | 0.3549142 |
| 817 | 0.6628353 | 0.5875054 | 0.2978034 | 1 | 0.6185836 | 0.4420975 | 0.8719508 | 0.3279001 |
| 818 | 1 | 0.6567508 | 0.3227702 | 1 | 0.621843 | 0.453701 | 1 | 0.3121682 |
| 819 | 0.6753355 | 0.5374975 | 0.4313883 | 1 | 0.7344944 | 0.5205127 | 0.6297607 | 0.5004301 |
| 820 | 0.5038894 | 0.5952101 | 0.3229847 | 1 | 1 | 0.5661507 | 1 | 0.4327846 |
| 821 | 1.6532425 | 1.6217736 | 3.0975324 | 3.437005 | 2.8054558 | 1.3090003 | 1.4884605 | 3.0477805 |
| 822 | 2.0915947 | 1.5109863 | 4.427608 | 1 | 2.7380667 | 1.5606519 | 1 | 3.1786218 |
| 823 | 2.4128479 | 2.4132888 | 2.3899634 | 2.3372635 | 1.579207 | 2.2337288 | 1.8658302 | 3.1043253 |
| 824 | 0.2441954 | 2.6651297 | 1 | 0.6053421 | 0.4010021 | 1 | 0.7007664 | 1.465298 |
| 825 | 0.4167359 | 0.5227745 | 1 | 0.5326829 | 0.6543474 | 0.5348712 | 0.4453601 | 0.4528558 |
| 826 | 3.3367705 | 2.4448312 | 2.4599945 | 4.122002 | 1.5917512 | 2.0897728 | 2.1495818 | 1.9994642 |
| 827 | 0.6004307 | 0.672337 | 0.2908385 | 1 | 0.6761189 | 0.5527197 | 1 | 0.3201604 |
| 828 | 0.4160051 | 0.6530566 | 1 | 1 | 0.5254157 | 0.408063 | 0.5162683 | 0.4471279 |
| 829 | 1.9945697 | 2.226404 | 1.8676149 | 1.856668 | 1.7093143 | 1.5135437 | 1 | 2.0353224 |
| 830 | 1 | 0.081116 | 0.0543335 | 0.0985817 | 0.0428873 | 0.0654514 | 0.1078604 | 0.0527736 |
| 831 | 0.0745598 | 0.5786212 | 1 | 1 | 0.3811632 | 0.1177465 | 0.2507606 | 0.3003891 |
| 832 | 1.4926428 | 3.9145974 | 2.8616308 | 3.3557466 | 1.874489 | 1.9484344 | 1 | 3.5045653 |
| 833 | 1 | 0.0701301 | 0.0395298 | 0.0981231 | 0.0306118 | 0.0478502 | 0.0700306 | 0.0424145 |

Table 4

| SEQ ID | Patient ID | | | | | | | |
|--------|------------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|
| | 10 | 15 | 52 | 121 | 125 | 128 | 130 | 133 |
| 834 | 0.6185934 | 0.6197824 | 0.2941866 | 1 | 0.7228671 | 0.4865195 | 0.8332184 | 0.3252887 |
| 835 | 0.299763 | 1 | 0.5447541 | 0.5626709 | 0.1753226 | 0.5507961 | 1 | 1 |
| 836 | 0.7750493 | 0.5483066 | 0.2948879 | 1 | 0.6791628 | 0.458359 | 1 | 0.3455097 |
| 837 | 1 | 0.6537644 | 0.3275119 | 1 | 0.7159957 | 0.4619932 | 1 | 0.3424486 |
| 838 | 1.4538356 | 2.8513925 | 2.9094243 | 3.6604907 | 2.0421113 | 3.5319431 | 2.6542419 | 3.210267 |
| 839 | 1 | 2.8075827 | 3.2453239 | 2.5432767 | 1.5901161 | 1.7474223 | 1 | 2.7533481 |
| 840 | 0.9605168 | 1.4328245 | 1.8969914 | 1.7766395 | 1 | 2.1406734 | 1 | 2.2062982 |
| 841 | 2.3579565 | 2.0130703 | 2.2103708 | 2.5779203 | 1.2372604 | 1.2203349 | 1.3223998 | 2.2668273 |
| 842 | 1.7148775 | 2.2746157 | 1.8272381 | 2.6301311 | 1.4683729 | 1.9312935 | 1.5819805 | 2.5519263 |
| 843 | 0.3648474 | 0.8886732 | 0.639716 | 0.5035389 | 0.6574853 | 0.4821638 | 0.7546179 | 0.4302126 |
| 844 | 2.0234582 | 3.675871 | 2.3923339 | 4.9208277 | 2.7978862 | 1.8679993 | 3.5524614 | 3.2702517 |
| 845 | 2.894463 | 3.2056136 | 3.94891 | 2.3557127 | 2.3729506 | 1.7788942 | 2.3673689 | 2.4426236 |
| 846 | 0.2212253 | 0.2510742 | 1 | 0.2869051 | 0.3993528 | 0.2783419 | 0.2280098 | 0.2442229 |
| 847 | 1.4727826 | 1.7621677 | 3.8547323 | 1.7021041 | 1.3761242 | 1.4069198 | 1 | 1.7466731 |
| 848 | 1 | 3.9746261 | 0.2788555 | 2.0957932 | 1.2556608 | 1 | 0.4513807 | 1 |
| 849 | 0.6682373 | 0.6695168 | 0.2916365 | 1 | 0.6495363 | 0.4649955 | 1 | 0.3278765 |
| 850 | 1.6866038 | 1.8701884 | 4.0688146 | 1.7751831 | 1.9281937 | 1.7163695 | 2.3834931 | 2.5684314 |
| 851 | 0.266558 | 0.2913614 | 0.1775767 | 0.276907 | 0.2440895 | 0.2086723 | 0.4191392 | 0.2456746 |
| 852 | 0.6935523 | 1.363606 | 2.8217161 | 2.7030482 | 1.2538477 | 1 | 1 | 3.1169802 |
| 853 | 1.7036769 | 1.818438 | 2.6428691 | 2.5172863 | 2.420215 | 2.2361196 | 2.5261102 | 2.5347585 |
| 854 | 1.42537 | 1.9807665 | 3.0914246 | 3.775215 | 1.7526215 | 2.5386236 | 1.925131 | 3.784749 |
| 855 | 0.7295529 | 1 | 1 | 0.6214918 | 0.4832196 | 0.5229035 | 0.6797734 | 0.6078709 |
| 856 | 1.6404267 | 1.2737344 | 3.0908152 | 2.201227 | 1.6156366 | 1.900433 | 2.0364151 | 2.0625732 |
| 857 | 0.5612511 | 0.2774105 | 0.2240745 | 0.650941 | 0.5228334 | 0.2565431 | 0.3919822 | 0.2853041 |
| 858 | 2.1407056 | 0.4214023 | 1 | 0.6716819 | 0.1659043 | 0.0913723 | 0.1024399 | 0.394378 |
| 859 | 0.65051 | 0.588063 | 0.6924982 | 0.6696915 | 0.6140069 | 0.5498618 | 1 | 0.3611627 |
| 860 | 0.1972375 | 1 | 0.5616191 | 0.4390352 | 0.1405961 | 0.5302064 | 1 | 1 |
| 861 | 1.6392743 | 2.6035139 | 2.5474303 | 2.8829892 | 2.320569 | 2.0036425 | 1.8221864 | 2.3078454 |
| 862 | 1.6392743 | 2.6035139 | 2.5474303 | 2.8829892 | 2.320569 | 2.0036425 | 1.8221864 | 2.3078454 |
| 863 | 0.6915081 | 0.576053 | 0.2899296 | 1 | 0.6545078 | 0.4342175 | 1 | 0.3203577 |
| 864 | 0.4359209 | 1.2664372 | 1 | 0.6012883 | 0.3581683 | 0.8906322 | 0.4837882 | 0.6251412 |
| 865 | 2.4383331 | 0.7602462 | 1 | 0.55647 | 0.320989 | 0.3369438 | 0.2971658 | 0.2723652 |
| 866 | 2.3886827 | 1.9821927 | 3.4491607 | 3.409069 | 3.8820378 | 1.3334991 | 2.1904732 | 3.4378823 |
| 867 | 2.0879528 | 2.0127701 | 3.0645348 | 2.8675403 | 3.0554556 | 1.8745877 | 2.1475207 | 3.8916454 |
| 868 | 0.6483557 | 0.512389 | 0.3184805 | 1 | 0.7192987 | 0.479725 | 1 | 0.3142432 |
| 869 | 1.8802443 | 1.9022294 | 3.3935411 | 5.2360064 | 1.4161563 | 1.9358209 | 2.0319809 | 2.9373653 |
| 870 | 2.6862555 | 1.4563192 | 3.6197772 | 1.5657217 | 2.1498462 | 1.7430117 | 2.5733483 | 3.585347 |
| 871 | 2.1114927 | 3.0746827 | 3.8188187 | 2.0354108 | 3.5031161 | 1.8423326 | 2.9051455 | 3.8513768 |
| 872 | 2.0540262 | 1.6373062 | 4.1844692 | 1.7604156 | 2.2408213 | 1.8173736 | 2.5318215 | 2.9165052 |
| 873 | 2.1309311 | 2.0782516 | 2.8696184 | 2.9306277 | 2.9548638 | 1.8494913 | 2.1148719 | 3.6426808 |
| 874 | 2.0722671 | 1.8696897 | 3.5454907 | 2.1793307 | 2.1970319 | 1.6307681 | 2.2587926 | 2.7375609 |
| 875 | 1.3914862 | 1.257108 | 2.0153819 | 1.6671782 | 1.6774749 | 1.5821484 | 1.6639606 | 2.1409801 |
| 876 | 2.2031983 | 1.9322545 | 2.8536877 | 2.1545701 | 2.286196 | 1.3610688 | 2.0989661 | 1.8854672 |
| 877 | 0.4168184 | 0.057793 | 0.8361016 | 0.0862004 | 0.4874539 | 0.5353796 | 0.0984446 | 0.0753695 |
| 878 | 1 | 0.1825901 | 1 | 0.5389106 | 1 | 0.3930038 | 0.5905041 | 0.7529608 |
| 879 | 1.6299899 | 2.3037722 | 2.7116634 | 2.2253215 | 1 | 1.8714344 | 1.8946361 | 2.6219703 |
| 880 | 0.5680978 | 0.6679459 | 0.360136 | 0.8125161 | 0.653099 | 0.4962888 | 1 | 0.4584811 |
| 881 | 0.2363831 | 0.6768622 | 0.1088357 | 1 | 0.277555 | 0.1375324 | 0.2365987 | 0.29889 |
| 882 | 0.4040364 | 0.319258 | 0.3534182 | 0.3916115 | 0.310291 | 0.3197479 | 0.5735338 | 0.4159403 |

Table 4

| SEQ ID NO | Patient ID | | | | | | | |
|--------------|------------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|
| | 10 | 15 | 52 | 121 | 125 | 128 | 130 | 133 |
| 883 | 0.1316716 | 0.6949631 | 0.0486907 | 1 | 0.1740798 | 0.0459953 | 0.1488488 | 0.2314181 |
| 884 | 3.0282676 | 2.144977 | 6.2725185 | 2.2905757 | 3.1945477 | 2.1928723 | 2.8359864 | 5.1309534 |
| 885 | 1.7907441 | 1 | 2.8477268 | 2.5269187 | 1.8609351 | 1.9201708 | 1.6943294 | 3.4858906 |
| 886 | 2.4028425 | 2.0837312 | 3.9538894 | 3.0807273 | 2.7320434 | 2.0416547 | 3.0386667 | 5.4560764 |
| 887 | 1.9350263 | 2.030635 | 1.5138839 | 4.0824229 | 1.9521944 | 1.5881048 | 1 | 2.678452 |
| 888 | 2.1561555 | 1.7813677 | 2.6710098 | 3.8009512 | 3.444038 | 1.2120702 | 2.4091965 | 2.9476534 |
| 889 | 0.5486366 | 0.5222491 | 1 | 0.4201858 | 0.5214601 | 0.7048511 | 0.640962 | 1 |
| 890 | 2.1755515 | 2.3254278 | 3.1824135 | 4.0268089 | 1.6034365 | 1.7706088 | 2.7569156 | 4.1807049 |
| 891 | 0.6186422 | 0.5681607 | 0.2816634 | 1 | 0.6948075 | 0.5462687 | 1 | 0.3293439 |
| 892 | 0.6421543 | 0.5422747 | 0.289508 | 1 | 0.7356023 | 0.4866294 | 0.8845726 | 0.3464565 |
| 893 | 1.5007115 | 1.6074044 | 1.526858 | 1 | 1.2964315 | 1.3073172 | 2.6342617 | 2.1810514 |
| 894 | 2.2204232 | 1 | 2.6324409 | 1.4510418 | 2.4379481 | 2.5122562 | 2.4415669 | 2.4581661 |
| 895 | 1 | 0.6742565 | 3.2669639 | 9.3758838 | 1.2178899 | 1.2218738 | 1.268043 | 4.2649108 |
| 896 | 3.3206006 | 2.3683852 | 2.3974555 | 1.6416062 | 2.4095135 | 1.416531 | 2.7958048 | 2.3749071 |
| 897 | 1.5228669 | 1.7856302 | 2.072734 | 1.7603823 | 1.739718 | 1.5522498 | 2.0016975 | 3.9205371 |
| 898 | 1.5199714 | 1.5560615 | 3.2173528 | 2.3797961 | 1.6556581 | 1.7136695 | 1.9321896 | 2.2260459 |
| 899 | 2.0955035 | 2.0713619 | 2.8397319 | 3.0271433 | 2.4036031 | 1.6375489 | 1.8798072 | 2.5086281 |
| 900 | 1.6063656 | 1.8601728 | 2.4536422 | 1.7274294 | 1.9408073 | 1.6365183 | 1.8371711 | 3.8818465 |
| 901 | 2.1165135 | 1.5101124 | 3.5221926 | 1 | 2.3380948 | 2.0059989 | 2.1227394 | 3.7751158 |
| 902 | 1.7297886 | 2.2027485 | 2.8165203 | 2.328205 | 1.9372167 | 1.7117253 | 1.7911463 | 4.2818655 |
| 903 | 0.6126849 | 0.5585794 | 0.2744259 | 1 | 0.6695661 | 0.5535029 | 1 | 0.2994739 |
| 904 | 1.6331657 | 1.9807451 | 3.3701978 | 2.0281399 | 2.3131309 | 2.095949 | 2.1631286 | 2.9711566 |
| 905 | 1 | 0.4092743 | 0.4813423 | 0.6589754 | 1 | 0.3782468 | 0.3474223 | 0.5526673 |
| 906 | 2.7153171 | 3.3162722 | 3.0211311 | 2.4075476 | 2.6686282 | 1 | 2.8687707 | 3.4021818 |
| 907 | 0.0527969 | 0.2759628 | 0.3741559 | 0.2970418 | 0.3657569 | 0.7887212 | 0.506064 | 1 |
| 908 | 0.5510281 | 1 | 1 | 1 | 0.6199085 | 0.5185479 | 0.8727068 | 0.491081 |
| 909 | 0.4710536 | 0.5945238 | 0.3983095 | 1 | 0.5350304 | 0.3885176 | 0.5085316 | 0.4416368 |
| 910 | 0.1602014 | 0.4445001 | 0.2088396 | 0.5725136 | 0.2440628 | 0.2323535 | 0.3743605 | 0.3555374 |
| 911 | 0.1786916 | 0.7464025 | 0.1509195 | 1 | 0.3373579 | 0.3116618 | 0.3887774 | 0.5716497 |
| 912 | 0.8934726 | 0.4108613 | 0.4915708 | 0.7495605 | 1 | 0.6175322 | 0.4950158 | 0.6433031 |
| 913 | 0.5949486 | 0.7054236 | 0.2689106 | 1 | 0.7893934 | 0.6432538 | 1 | 0.4766272 |
| 914 | 0.8019742 | 0.6380065 | 0.3252106 | 1 | 0.7117492 | 0.488608 | 1 | 0.3687052 |
| 915 | 0.4722129 | 0.0447696 | 1 | 0.419153 | 0.0851143 | 0.0574752 | 0.1572536 | 0.4217865 |
| 916 | 1 | 0.4481514 | 0.3048446 | 1 | 1 | 1 | 0.588518 | 1 |
| 917 | 1.8388375 | 2.0749488 | 1.5819747 | 2.5804923 | 1.8209586 | 1.5245908 | 1 | 2.5832007 |
| 918 | 0.7254824 | 0.6180184 | 0.2941949 | 1 | 0.6444687 | 0.4409158 | 1 | 0.3255175 |
| 919 | 2.1865708 | 3.1936733 | 2.8738264 | 3.8020377 | 2.4141974 | 2.4337928 | 2.6279253 | 4.3110255 |
| 920 | 1.7565344 | 3.21883 | 5.6702206 | 5.6034123 | 2.807742 | 1.7384431 | 2.4552847 | 6.732931 |
| 921 | 0.5982921 | 0.6773555 | 0.5505745 | 1 | 0.4991868 | 0.4813669 | 0.7400864 | 0.3557899 |
| 922 | 1.560408 | 1.6711917 | 3.5192278 | 2.5314529 | 2.3667458 | 1.9225616 | 2.0343341 | 2.5450623 |
| 923 | 1.504084 | 2.4353572 | 1.9840749 | 3.6747929 | 1.9692554 | 1.8721351 | 2.1119801 | 2.7729222 |
| 924 | 0.4509667 | 0.0427697 | 1 | 0.4153425 | 0.0600127 | 0.0235095 | 0.1219921 | 0.4113407 |
| 925 | 1.4328211 | 2.0808895 | 2.5254768 | 1.7518373 | 1.9529083 | 1.6518387 | 2.1009844 | 2.6793435 |
| 926 | 0.8159115 | 0.6498343 | 0.2960993 | 1 | 0.665739 | 0.4977658 | 1 | 0.3220776 |
| 927 | 1.2330082 | 0.8009839 | 2.8871894 | 2.7124185 | 0.6890476 | 1.4006062 | 1.3603106 | 2.6395089 |
| 928 | 0.5674332 | 0.4797207 | 0.6485278 | 1 | 0.6143531 | 0.3081581 | 0.3379659 | 0.2272287 |
| 929 | 2.1670332 | 0.7177929 | 1 | 0.3931725 | 0.3657895 | 0.3363461 | 0.1859726 | 0.3337306 |
| 930 | 0.5007507 | 1 | 1 | 0.224756 | 0.140628 | 0.1550855 | 0.2868679 | 0.336342 |
| 931 | 2.5788983 | 1.5820761 | 3.6691224 | 1.8772561 | 2.4041441 | 2.2352402 | 2.6268465 | 5.4215909 |

Table 4

| SEQ ID NO | Patient ID | | | | | | | |
|--------------|------------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|
| | 10 | 15 | 52 | 121 | 125 | 128 | 130 | 133 |
| 932 | 4.9421257 | 6.3649564 | 5.6892534 | 14.874106 | 2.518665 | 2.1476671 | 4.3811606 | 4.7868796 |
| 933 | 1.9758098 | 1.4764306 | 1.8662254 | 2.7516964 | 2.3212246 | 2.1422878 | 2.1388557 | 2.9926794 |
| 934 | 1.3309122 | 2.1213483 | 3.2930393 | 1.9230844 | 1.2574792 | 1.3702816 | 1.946844 | 3.0002377 |
| 935 | 1 | 1.7298371 | 6.3901202 | 1 | 2.4332272 | 1.5992412 | 1 | 2.3739209 |
| 936 | 1 | 0.6956172 | 1.6311876 | 0.3229072 | 0.7294978 | 0.6301251 | 0.4638396 | 0.818918 |
| 937 | 0.3046809 | 0.5928831 | 0.6404346 | 0.437486 | 0.3237395 | 0.7178218 | 0.5706694 | 0.8015135 |
| 938 | 2.423277 | 3.5287641 | 3.7242497 | 2.2302252 | 2.3159397 | 1.6295383 | 2.291553 | 3.9770189 |
| 939 | 2.5007657 | 1.4564103 | 4.0730428 | 1 | 1.488966 | 1 | 2.2221499 | 1.7040219 |
| 940 | 0.5798724 | 0.5678443 | 0.2926395 | 1 | 0.6251369 | 0.5102969 | 1 | 0.3126653 |
| 941 | 1.647501 | 3.7686164 | 0.5077535 | 0.2863211 | 1.711204 | 1 | 2.7526801 | 2.0705653 |
| 942 | 0.185334 | 0.6581984 | 1 | 0.0688048 | 0.1720956 | 0.053099 | 0.1268612 | 0.209122 |
| 943 | 0.39676 | 0.6503812 | 0.3358934 | 0.2502921 | 0.4010488 | 0.3197136 | 0.3576158 | 0.4849981 |
| 944 | 2.0183023 | 1.9201855 | 1.8484582 | 2.3090366 | 2.2666916 | 1.4833358 | 2.0851889 | 2.9964349 |
| 945 | 2.3584074 | 2.570942 | 6.9112453 | 2.1051753 | 3.7045717 | 1.896043 | 3.1343493 | 3.6862946 |
| 946 | 0.5672953 | 0.0530372 | 1 | 0.4173681 | 0.0879548 | 0.0489906 | 0.1480838 | 0.4487926 |
| 947 | 2.5213602 | 2.8571348 | 2.8256574 | 3.1849462 | 2.381416 | 1.8792319 | 1.9068148 | 3.772386 |
| 948 | 2.512994 | 1 | 1 | 5.1174445 | 3.3167662 | 3.7653889 | 3.9129056 | 2.1368302 |
| 949 | 1.6700634 | 1.6023806 | 4.1493079 | 3.3248314 | 1.6390164 | 2.4159924 | 2.2293941 | 3.1911031 |
| 950 | 1.9744543 | 2.7303646 | 2.476118 | 2.6258292 | 1.3700519 | 2.4294647 | 1.5978093 | 2.7671943 |
| 951 | 0.5841764 | 0.4949745 | 0.2809404 | 1 | 0.6667156 | 0.427739 | 1 | 0.3202551 |
| 952 | 1.2511983 | 1.9562585 | 2.184044 | 3.6046573 | 1 | 1 | 1.8713647 | 2.4847541 |
| 953 | 1.8421331 | 1.7351826 | 1.8652263 | 3.0410837 | 2.098236 | 1.7901749 | 2.2292277 | 2.4748921 |
| 954 | 0.5680604 | 0.3570413 | 0.2281215 | 1 | 1 | 0.5451901 | 1.2894892 | 0.7696473 |
| 955 | 0.2567999 | 0.6279589 | 1 | 0.3636204 | 0.3357418 | 0.4936438 | 0.5080586 | 0.5308762 |
| 956 | 1.652072 | 1 | 3.9107408 | 2.187163 | 1.5657564 | 1.1556323 | 1.6219059 | 2.4794444 |
| 957 | 1 | 2.9602764 | 3.7640382 | 1.5609184 | 3.1052014 | 1.6540165 | 1.9033308 | 3.9383913 |
| 958 | 1.9254033 | 1.8681509 | 3.3004916 | 1.7423634 | 2.3824253 | 1.8147149 | 2.7232262 | 3.2629538 |
| 959 | 1.8827864 | 1.6759957 | 2.3509012 | 2.1976422 | 2.2038318 | 1.7128588 | 2.424847 | 2.6048577 |
| 960 | 2.0606935 | 1.4794439 | 1.2776595 | 3.1668561 | 2.4046854 | 1.3341037 | 2.0489439 | 1.9804975 |
| 961 | 1.8687677 | 1.5666561 | 4.5434065 | 2.1128662 | 3.2290264 | 1.820843 | 3.4865138 | 3.2166813 |
| 962 | 1.7961459 | 1.5158064 | 3.0490393 | 2.4749323 | 2.0238471 | 1.6704291 | 1.9395521 | 2.5101902 |
| 963 | 1.9227449 | 1.5860222 | 3.1559881 | 2.6869795 | 2.1844055 | 1.5083705 | 2.3266667 | 3.1792529 |
| 964 | 2.0309787 | 0.5222223 | 19.554924 | 0.7039905 | 1.9036896 | 1.2518824 | 2.8433673 | 1 |
| 965 | 1.7929754 | 1.7296923 | 2.0058417 | 1 | 2.5351049 | 1.661285 | 1.9623669 | 2.9760797 |
| 966 | 2.0551018 | 2.2707017 | 2.4341189 | 2.1597676 | 2.452841 | 1.1386014 | 2.7709859 | 1.9413177 |
| 967 | 1 | 1 | 1 | 0.4065383 | 1 | 1 | 1 | 1 |
| 968 | 1.9572221 | 1.7161864 | 3.7253558 | 1 | 3.0201189 | 1.39702 | 1 | 3.1685546 |
| 969 | 0.611314 | 0.5269459 | 0.2949004 | 1 | 0.736683 | 0.5441664 | 1 | 0.3157107 |
| 970 | 2.6126895 | 3.0284387 | 3.164109 | 2.0293333 | 1.5897611 | 2.7322984 | 1.5628277 | 4.274039 |
| 971 | 1.5464336 | 2.0135528 | 1 | 1.9698718 | 1.1304908 | 1 | 1.3118846 | 3.2219989 |
| 972 | 0.3008986 | 0.2774963 | 0.3972473 | 0.3317239 | 0.1975385 | 0.3640188 | 0.3398184 | 0.5598941 |
| 973 | 1 | 0.3922618 | 0.5350999 | 0.7751832 | 1 | 0.7033878 | 0.4003216 | 0.6665065 |
| 974 | 0.6614997 | 0.6986251 | 0.3115908 | 1 | 0.690415 | 1 | 1 | 0.3436162 |
| 975 | 1 | 0.395586 | 0.6248831 | 1 | 1 | 1 | 0.3890036 | 0.6233582 |
| 976 | 1 | 0.5175255 | 0.627685 | 1 | 0.8676613 | 0.4721747 | 0.6043836 | 0.6279973 |
| 977 | 2.4002373 | 3.0260474 | 2.6654471 | 1.9285013 | 3.3357227 | 1.4460999 | 2.2704134 | 3.8629193 |
| 978 | 2.3426019 | 2.281484 | 3.4819077 | 1.4993382 | 1.9286812 | 1.9277691 | 2.1667386 | 3.9123714 |
| 979 | 1.906526 | 1 | 1.8613511 | 2.823712 | 1.7003074 | 1 | 1.3480697 | 2.8843866 |
| 980 | 1.3155207 | 0.7446761 | 2.0362569 | 4.5663235 | 1.8140308 | 1.4895121 | 2.2092174 | 4.5408184 |

Table 4

| SEQ ID NO | Patient ID | | | | | | | |
|--------------|------------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|
| | 10 | 15 | 52 | 121 | 125 | 128 | 130 | 133 |
| 981 | 1 | 0.4872108 | 1.8693406 | 0.7156674 | 0.498425 | 0.726911 | 0.3620425 | 0.7811662 |
| 982 | 1 | 2.6978677 | 1.9196963 | 2.1913323 | 1.0971054 | 1 | 1.3915835 | 2.3006658 |
| 983 | 1.6710331 | 1.3953361 | 2.7456171 | 2.5728627 | 1.8445445 | 1 | 1 | 2.7785475 |
| 984 | 3.502878 | 2.6661269 | 4.0105289 | 2.1632801 | 1.7840035 | 1.8109844 | 3.8743231 | 2.134487 |
| 985 | 0.4807719 | 0.0460135 | 1 | 0.4612057 | 0.1164957 | 1 | 0.1606215 | 0.493511 |
| 986 | 1.7934968 | 2.9359185 | 2.2040783 | 2.2542526 | 2.2937571 | 1 | 2.4449653 | 3.4282254 |
| 987 | 0.3168646 | 0.2285607 | 0.4852154 | 0.2073859 | 0.2933221 | 1 | 0.2074119 | 0.328697 |
| 988 | 0.5915895 | 0.6595281 | 0.30202 | 1 | 0.6343974 | 0.5362521 | 1 | 0.3493125 |
| 989 | 0.7999457 | 0.4533147 | 0.2035669 | 1 | 0.5394186 | 0.7672384 | 0.5706513 | 1 |
| 990 | 1.4580832 | 1.8137573 | 2.4381883 | 2.3342752 | 1.4360732 | 1 | 2.1231419 | 1.7111225 |
| 991 | 1 | 1.3521482 | 6.2882423 | 0.6035372 | 1.2870115 | 1 | 1.6339159 | 0.5842178 |
| 992 | 0.6994915 | 0.6418723 | 0.3249461 | 1 | 0.7758323 | 0.4389784 | 1 | 0.3236082 |
| 993 | 0.268848 | 0.7003891 | 1 | 0.2068799 | 0.3014536 | 1 | 1 | 1 |
| 994 | 1.9293186 | 2.1594105 | 1 | 1 | 2.0769778 | 1 | 3.1569924 | 1 |
| 995 | 0.5745702 | 0.5163835 | 0.2896337 | 0.8305257 | 0.7796551 | 1.3802432 | 0.7854078 | 0.494363 |
| 996 | 2.3438738 | 2.3281515 | 3.2078077 | 1.3888178 | 2.7028674 | 1 | 2.6490618 | 3.1277417 |
| 997 | 2.2120039 | 2.471693 | 1 | 1 | 2.9150247 | 1 | 1 | 1 |
| 998 | 1.9350263 | 1.2769889 | 3.91954 | 2.7503146 | 0.7497982 | 1.5865934 | 1.8048588 | 4.2087525 |
| 999 | 0.5072733 | 0.4880526 | 1 | 1 | 0.4275527 | 0.5201142 | 0.6186919 | 0.861585 |
| 1000 | 1 | 0.4688848 | 0.3285311 | 1 | 1 | 1 | 1 | 1 |
| 1001 | 0.103764 | 1 | 0.0651199 | 1 | 0.2531524 | 0.223862 | 0.2033665 | 0.4923512 |
| 1002 | 0.4193572 | 0.6722781 | 0.2800021 | 1 | 0.4661678 | 0.3547717 | 0.6076468 | 0.5786162 |
| 1003 | 2.3645434 | 2.562846 | 3.0742997 | 1.7331206 | 3.0495234 | 2.0186399 | 1.9713054 | 3.5339856 |
| 1004 | 1.2995806 | 1.4497887 | 3.0619911 | 2.1947931 | 1 | 1.4221577 | 2.0103219 | 2.2485628 |
| 1005 | 0.7553779 | 0.6790444 | 0.3300926 | 1 | 0.6792406 | 0.499765 | 1 | 0.3286812 |
| 1006 | 1 | 1 | 0.3078525 | 0.7138348 | 1.6629275 | 1 | 1 | 1.259395 |
| 1007 | 0.3519126 | 0.0614978 | 0.3528634 | 0.186879 | 0.0926434 | 0.1255922 | 0.4313343 | 0.2848702 |
| 1008 | 0.7072093 | 0.6217876 | 0.2900637 | 1 | 0.6854392 | 0.4488301 | 1 | 0.3316635 |
| 1009 | 0.6387859 | 0.6168496 | 0.2931703 | 1 | 0.6693269 | 0.4772311 | 1 | 0.3498096 |
| 1010 | 1.9244163 | 2.2722352 | 1.8025535 | 4.121637 | 1.4600627 | 1.9163579 | 1.8563578 | 2.7026415 |
| 1011 | 0.6954629 | 0.6797522 | 0.3185388 | 1 | 0.6944687 | 0.4823699 | 0.8656904 | 0.3873799 |
| 1012 | 2.1102025 | 2.1014138 | 3.6095683 | 2.0163256 | 1.5013144 | 1.4852595 | 1.806533 | 2.4757284 |
| 1013 | 1.6281764 | 2.4474477 | 2.5226323 | 3.0055488 | 1.3879086 | 3.0845969 | 2.4370504 | 3.0426759 |
| 1014 | 0.5437337 | 0.5748627 | 0.3452047 | 0.7208366 | 0.67187 | 0.4994696 | 1 | 0.4353172 |
| 1015 | 2.0171235 | 1.7626074 | 3.2006043 | 4.4053701 | 3.2879727 | 1.493428 | 1.6740974 | 3.2317899 |
| 1016 | 0.5241812 | 1 | 0.2619576 | 1 | 0.7384912 | 0.4943789 | 1 | 0.3659438 |
| 1017 | 2.4730447 | 2.2466227 | 2.9171383 | 1 | 2.5333011 | 2.0058271 | 1 | 2.7836442 |
| 1018 | 1.0948104 | 0.1600016 | 0.7582599 | 0.432831 | 1 | 0.4267497 | 0.5920339 | 0.7670122 |
| 1019 | 1.7602589 | 2.8350288 | 0.5821009 | 4.2985967 | 1.5283618 | 2.851419 | 0.8833079 | 2.0370187 |
| 1020 | 2.6729493 | 6.892165 | 1.4122242 | 1.5323531 | 2.0730674 | 3.3082597 | 3.0132176 | 4.0493035 |
| 1021 | 2.2629066 | 2.7174645 | 2.5647244 | 2.3824754 | 2.5893742 | 2.3684582 | 2.6464794 | 4.1581249 |
| 1022 | 1 | 1 | 3.0823081 | 3.3501926 | 1.6739782 | 1.9592754 | 1.6919614 | 1 |
| 1023 | 0.7220544 | 0.6122279 | 0.2856599 | 1 | 0.7239303 | 0.4820608 | 0.8646794 | 0.4005871 |
| 1024 | 0.5930483 | 0.4448272 | 0.4788065 | 0.7233734 | 0.5189417 | 0.5838825 | 0.6164908 | 0.7164714 |
| 1025 | 1 | 3.1271516 | 3.0868596 | 3.6322178 | 1 | 1.5127536 | 1.6556575 | 3.0327192 |
| 1026 | 2.1685027 | 3.5833883 | 2.1725435 | 2.0648402 | 2.1764821 | 1 | 2.2938413 | 2.9858155 |
| 1027 | 3.3994384 | 2.3457377 | 4.9704874 | 2.344207 | 1.6692429 | 1.7387316 | 2.6352691 | 2.8398498 |
| 1028 | 2.0794041 | 1.7228831 | 1.9212254 | 3.1291807 | 2.8076682 | 2.2825065 | 2.9844084 | 2.2848551 |
| 1029 | 1.5717993 | 2.3269559 | 2.3517828 | 3.9981065 | 1 | 1.8283245 | 1.7812811 | 2.5256697 |

Table 4

| SEQ ID NO | Patient ID | | | | | | | |
|--------------|------------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|
| | 10 | 15 | 52 | 121 | 125 | 128 | 130 | 133 |
| 1030 | 0.8559427 | 0.4422483 | 0.4130179 | 1 | 0.458051 | 0.3693225 | 0.315297 | 0.400169 |
| 1031 | 2.6632202 | 3.1530697 | 4.056445 | 3.3744755 | 3.2497568 | 2.204682 | 2.4207191 | 3.1301401 |
| 1032 | 0.5604896 | 0.853324 | 0.327218 | 0.2092365 | 0.4675801 | 0.4816142 | 0.5996143 | 0.4873571 |
| 1033 | 2.0300714 | 2.0291016 | 2.3594808 | 3.7666627 | 3.5136031 | 1.2462626 | 2.3151821 | 2.5432083 |
| 1034 | 2.2220233 | 2.059443 | 3.6256368 | 2.4574268 | 1.919013 | 2.1217256 | 2.1463373 | 3.7762835 |
| 1035 | 1.5456308 | 1.483567 | 2.334536 | 2.4216989 | 1.9338495 | 1.7417201 | 1.9822537 | 2.0539183 |
| 1036 | 0.5095396 | 0.7229883 | 0.3625637 | 2.4660179 | 1 | 0.3791949 | 0.4990556 | 1.1673311 |
| 1037 | 1 | 0.449465 | 0.5530898 | 0.7379233 | 1 | 0.8892444 | 0.4390415 | 1 |
| 1038 | 1.2203383 | 1.7766119 | 1 | 2.562948 | 1.7282606 | 2.9112369 | 1.6357954 | 2.0078114 |
| 1039 | 2.1059304 | 3.8481293 | 1 | 4.4290492 | 2.9642948 | 3.2641193 | 2.3282993 | 6.207049 |
| 1040 | 2.1894542 | 1.4399126 | 4.0948508 | 3.4580666 | 2.1514918 | 3.8281884 | 1.6582318 | 3.6064202 |
| 1041 | 1.8334877 | 1 | 1 | 1 | 2.2544433 | 1 | 1 | 1 |
| 1042 | 1.9332065 | 1.7176716 | 3.3776399 | 2.7942233 | 3.0017005 | 1.4288216 | 1.6596757 | 3.3732111 |
| 1043 | 2.9099743 | 2.6356568 | 4.2974467 | 1.8301734 | 3.6748729 | 2.4326799 | 2.7088163 | 4.7312183 |
| 1044 | 1.8388375 | 1.3929501 | 2.4229278 | 2.1894773 | 1.939292 | 2.0100729 | 1.7607652 | 3.1986772 |
| 1045 | 3.061773 | 3.1749237 | 14.443261 | 1 | 3.2733613 | 3.3738897 | 3.1191801 | 5.9678597 |
| 1046 | 0.340201 | 0.1952597 | 0.3301621 | 0.3161018 | 0.1352791 | 0.1967595 | 0.6270322 | 0.2954186 |
| 1047 | 0.5048765 | 0.0425391 | 1 | 0.4675161 | 0.0958619 | 0.0572966 | 0.1637054 | 0.4365559 |
| 1048 | 0.711569 | 0.0379818 | 0.3716701 | 0.48003 | 0.1109732 | 0.0991973 | 0.0840915 | 0.1281115 |
| 1049 | 1 | 2.3161254 | 1.8001217 | 2.7490154 | 1.1867917 | 1.2758246 | 1.2167378 | 2.254125 |
| 1050 | 1 | 1.4422449 | 5.5863745 | 1 | 2.8221346 | 1.7609426 | 1 | 3.4033021 |
| 1051 | 0.1613758 | 0.1852763 | 0.5705662 | 0.3678408 | 0.0855494 | 0.2621559 | 0.3828771 | 0.4186938 |
| 1052 | 0.6483557 | 0.5847817 | 0.3040775 | 1 | 0.754667 | 0.5402368 | 0.8346079 | 0.4037272 |
| 1053 | 1.082973 | 0.5140029 | 0.7156608 | 1 | 1 | 0.6122147 | 0.5053332 | 0.7225937 |
| 1054 | 0.7306086 | 0.3283513 | 0.6051591 | 0.6914849 | 0.8488969 | 0.5171051 | 0.5878268 | 0.6592401 |
| 1055 | 0.859804 | 0.6594906 | 0.5397886 | 1 | 0.7908605 | 0.6588008 | 0.6552418 | 0.7247555 |
| 1056 | 1 | 0.3912699 | 0.5664689 | 0.7691512 | 1 | 1 | 0.4512443 | 1 |
| 1057 | 1 | 0.4850608 | 0.5754139 | 1 | 0.8209128 | 0.6258313 | 0.4734538 | 0.7140808 |
| 1058 | 1 | 0.4174722 | 0.5741233 | 1 | 1 | 1 | 0.5557615 | 1 |
| 1059 | 2.5020702 | 2.101328 | 5.6691954 | 1.8307852 | 2.9540465 | 2.7744808 | 3.208207 | 4.1390478 |
| 1060 | 0.4027153 | 0.4994568 | 0.5646532 | 0.4072727 | 0.6203297 | 0.3754301 | 0.615432 | 0.374512 |
| 1061 | 1 | 0.8088547 | 2.6784249 | 2.3505984 | 0.6615864 | 1.4045221 | 1.3991468 | 2.7678728 |
| 1062 | 1.9886891 | 3.1132543 | 1.9879744 | 5.9530658 | 2.0138872 | 1.1671054 | 1.4466617 | 2.7498687 |
| 1063 | 1.6105607 | 2.5888981 | 2.4774875 | 2.0218862 | 1.3144122 | 1.3458446 | 1.6176885 | 2.698247 |
| 1064 | 2.939498 | 2.8959476 | 3.3807353 | 3.2947136 | 2.0995971 | 2.4712829 | 2.4147162 | 4.6541763 |
| 1065 | 2.4458622 | 3.169042 | 1.7747521 | 3.7640741 | 1.8544084 | 5.1656515 | 3.4603875 | 5.2602562 |
| 1066 | 0.6711723 | 0.6574746 | 0.2973403 | 1 | 0.6834129 | 0.4850562 | 1 | 0.3494782 |
| 1067 | 4.0523297 | 5.0652932 | 19.433728 | 1 | 4.7798839 | 4.7849109 | 5.1509874 | 9.9478371 |
| 1068 | 2.4531592 | 3.5318363 | 2.7337681 | 4.0768817 | 3.673988 | 2.4593564 | 3.6017357 | 5.4889682 |
| 1069 | 0.6815461 | 0.6659996 | 0.3072402 | 1 | 0.5174383 | 0.5336827 | 0.8603447 | 0.3797664 |
| 1070 | 1.6162287 | 2.5071655 | 2.8739581 | 2.5300085 | 1.1441879 | 2.1197745 | 1.4536806 | 2.6386962 |
| 1071 | 0.936299 | 0.4581884 | 0.4552014 | 0.5985748 | 0.7708211 | 0.5007062 | 0.4092141 | 0.6663802 |
| 1072 | 1.7989902 | 1.882874 | 4.3971841 | 2.6876776 | 2.5773771 | 2.4306188 | 2.908069 | 2.505275 |
| 1073 | 2.4346889 | 2.7431949 | 2.5865149 | 3.0988752 | 3.2574877 | 2.337268 | 1.761804 | 6.7570022 |
| 1074 | 0.6685478 | 0.5801707 | 1 | 0.6573378 | 0.7712441 | 1 | 0.3810807 | 1 |
| 1075 | 0.0423755 | 0.6352239 | 1 | 1 | 0.0515781 | 0.0187828 | 0.0971154 | 0.1963014 |
| 1076 | 1.9371971 | 1000 | 1 | 1 | 2.4876326 | 1 | 1 | 3.2143223 |
| 1077 | 3.0504147 | 3.554768 | 3.9721713 | 3.508361 | 1.9835551 | 1.8823647 | 2.7528492 | 4.0275834 |
| 1078 | 2.2840989 | 2.5771722 | 2.0004032 | 2.5659851 | 2.4547577 | 2.41591 | 2.4495112 | 3.8386035 |

Table 4

| SEQ ID NO | Patient ID | | | | | | | |
|--------------|------------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|
| | 10 | 15 | 52 | 121 | 125 | 128 | 130 | 133 |
| 1079 | 1 | 1 | 4.5688941 | 1 | 3.0448289 | 1.7902161 | 1 | 3.9010261 |
| 1080 | 2.4558107 | 2.5367563 | 6.4413147 | 1.7862509 | 3.7477282 | 1.7885467 | 3.1298597 | 4.0244828 |
| 1081 | 0.5201329 | 0.1185562 | 0.904618 | 0.2212746 | 1 | 0.8106093 | 0.1873862 | 0.1891613 |
| 1082 | 2.1437352 | 2.431529 | 3.1099747 | 1.989528 | 2.4919857 | 1.5831514 | 1.6436587 | 2.8949981 |
| 1083 | 2.1228624 | 1.6078441 | 2.5578204 | 1.7466778 | 3.559505 | 1.9581075 | 2.0230331 | 2.9055702 |
| 1084 | 1 | 2.4995144 | 9.5279003 | 2.8531301 | 2.1949098 | 3.6306526 | 2.3510293 | 5.0282306 |
| 1085 | 0.376508 | 1 | 0.8175822 | 0.0981597 | 0.50418 | 0.5928823 | 0.1032478 | 0.0892157 |
| 1086 | 1.2970816 | 2.2365804 | 1.9446986 | 2.6919513 | 1.8039507 | 2.3948737 | 1 | 2.2811864 |
| 1087 | 0.8618295 | 2.1793128 | 0.356164 | 0.3779874 | 0.5810575 | 0.1451376 | 0.2433284 | 0.7417734 |
| 1088 | 0.6881406 | 0.3107973 | 0.2903323 | 0.6900705 | 0.5402672 | 0.3013979 | 0.4220995 | 0.3287364 |
| 1089 | 0.2865728 | 0.6662141 | 0.198957 | 1 | 0.395565 | 0.4025807 | 0.3915488 | 0.544612 |
| 1090 | 1 | 2.3098148 | 2.1113234 | 2.6704113 | 2.1635641 | 2.0534919 | 1.787287 | 2.2982911 |
| 1091 | 0.5939418 | 0.6500756 | 0.6422712 | 1 | 0.4579195 | 0.496433 | 0.2849445 | 0.5853855 |
| 1092 | 2.6775084 | 1 | 2.0179111 | 7.3833877 | 2.34415 | 1.6313933 | 1.5784406 | 3.3752467 |
| 1093 | 0.7255556 | 2.3856282 | 2.8905162 | 2.6479326 | 1 | 2.365985 | 1 | 2.8124018 |
| 1094 | 3.3587076 | 3.0272967 | 3.7771873 | 2.829719 | 2.6063081 | 1.9335537 | 1.8836808 | 2.1016425 |
| 1095 | 1 | 0.577136 | 0.3383617 | 1 | 0.7343682 | 0.5000879 | 0.9034943 | 0.3714666 |
| 1096 | 2.557736 | 2.5534953 | 1.5660933 | 2.0698433 | 1.5565604 | 2.2407912 | 2.0165212 | 3.2873879 |
| 1097 | 0.5809063 | 0.5232731 | 0.2766278 | 1 | 0.6797247 | 0.4932316 | 0.8769183 | 0.3830485 |
| 1098 | 2.3690851 | 2.9002798 | 3.286826 | 2.9710243 | 1.394359 | 3.3047834 | 1 | 3.1544796 |
| 1099 | 3.9525241 | 2.2226669 | 3.0043422 | 2.3708281 | 2.9186093 | 2.8786108 | 2.944292 | 4.0095241 |
| 1100 | 2.209174 | 1.5899738 | 3.3767306 | 1 | 2.6518648 | 1.462121 | 2.5014931 | 3.2792616 |
| 1101 | 1.8861592 | 1 | 2.3307184 | 4.4457554 | 2.1721443 | 2.7796265 | 2.0229874 | 3.3158458 |
| 1102 | 2.3129805 | 1.5469521 | 1 | 1.8541539 | 2.3744805 | 1.9909946 | 1.7239675 | 1 |
| 1103 | 1 | 2.0310103 | 3.2092851 | 1 | 2.4049561 | 0.6971841 | 1.9956777 | 2.4690775 |
| 1104 | 1.3964149 | 1.7495143 | 2.7717069 | 2.3500644 | 2.2236531 | 1.5709364 | 1.7309292 | 2.4231599 |
| 1105 | 0.6500104 | 0.6678118 | 0.5404818 | 1 | 0.5518975 | 0.5295744 | 0.4791155 | 0.606072 |
| 1106 | 2.0850283 | 1.7885201 | 1.8137621 | 1.9293405 | 2.5633357 | 1.6486028 | 1.9648201 | 2.7913208 |
| 1107 | 2.6785052 | 2.708146 | 1 | 2.2813716 | 1.247317 | 1 | 1 | 3.0782107 |
| 1108 | 1 | 1.8584303 | 1.8401596 | 2.7697038 | 1.6660142 | 2.5475822 | 1.5918188 | 3.555469 |
| 1109 | 0.4765684 | 0.5198685 | 0.3557175 | 0.1771471 | 0.3871372 | 0.465813 | 1 | 0.3694074 |
| 1110 | 2.327697 | 2.6888334 | 3.5402868 | 1.9591782 | 2.2504532 | 1.818782 | 2.154493 | 3.53782 |
| 1111 | 1.9783451 | 1.880354 | 2.1530019 | 2.3826583 | 2.6588625 | 1.9803047 | 3.3390225 | 2.8541931 |
| 1112 | 1 | 1.8694645 | 1.9361131 | 1 | 1.5197932 | 2.2561459 | 2.2498863 | 2.8128673 |
| 1113 | 3.489993 | 2.5948066 | 4.357768 | 1.9176584 | 3.2538159 | 2.6792613 | 3.133034 | 5.7647653 |
| 1114 | 0.6366615 | 0.6783742 | 0.7328897 | 1 | 0.5951516 | 0.5839099 | 0.4928643 | 0.5920285 |
| 1115 | 1 | 1 | 0.326426 | 1 | 1.8434939 | 1 | 1 | 1.2245308 |
| 1116 | 2.7855763 | 2.4676342 | 4.5909693 | 1 | 2.7545909 | 2.3104815 | 3.2313509 | 4.3523356 |
| 1117 | 0.7393172 | 0.5842777 | 0.2908898 | 1 | 0.6624234 | 0.4561949 | 1 | 0.3581173 |
| 1118 | 0.3615382 | 1 | 0.6524411 | 0.3054401 | 0.3021341 | 0.5561616 | 0.488625 | 0.6021982 |
| 1119 | 0.6450328 | 0.4775546 | 0.3320132 | 0.3678262 | 0.1528721 | 0.4271344 | 0.2761309 | 0.5040751 |
| 1120 | 2.6301196 | 1.7540234 | 3.7993845 | 2.2287305 | 1.8753118 | 1 | 2.2851816 | 2.3277351 |
| 1121 | 2.146987 | 2.28995 | 1.5377152 | 2.107367 | 1.6330771 | 1.872403 | 1.8105858 | 2.0608374 |
| 1122 | 2.3192558 | 1.4665063 | 3.2861371 | 2.3705263 | 1.5396198 | 1.3706732 | 1.8421956 | 1.8143739 |
| 1123 | 1 | 1 | 14.406763 | 3.5664127 | 1 | 2.3931493 | 1 | 2.2431348 |
| 1124 | 2.816931 | 2.7129178 | 2.2203094 | 3.2868051 | 2.3189063 | 1.9120504 | 1.6630956 | 4.6811193 |
| 1125 | 1.1470564 | 1.321351 | 3.5129196 | 1.5413326 | 1.1933821 | 2.0792547 | 1.4712273 | 1.7084637 |
| 1126 | 2.7082477 | 2.7963286 | 4.6241439 | 3.9444168 | 2.7401038 | 1.7223258 | 2.7485418 | 3.1806415 |
| 1127 | 2.2150116 | 2.2822936 | 4.2514162 | 3.781194 | 1.5784368 | 1.458734 | 2.3957312 | 3.1487359 |

Table 4

| SEQ ID NO | Patient ID | | | | | | | |
|--------------|------------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|
| | 10 | 15 | 52 | 121 | 125 | 128 | 130 | 133 |
| 1128 | 2.1444274 | 2.3925393 | 3.6131036 | 3.6599152 | 1.3991263 | 2.9179971 | 2.2689184 | 2.8623509 |
| 1129 | 2.1711202 | 1000 | 3.4213115 | 1.3867288 | 1.8895446 | 1.8804479 | 1.4809557 | 1 |
| 1130 | 6.0571725 | 6.132085 | 1 | 8.6720594 | 2.6368722 | 2.7381449 | 4.5758491 | 1 |
| 1131 | 1.7009247 | 1.4011749 | 2.6815171 | 2.9506877 | 1.3501183 | 2.0809997 | 2.0102316 | 3.2852499 |
| 1132 | 0.6154099 | 0.6416793 | 0.2690006 | 1 | 0.7111521 | 0.5794306 | 0.8092315 | 0.3448786 |
| 1133 | 1 | 1.7841236 | 2.8322934 | 1.5194005 | 1.9627776 | 1.3283328 | 1.7366334 | 3.429472 |
| 1134 | 1 | 2.4442683 | 4.4366919 | 1 | 2.1423859 | 1.7861147 | 1 | 4.0169718 |
| 1135 | 2.9523641 | 1.921038 | 2.661262 | 3.0628915 | 1.8032806 | 1.9652798 | 2.1146223 | 3.1148027 |
| 1136 | 2.3141584 | 1.7210977 | 2.9591205 | 3.5087577 | 2.8090712 | 1.6723802 | 2.6751664 | 3.7897589 |
| 1137 | 3.2450927 | 2.1814629 | 2.7570843 | 1.7112069 | 2.2929692 | 2.2134551 | 2.5906126 | 2.9720639 |
| 1138 | 2.3927208 | 2.387301 | 3.1660258 | 1.9803459 | 1.8650946 | 1.7878184 | 1 | 2.5482103 |
| 1139 | 1.9033737 | 1.7388286 | 3.0065027 | 1.9683727 | 1.5757355 | 1.8006174 | 1.8323987 | 2.656369 |
| 1140 | 2.4242296 | 4.0928875 | 1 | 1.7494345 | 1.9209458 | 2.4016957 | 2.5604039 | 3.6908627 |
| 1141 | 2.5178308 | 2.2892905 | 2.6410882 | 1 | 2.9170151 | 1.762564 | 1 | 3.7374271 |
| 1142 | 2.3412044 | 2.3542948 | 2.4457954 | 1 | 1.6215973 | 2.3219477 | 1 | 3.4601389 |
| 1143 | 1 | 0.4603277 | 1 | 1 | 0.7637656 | 0.667732 | 0.4293086 | 1 |
| 1144 | 1 | 0.6076758 | 0.508305 | 0.7790096 | 1 | 0.5201349 | 0.37266 | 0.7712016 |
| 1145 | 1.9592207 | 1.6113666 | 3.4755398 | 1.9624816 | 2.5125031 | 1.5566878 | 1 | 4.3502921 |
| 1146 | 2.5795147 | 1.9729385 | 2.8775186 | 2.7148702 | 2.3688455 | 1.2788612 | 1.5909425 | 3.0314332 |
| 1147 | 2.2458949 | 2.708146 | 3.0526012 | 1 | 2.6562836 | 2.0757853 | 1 | 3.7033282 |
| 1148 | 2.2177996 | 2.1756562 | 3.0323795 | 2.6301311 | 1.8840449 | 1.6686566 | 1.7649279 | 4.3097317 |
| 1149 | 1 | 1.30184 | 2.9783739 | 4.4043282 | 0.7945494 | 1 | 1.321327 | 2.5021586 |
| 1150 | 0.3793334 | 0.6022284 | 0.2456882 | 0.2598938 | 0.2548789 | 0.3344843 | 0.2444885 | 0.2758681 |
| 1151 | 2.6073243 | 3.1350225 | 2.994873 | 1 | 1.7698434 | 3.119813 | 1 | 4.3914601 |
| 1152 | 1 | 6.222498 | 1 | 1 | 4.8324363 | 3.4957583 | 3.9245618 | 8.5927885 |
| 1153 | 1 | 2.4988228 | 1.6594157 | 2.9094742 | 1.267372 | 1.3061424 | 1.7045813 | 2.5445889 |
| 1154 | 1.9517799 | 2.2225115 | 2.5576117 | 1.63171 | 1.2735376 | 1.7512489 | 1.5472801 | 2.8597 |
| 1155 | 1.490607 | 1 | 2.0874988 | 5.7693725 | 1.8024894 | 1.8547263 | 2.4530661 | 5.5989888 |
| 1156 | 0.7668437 | 0.6634689 | 0.3037505 | 1 | 0.6406878 | 0.513251 | 0.8465803 | 0.3578807 |
| 1157 | 2.2707626 | 2.9651394 | 3.1245399 | 2.2504931 | 2.4557172 | 2.2801981 | 2.0255488 | 2.7301842 |
| 1158 | 0.9499382 | 0.4378249 | 0.4398665 | 0.7969999 | 0.7598425 | 0.577191 | 0.7180262 | 0.5067261 |
| 1159 | 0.9216073 | 0.3608802 | 0.5454791 | 0.6987445 | 0.7582997 | 1 | 0.5302106 | 0.630301 |
| 1160 | 0.4465607 | 1.2041834 | 2.8146241 | 0.6109384 | 1 | 1 | 1 | 0.70242 |
| 1161 | 0.7864867 | 0.4115905 | 0.4914476 | 0.6001373 | 0.74795 | 0.6184803 | 0.5332943 | 0.8229022 |
| 1162 | 1.0921652 | 0.2793192 | 0.5656616 | 0.6323904 | 0.8583248 | 0.5020253 | 0.6852486 | 0.6281077 |
| 1163 | 1 | 0.4218634 | 0.5709142 | 0.4421709 | 0.751127 | 1 | 0.5006145 | 0.5693222 |
| 1164 | 2.078453 | 2.1273104 | 4.3702188 | 3.1773384 | 2.8682898 | 2.2652213 | 2.1716232 | 3.5270428 |
| 1165 | 1.8564319 | 1 | 3.5575584 | 2.0320792 | 1.7068559 | 2.144129 | 1.5533164 | 2.9848056 |
| 1166 | 2.0066689 | 2.393676 | 2.2998621 | 4.7615394 | 1.5123045 | 2.7133232 | 2.2280634 | 3.1834423 |
| 1167 | 2.236007 | 2.4291699 | 2.5891846 | 4.9765848 | 3.1575269 | 2.2096628 | 3.4774463 | 7.5747604 |
| 1168 | 1.6392743 | 2.1373635 | 3.2673044 | 2.0715472 | 2.1110926 | 1.2799742 | 1.9941673 | 2.784725 |
| 1169 | 0.6107735 | 0.3486504 | 0.1335394 | 0.2066018 | 0.4954885 | 0.1396415 | 0.1661818 | 0.0231166 |
| 1170 | 1 | 0.2523931 | 0.3520295 | 0.6408473 | 0.6941708 | 0.4205116 | 0.4449332 | 0.4267964 |
| 1171 | 0.7264958 | 0.5155846 | 0.2770152 | 1 | 0.6773839 | 0.4871309 | 0.861238 | 0.343561 |
| 1172 | 0.1307611 | 0.0955066 | 1 | 0.0218481 | 0.0534643 | 0.1664006 | 0.2069931 | 0.2749924 |
| 1173 | 1.5308322 | 1.9479266 | 2.5281238 | 1 | 2.5839867 | 1.5645678 | 1.6770432 | 3.3582209 |
| 1174 | 1.5642529 | 3.5935379 | 7.8973228 | 2.9793902 | 2.0809841 | 3.4015075 | 2.2823289 | 7.2716731 |
| 1175 | 0.5905374 | 0.047445 | 1 | 0.4165615 | 0.1024021 | 0.1164687 | 0.1801632 | 0.4908206 |
| 1176 | 1 | 0.3949158 | 0.5057471 | 0.7185447 | 1.0946542 | 0.4442821 | 0.3148781 | 0.6981438 |

Table 4

| SEQ ID NO | Patient ID | | | | | | | |
|--------------|------------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|
| | 10 | 15 | 52 | 121 | 125 | 128 | 130 | 133 |
| 1177 | 1.1355456 | 0.402599 | 0.4927179 | 0.6559948 | 1 | 0.4225177 | 0.3093855 | 0.7027671 |
| 1178 | 1 | 1.3894651 | 0.7354337 | 0.5898235 | 1 | 0.4364159 | 0.3053207 | 0.5187656 |
| 1179 | 1.9617581 | 1.5399659 | 2.8677812 | 1.7227313 | 2.8172959 | 1.749978 | 2.513283 | 3.0783448 |
| 1180 | 1.877954 | 2.0502961 | 2.7526068 | 1.9341096 | 2.6486424 | 1.6677704 | 2.1177716 | 3.3331004 |
| 1181 | 2.2075359 | 2.3563483 | 3.4709232 | 1.74093 | 2.846807 | 1.9953846 | 1.6609373 | 3.8210886 |
| 1182 | 2.3653855 | 1.7763385 | 2.726518 | 3.705209 | 4.5875142 | 1.4824702 | 3.2222852 | 2.9870699 |
| 1183 | 2.074109 | 1.5112651 | 3.2502016 | 1 | 2.7577203 | 1.6582622 | 2.235179 | 3.31983 |
| 1184 | 2.3739053 | 2.4486058 | 6.2518832 | 1.7217756 | 3.7462822 | 2.0158163 | 2.9645578 | 4.0200093 |
| 1185 | 2.5646498 | 2.1996441 | 2.164296 | 2.2007588 | 1.5999297 | 1.6887585 | 2.0922503 | 2.6385384 |
| 1186 | 2.2236256 | 2.0189466 | 3.4968574 | 1 | 2.5525538 | 1.910855 | 1 | 5.440163 |
| 1187 | 2.1942953 | 2.5873325 | 2.5502273 | 2.5533895 | 2.3820002 | 1.8252604 | 2.6249992 | 3.6223493 |
| 1188 | 1 | 1.9681452 | 2.1564816 | 2.7572373 | 1.5628467 | 2.0864683 | 1.4185545 | 3.1060058 |
| 1189 | 0.6218682 | 1 | 0.3895364 | 1 | 0.6899734 | 0.5701285 | 1 | 0.4871914 |
| 1190 | 0.8113189 | 1.4576274 | 5.8874052 | 0.6875685 | 1.2039962 | 0.61971 | 1.4345232 | 0.541393 |
| 1191 | 1.2186331 | 0.7704762 | 2.4180698 | 2.3891387 | 0.721456 | 1.4378627 | 1 | 2.5040363 |
| 1192 | 0.2425162 | 0.7017616 | 0.1044772 | 1 | 0.1685528 | 0.0847014 | 0.1975348 | 0.2762863 |
| 1193 | 0.6711984 | 0.5744338 | 0.2863107 | 1 | 0.6264421 | 0.5085587 | 0.8695641 | 0.3610602 |
| 1194 | 1 | 0.2357238 | 1 | 0.3113444 | 0.2071961 | 0.2108363 | 0.4053242 | 0.4163032 |
| 1195 | 2.3077256 | 2.3242268 | 3.0540879 | 3.1394148 | 1.7162083 | 2.003244 | 2.5715754 | 3.7210799 |
| 1196 | 0.6454427 | 0.5087431 | 0.3929117 | 0.5877868 | 0.7178918 | 0.5208287 | 0.6470076 | 0.5261661 |
| 1197 | 0.5177002 | 0.7811941 | 0.3275256 | 1.9944715 | 0.8548077 | 0.4789624 | 0.4998157 | 1 |
| 1198 | 0.7745486 | 0.4566764 | 0.370767 | 0.4630268 | 0.6971568 | 0.4485897 | 0.6105415 | 0.5042014 |
| 1199 | 1 | 0.0406572 | 0.1884694 | 0.254578 | 0.0893643 | 0.0723009 | 0.0903817 | 0.1218235 |
| 1200 | 1 | 0.5856503 | 0.3131076 | 0.6765821 | 0.7181621 | 0.51648 | 0.6954515 | 0.4500471 |
| 1201 | 2.3342418 | 3.1567317 | 2.7766156 | 2.369742 | 2.29292 | 2.3879143 | 2.3030405 | 4.0222421 |
| 1202 | 1 | 1.921483 | 3.7918036 | 1.9648006 | 1 | 1.6125142 | 1.5139926 | 2.1357098 |
| 1203 | 1 | 0.0960803 | 1 | 0.206937 | 0.7211247 | 0.7275293 | 0.2096628 | 0.2117651 |
| 1204 | 3.3894295 | 2.4325746 | 2.6098731 | 3.0884935 | 1.7819795 | 2.0668611 | 2.0045192 | 2.3736526 |
| 1205 | 1.315661 | 1.3326747 | 2.6619398 | 2.0273009 | 1.5608825 | 2.012443 | 1.809379 | 1.9412073 |
| 1206 | 2.6362229 | 2.496839 | 2.404257 | 1.9093611 | 1.8720249 | 2.0821127 | 1.6266178 | 2.2597819 |
| 1207 | 2.496716 | 2.3460594 | 2.9820561 | 2.9041202 | 1.567848 | 1.9722049 | 2.3936189 | 4.3976061 |
| 1208 | 2.2349072 | 1 | 1 | 1 | 0.2735682 | 2.398563 | 0.39343 | 1 |
| 1209 | 1.9919007 | 2.4775586 | 3.8981004 | 2.6790937 | 2.0963827 | 2.3686574 | 2.1427437 | 2.3251552 |
| 1210 | 1 | 2.0548856 | 2.7207219 | 2.1683683 | 1.1661881 | 2.0132949 | 1 | 2.7879677 |
| 1211 | 2.7697593 | 2.3204469 | 2.9470226 | 2.1164682 | 3.2310778 | 2.0045493 | 1.9661569 | 3.453409 |
| 1212 | 1 | 0.6266882 | 0.3140594 | 0.7080968 | 0.7771702 | 0.4790654 | 0.8432335 | 0.3739518 |
| 1213 | 1.8352025 | 1.742512 | 2.1175257 | 1.8845893 | 1.6378352 | 1.777369 | 1.8577051 | 3.8455385 |
| 1214 | 2.3530725 | 2.1435991 | 5.466583 | 1 | 3.2143526 | 2.9699006 | 2.8820606 | 4.6947683 |
| 1215 | 0.6460996 | 0.6834678 | 0.2724682 | 0.6972846 | 0.6630979 | 0.5173662 | 0.784088 | 0.3407207 |
| 1216 | 1.8702655 | 2.1569495 | 2.1789597 | 1 | 1.5546572 | 1.646054 | 1.6280662 | 3.6900343 |
| 1217 | 1 | 1.8326999 | 5.5025568 | 1 | 2.0229654 | 1 | 1 | 3.9725849 |
| 1218 | 1 | 4.569863 | 1 | 2.7331993 | 1 | 3.1157871 | 1.8650534 | 2.8194314 |
| 1219 | 0.2325233 | 0.4534058 | 0.1077592 | 0.2131107 | 0.0903142 | 0.2519195 | 0.1272127 | 0.1226756 |
| 1220 | 1.6193814 | 1 | 1 | 2.5834277 | 2.0054547 | 1 | 1 | 2.7060341 |
| 1221 | 3.1696808 | 0.4902455 | 3.7957051 | 0.3716612 | 2.5016163 | 1.3413791 | 1 | 1.3065591 |
| 1222 | 0.5205531 | 0.0430002 | 1 | 0.3405117 | 0.0732439 | 0.040829 | 0.1536514 | 0.4357038 |
| 1223 | 1.4768386 | 2.2491158 | 2.6373119 | 1 | 3.0037265 | 4.3419684 | 2.9579995 | 1.6308931 |
| 1224 | 2.5550868 | 3.2749984 | 3.5652439 | 1 | 1.8749496 | 1.1775067 | 1.934568 | 3.5877297 |
| 1225 | 2.0130788 | 1.2254423 | 1.6298734 | 2.5827111 | 3.0202898 | 1.3479194 | 2.5305342 | 3.2337702 |

Table 4

| SEQ ID NO | Patient ID | | | | | | | |
|--------------|------------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|
| | 10 | 15 | 52 | 121 | 125 | 128 | 130 | 133 |
| 1226 | 0.2008331 | 0.6015904 | 1 | 0.0365277 | 0.1527249 | 0.046964 | 0.0583303 | 0.1304153 |
| 1227 | 0.7971244 | 0.1995329 | 0.5821117 | 0.2779908 | 0.9030201 | 0.5755628 | 0.2233279 | 0.2792449 |
| 1228 | 2.0903287 | 1.5088792 | 1.7482337 | 1.5509861 | 3.413439 | 2.1107884 | 2.2545292 | 2.4982769 |
| 1229 | 1.9921305 | 2.1737475 | 2.1679621 | 2.2717423 | 1.9453674 | 1.4938952 | 1.843219 | 2.5687233 |
| 1230 | 2.241289 | 2.4989836 | 2.1549254 | 2.7782158 | 1.5142771 | 4.7295517 | 2.8009621 | 4.0223052 |
| 1231 | 1.3053375 | 1.9075964 | 3.6801033 | 1.6670588 | 1.5583546 | 1.8629635 | 1 | 2.5579934 |
| 1232 | 0.6482827 | 0.4798118 | 0.3029699 | 0.3884162 | 0.6956402 | 0.5601738 | 0.4703194 | 0.5684623 |
| 1233 | 2.1374198 | 2.3054236 | 2.4650226 | 1.8785817 | 2.3651212 | 1.4241431 | 2.354799 | 2.071662 |
| 1234 | 1 | 1.6648328 | 18.057196 | 6.0235413 | 2.1572278 | 4.8796152 | 1.8971638 | 1.8812541 |
| 1235 | 1.1368314 | 1.9915648 | 2.6342101 | 1 | 1.7862412 | 0.7208309 | 1.7631216 | 2.0637487 |
| 1236 | 0.5474816 | 0.5931834 | 1 | 0.2629983 | 0.2984264 | 0.4022921 | 0.4417236 | 0.5289984 |
| 1237 | 1.4926686 | 2.5641381 | 2.9538241 | 1.44009 | 1.5090994 | 1 | 1.9601342 | 2.5136301 |
| 1238 | 0.6564001 | 0.5733882 | 0.2964198 | 0.3439227 | 0.5431272 | 0.3972838 | 1 | 0.301178 |
| 1239 | 1 | 2.8672361 | 3.6093606 | 1 | 2.8168501 | 2.0958116 | 1.9255862 | 4.0585028 |
| 1240 | 2.5752061 | 1.7473106 | 4.6309733 | 1 | 2.137926 | 1.8593499 | 1 | 3.0782501 |
| 1241 | 2.1442144 | 2.4758804 | 3.3304642 | 1 | 2.2358022 | 1.9672722 | 2.2767605 | 3.5186167 |
| 1242 | 2.013971 | 1.6687682 | 2.8525194 | 1 | 2.009681 | 1.8572682 | 1 | 3.6211737 |
| 1243 | 1.9884601 | 1.7700815 | 2.5994877 | 1 | 2.0517617 | 1.451383 | 1 | 2.859274 |
| 1244 | 2.1034677 | 1.7650415 | 2.720958 | 1 | 2.1460017 | 1.6188416 | 1 | 3.4138505 |
| 1245 | 2.4309871 | 2.0553306 | 3.6195683 | 1 | 2.6485111 | 2.060678 | 1 | 4.1335724 |
| 1246 | 2.660676 | 1.8574277 | 6.1640102 | 1 | 2.7778025 | 2.0948773 | 2.8855883 | 4.6639831 |
| 1247 | 1.9736419 | 2.0216221 | 2.060882 | 1 | 2.2040592 | 1.5373073 | 1 | 1.8600626 |
| 1248 | 1.8386808 | 2.1628741 | 3.8706728 | 1 | 2.0450047 | 2.6160152 | 1 | 4.1667324 |
| 1249 | 1 | 3.5069369 | 3.250707 | 1 | 2.9745316 | 2.0050783 | 1 | 4.5547199 |
| 1250 | 0.7337005 | 0.5532929 | 0.2868778 | 0.546627 | 0.6907811 | 0.4726762 | 1 | 0.3371862 |
| 1251 | 1.0327995 | 0.4400071 | 0.453185 | 0.3897298 | 0.8507835 | 0.4287901 | 0.325372 | 0.6958085 |
| 1252 | 0.553831 | 0.5302808 | 0.322026 | 0.3516178 | 0.5654159 | 0.4310229 | 1 | 0.3627249 |
| 1253 | 1 | 2.3393091 | 2.8330611 | 1 | 1 | 1.6062899 | 1 | 2.2917742 |
| 1254 | 1 | 1.8037257 | 4.3671755 | 1 | 2.8582345 | 1.5066529 | 1 | 3.499579 |
| 1255 | 2.4985946 | 2.8376882 | 3.6721302 | 1 | 2.5759474 | 2.1320308 | 1.9137804 | 2.0296735 |
| 1256 | 2.4117021 | 1.2776752 | 3.431796 | 1 | 1.927463 | 1.543408 | 2.3416272 | 3.7228708 |
| 1257 | 0.339128 | 1 | 1 | 0.2935599 | 0.6422365 | 1 | 0.6430831 | 0.5778036 |
| 1258 | 1 | 1.5693798 | 1.674391 | 1 | 1 | 1 | 1 | 2.0086871 |
| 1259 | 0.706914 | 0.3923047 | 0.4323519 | 0.4260283 | 0.3488368 | 0.4730884 | 0.6600259 | 0.4931165 |
| 1260 | 0.6434609 | 1 | 0.3387931 | 0.599801 | 0.5520686 | 0.4955056 | 1 | 0.4287294 |
| 1261 | 0.6009991 | 0.6463332 | 0.2780333 | 0.7030391 | 0.6517997 | 0.4877973 | 0.8562251 | 0.334985 |
| 1262 | 1.8893373 | 1.3721309 | 2.2639125 | 1 | 2.0340997 | 2.5107516 | 2.4948056 | 2.994778 |
| 1263 | 1 | 2.171517 | 2.9600982 | 2.6282009 | 1.2905883 | 1.4615164 | 1.4472694 | 3.0223917 |
| 1264 | 1.1314236 | 0.213827 | 0.70531 | 0.4595237 | 1 | 0.5060099 | 0.5722515 | 0.7235878 |
| 1265 | 1 | 0.5124051 | 0.4704836 | 0.3977951 | 0.6603593 | 0.6600237 | 1 | 0.553259 |
| 1266 | 1.0835438 | 0.2870131 | 0.5877914 | 0.4142302 | 0.8275533 | 0.4199757 | 1 | 0.5680047 |
| 1267 | 1 | 1.5582115 | 3.8773736 | 1 | 1 | 2.1064534 | 1 | 3.4203042 |
| 1268 | 1 | 2.470878 | 2.989163 | 1.7488102 | 1 | 1 | 1 | 2.34039 |
| 1269 | 3.1999902 | 1.6801777 | 2.9546591 | 3.8741742 | 3.2853432 | 1 | 6.4404006 | 5.8178939 |
| 1270 | 2.2017376 | 2.1110111 | 3.5194253 | 2.5508014 | 3.3208913 | 2.1556502 | 2.403444 | 3.5013069 |
| 1271 | 7.3567601 | 1 | 19.260639 | 18.837124 | 3.2192937 | 5.4625702 | 5.6124529 | 9.6892788 |
| 1272 | 1.1459146 | 0.4597325 | 0.4715803 | 0.6322874 | 0.8087481 | 0.4849668 | 0.5476819 | 0.4990731 |
| 1273 | 1.6882528 | 2.4731835 | 2.6396431 | 1 | 2.283996 | 3.5300263 | 1 | 3.4558233 |
| 1274 | 1 | 2.2984696 | 0.2844317 | 0.2024379 | 0.5503816 | 0.0998362 | 0.0781247 | 0.7711937 |

Table 4

| SEQ ID NO | Patient ID | | | | | | | |
|--------------|------------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|
| | 10 | 15 | 52 | 121 | 125 | 128 | 130 | 133 |
| 1275 | 1 | 0.1467423 | 1 | 1 | 0.3144466 | 0.4901057 | 0.3549393 | 0.3639557 |
| 1276 | 0.7719931 | 0.5554858 | 0.2851793 | 0.646853 | 0.6126439 | 0.3645547 | 0.5146903 | 0.395522 |
| 1277 | 2.9980879 | 2.7920447 | 3.9957082 | 1.6112113 | 2.8814446 | 2.0687435 | 1.8948765 | 2.2221484 |
| 1278 | 1 | 1.9276382 | 3.7297871 | 1 | 2.511794 | 1.5528062 | 1.9432544 | 3.8144219 |
| 1279 | 3.2870988 | 2.1460386 | 6.8463581 | 1 | 3.2172573 | 2.5222384 | 1 | 5.5854739 |
| 1280 | 0.7625228 | 0.1909007 | 1 | 0.1411982 | 0.3067028 | 1 | 0.6385224 | 0.5419689 |
| 1281 | 1.1689064 | 1.3544001 | 1.8051478 | 1 | 2.0140771 | 1.6627278 | 2.0391499 | 1.7324245 |
| 1282 | 2.5910491 | 2.8688553 | 5.3096808 | 2.8023807 | 2.8580815 | 1.9979609 | 2.8063143 | 3.6814425 |
| 1283 | 0.6543406 | 0.563051 | 0.2933293 | 0.6163861 | 0.6990549 | 0.610085 | 0.8037644 | 0.3683817 |
| 1284 | 2.4717703 | 2.4150903 | 3.1449095 | 2.1899923 | 1.6956644 | 2.1627745 | 2.4902286 | 4.353448 |
| 1285 | 2.3038461 | 2.3625893 | 2.2230642 | 1 | 2.1897348 | 1 | 1 | 2.3996252 |
| 1286 | 1.3629092 | 1.8173388 | 2.024229 | 1 | 1.7579871 | 1 | 1 | 3.5485735 |
| 1287 | 1.7399326 | 1 | 1.8075932 | 1.9361204 | 1.4245996 | 2.87104 | 1 | 4.1469532 |
| 1288 | 2.0813089 | 1 | 2.7334106 | 1.8104237 | 1 | 2.1385161 | 1 | 1.6301593 |
| 1289 | 2.6829165 | 3.3098061 | 3.0153207 | 3.0137203 | 1.3874579 | 1 | 1.784048 | 4.8508485 |
| 1290 | 3.6969657 | 2.4844965 | 3.8862639 | 1 | 2.6946163 | 2.4406286 | 1 | 4.2362084 |
| 1291 | 2.5343119 | 2.1117939 | 6.2825726 | 1 | 3.5031161 | 3.3852597 | 1 | 5.5070906 |
| 1292 | 1 | 0.0386198 | 1 | 0.3360761 | 0.092462 | 0.1076132 | 0.1799378 | 0.4263072 |
| 1293 | 0.6842088 | 0.6599302 | 0.292757 | 1 | 0.7360129 | 0.490669 | 0.843869 | 0.3212729 |
| 1294 | 1.2589521 | 1.5194952 | 2.1948217 | 2.5198068 | 2.0448873 | 1.4213332 | 2.1837987 | 3.6591149 |
| 1295 | 0.5936804 | 0.7066353 | 0.2928486 | 1 | 1 | 0.4945918 | 0.8631881 | 0.3155213 |
| 1296 | 0.5269518 | 0.5842884 | 1 | 0.287323 | 0.3304994 | 1 | 0.437765 | 0.5872316 |
| 1297 | 0.285519 | 1 | 0.6474432 | 0.5365938 | 0.4586963 | 0.6152032 | 0.4693879 | 1 |
| 1298 | 1.4963161 | 1 | 3.286826 | 1.6277451 | 1 | 2.6483046 | 1.2249398 | 3.2408314 |
| 1299 | 2.6906085 | 1 | 1 | 1 | 1 | 1 | 1 | 0.5251404 |
| 1300 | 0.5243022 | 0.6275237 | 0.3252376 | 0.5569527 | 0.6672154 | 0.4100141 | 0.808399 | 0.3735021 |
| 1301 | 1 | 1 | 5.1177281 | 1.6998047 | 1.2829919 | 2.5707619 | 1.5219403 | 4.616748 |
| 1302 | 1.7764482 | 1 | 1 | 1 | 1 | 1 | 0.4341436 | 0.480856 |
| 1303 | 0.4865289 | 1 | 0.1170593 | 0.3118501 | 0.5948268 | 0.4278283 | 0.55355 | 0.2617773 |

Table 4

| SEQ ID NO | Patient ID | | | | | | | |
|--------------|------------|-----------|-----------|-----------|-----------|-----|-----------|-----------|
| | 141 | 156 | 228 | 264 | 266 | 267 | 268 | 278 |
| 1 | 1 | 1 | 1.8454224 | 1 | 1000 | | 1000 | 1000 |
| 2 | 0.8164474 | 0.8178862 | 0.7936883 | 0.8687693 | 0.8841135 | | 0.30259 | 0.8741052 |
| 3 | 2.0365961 | 1 | 1 | 2.0287516 | 1.7233415 | | 1 | 4.9176463 |
| 4 | 0.6389055 | 0.5757827 | 0.3848124 | 0.2982074 | 0.2948369 | | 0.3210765 | 0.5209778 |
| 5 | 0.8303428 | 0.4766504 | 0.6754531 | 0.6150867 | 0.7361969 | | 0.5658911 | 0.2548084 |
| 6 | 0.8620319 | 0.5081246 | 0.7607838 | 0.6420504 | 0.8582275 | | 0.6269873 | 0.2753265 |
| 7 | 0.7601867 | 0.4628901 | 1.1769849 | 2.3942662 | 1.3424934 | | 1 | 2.6778042 |
| 8 | 1 | 4.622082 | 2.1632955 | 2.7848672 | 2.2634272 | | 2.1258811 | 2.3332255 |
| 9 | 0.4946185 | 0.2560052 | 0.6223539 | 0.6177607 | 0.4746162 | | 0.4591715 | 0.7039204 |
| 10 | 0.2611992 | 0.1800528 | 0.5926713 | 1 | 0.3901546 | | 0.2763202 | 1 |
| 11 | 0.2267179 | 1 | 0.1857397 | 0.8586105 | 0.6968087 | | 0.1638946 | 0.794684 |
| 12 | 1.3699983 | 1.4593534 | 1 | 1.3311263 | 0.8214031 | | 2.143429 | 3.0080234 |
| 13 | 0.3787027 | 0.3503233 | 0.3959456 | 0.4740781 | 0.2747502 | | 0.313614 | 0.7567147 |
| 14 | 1 | 1.7326482 | 1.4638074 | 1.6965099 | 2.1403422 | | 1 | 2.1122703 |
| 15 | 0.5508901 | 0.4619248 | 1.3173064 | 1 | 0.5475913 | | 0.286754 | 0.6256477 |
| 16 | 2.1300208 | 3.086192 | 1.9996034 | 2.7577431 | 2.0065399 | | 2.134902 | 2.6926852 |
| 17 | 2.5677654 | 1.7380651 | 1.5175083 | 3.6557933 | 2.1953751 | | 1 | 3.2402651 |
| 18 | 1 | 3.080972 | 1.88923 | 1.8154843 | 1.4170157 | | 1.8174038 | 1.2712361 |
| 19 | 0.5969454 | 1.5851579 | 0.6753138 | 0.6961726 | 0.5535283 | | 0.5050108 | 0.3274752 |
| 20 | 3.060172 | 1 | 1 | 3.1180237 | 1.8402879 | | 1 | 1 |
| 21 | 1 | 1.3965895 | 1 | 0.2467344 | 0.1222395 | | 0.0791483 | 2.2133767 |
| 22 | 2.4538425 | 1.3013615 | 1.7778602 | 3.1075427 | 3.8044287 | | 3.0324295 | 3.1140963 |
| 23 | 1.4825086 | 1.1889853 | 1.5536715 | 2.8380162 | 1.4991341 | | 3.0794953 | 2.7531218 |
| 24 | 1.2636418 | 3.088467 | 1.4877327 | 2.1169631 | 1.633915 | | 1 | 1.8214606 |
| 25 | 0.7840685 | 0.53642 | 0.670591 | 0.6825002 | 0.7165255 | | 0.6263949 | 0.4026313 |
| 26 | 1 | 1 | 1 | 4.3228983 | 3.9827613 | | 1 | 3.1348068 |
| 27 | 1 | 0.46115 | 0.7198244 | 0.6154172 | 0.7581749 | | 0.5622435 | 0.282857 |
| 28 | 0.3813088 | 0.2089507 | 1 | 1.5873939 | 0.6352755 | | 0.5292887 | 0.6119835 |
| 29 | 2.2373299 | 1.319727 | 3.1787031 | 1 | 1.9910388 | | 2.5175858 | 1 |
| 30 | 2.2571273 | 6.5869592 | 3.0762062 | 5.642018 | 2.880487 | | 8.3454687 | 3.2442694 |
| 31 | 2.0340667 | 6.371903 | 2.1925598 | 6.2673728 | 5.5161954 | | 4.2418401 | 8.7507054 |
| 32 | 1.6639487 | 1.5592666 | 1 | 1.7393899 | 1 | | 2.6272195 | 2.6953982 |
| 33 | 1 | 1.7466545 | 1.5704741 | 2.3509849 | 1 | | 2.3784815 | 3.1826904 |
| 34 | 1.2310329 | 2.1145564 | 1.1943497 | 2.0346692 | 1.4778661 | | 1.5136082 | 1.6466073 |
| 35 | 1.3891168 | 2.0894766 | 1 | 2.2595319 | 2.0908869 | | 1.9086987 | 1.8778185 |
| 36 | 1.8831769 | 1.8187826 | 1.3111874 | 2.0607897 | 1.5824534 | | 1.6744006 | 1.2623335 |
| 37 | 1.9214687 | 2.5502209 | 1.3304216 | 2.5222354 | 1.9635657 | | 2.3632194 | 1.5326873 |
| 38 | 1 | 1.2107756 | 2.7569613 | 2.0645602 | 1.9791469 | | 1.39532 | 5.2200653 |
| 39 | 0.2425515 | 0.4414318 | 0.3895461 | 0.506044 | 0.4407241 | | 0.2113942 | 0.7377177 |
| 40 | 1.201063 | 2.6709467 | 1.3903821 | 3.5591375 | 2.9660631 | | 2.0500093 | 2.1452854 |
| 41 | 0.2876213 | 0.7686121 | 1.4842169 | 3.533406 | 2.0625035 | | 1.6152211 | 1.1725757 |
| 42 | 2.7697803 | 3.1248723 | 2.2702971 | 1.8541331 | 2.6517341 | | 2.7531443 | 1.9142232 |
| 43 | 1 | 0.5115862 | 0.7034905 | 0.691511 | 0.8152347 | | 0.5966288 | 0.2993583 |
| 44 | 0.3488095 | 1.2815448 | 0.3388898 | 1 | 0.769221 | | 0.4410781 | 0.6477799 |
| 45 | 1.129593 | 1.7203697 | 0.6396199 | 1.7953916 | 2.3663347 | | 2.2958199 | 0.8448274 |
| 46 | 1 | 2.3158707 | 1 | 2.0247366 | 1.5949302 | | 1.5575379 | 2.1783253 |
| 47 | 2.4590547 | 2.3877282 | 1.3540613 | 4.5902994 | 2.3103189 | | 2.1731885 | 2.0342832 |
| 48 | 0.4569398 | 0.2674414 | 0.5339349 | 0.5481679 | 1 | | 0.4777492 | 0.6475067 |
| 49 | 1 | 3.6415863 | 2.2768126 | 1 | 2.0590858 | | 1 | 1 |

Table 4

| SEQ ID NO | Patient ID | | | | | | | |
|--------------|------------|-----------|-----------|-----------|-----------|-----|-----------|-----------|
| | 141 | 156 | 228 | 264 | 266 | 267 | 268 | 278 |
| 50 | 1 | 1 | 0.1808417 | 0.1765293 | 0.1833954 | | 0.1135145 | 0.0721949 |
| 51 | 1 | 2.6636177 | 1.6224367 | 2.8016447 | 3.9591947 | | 4.7280252 | 3.5682493 |
| 52 | 1 | 0.4729306 | 1 | 0.614407 | 0.8400957 | | 0.6354079 | 0.3006248 |
| 53 | 1 | 1 | 1 | 1 | 1000 | | 1000 | 1000 |
| 54 | 1 | 1 | 1 | 3.7674397 | 2.3381877 | | 1 | 1 |
| 55 | 1 | 1 | 1 | 0.2521423 | 0.3751351 | | 0.3212522 | 0.177765 |
| 56 | 1.298134 | 1.2975125 | 1 | 1.9023067 | 1.8333063 | | 1.8364165 | 2.1370099 |
| 57 | 0.2664442 | 0.3117722 | 0.2541745 | 0.4827274 | 0.2742164 | | 0.3522382 | 0.6097858 |
| 58 | 1 | 0.4367097 | 1 | 0.7676061 | 1 | | 0.4552797 | 0.3566225 |
| 59 | 0.7553469 | 2.1005562 | 2.1964577 | 1.705636 | 1.6313868 | | 1.5730606 | 2.5473766 |
| 60 | 2.1556983 | 1 | 1 | 2.2472893 | 2.374085 | | 1.8553424 | 2.8459465 |
| 61 | 3.7608569 | 1.6106619 | 3.165087 | 4.5160052 | 2.4678798 | | 4.0582358 | 4.6508871 |
| 62 | 1.6968751 | 1.865831 | 1.4976363 | 2.1390941 | 3.1434614 | | 2.9111699 | 1.2717203 |
| 63 | 1.1758235 | 2.0026597 | 1.2811425 | 2.0840176 | 2.004286 | | 2.3803905 | 1.8804507 |
| 64 | 1 | 2.0324677 | 1 | 2.1899493 | 2.231777 | | 2.1119375 | 1.5900943 |
| 65 | 1.4085967 | 3.4269298 | 1.7564802 | 2.7030487 | 2.0060772 | | 2.3598544 | 3.0207129 |
| 66 | 1 | 0.4652695 | 0.7369059 | 0.6209905 | 0.7951415 | | 0.5641913 | 0.2910642 |
| 67 | 1.8183424 | 2.1152081 | 1 | 2.7910463 | 2.3361468 | | 1.4661897 | 2.3858833 |
| 68 | 1.4696315 | 3.097493 | 1.4655722 | 3.3953469 | 2.761162 | | 2.0069311 | 3.8093873 |
| 69 | 1.4600175 | 1.9740016 | 1 | 2.4541497 | 2.3079435 | | 1.7175263 | 1.8624036 |
| 70 | 1 | 1 | 1.9293718 | 7.7522171 | 1 | | 1 | 4.5870795 |
| 71 | 0.5099593 | 2.2727389 | 1 | 1.6165219 | 1.7770776 | | 2.4154923 | 0.5330589 |
| 72 | 0.3118207 | 0.2171221 | 0.25599 | 0.7731907 | 0.5546754 | | 0.3312461 | 0.4270481 |
| 73 | 2.5668237 | 1 | 1 | 1 | 1.272363 | | 1 | 1 |
| 74 | 1.7063686 | 2.4321388 | 1.621006 | 1.7231018 | 2.1533236 | | 2.0592992 | 1.7426602 |
| 75 | 1 | 1 | 1 | 1 | 1 | | 1 | 1000 |
| 76 | 1.9014851 | 1.5366216 | 1.8049827 | 2.2306301 | 1.7352453 | | 1 | 2.0693407 |
| 77 | 0.8551006 | 0.4997872 | 0.7169075 | 0.6587012 | 0.8378501 | | 0.6118663 | 0.3509979 |
| 78 | 1 | 0.4237548 | 0.7049381 | 0.6021695 | 0.8174469 | | 0.5640106 | 0.2502082 |
| 79 | 0.8646927 | 0.428108 | 0.7988452 | 0.6319662 | 0.7478512 | | 0.5197252 | 0.2659211 |
| 80 | 1.7007951 | 2.429661 | 1.9207179 | 4.5700682 | 3.024067 | | 2.2690104 | 3.7515954 |
| 81 | 2.5961804 | 1.9505389 | 2.3266462 | 6.624488 | 5.8872086 | | 1 | 4.4084392 |
| 82 | 1 | 1.7796781 | 1.4974281 | 2.5577148 | 1.7290795 | | 1.2081605 | 3.6245575 |
| 83 | 2.0870533 | 2.4139024 | 1 | 4.3042264 | 2.2769061 | | 1.9618621 | 1.9161788 |
| 84 | 8.6605923 | 3.281364 | 1 | 2.5583118 | 1.7372814 | | 2.1371692 | 4.5224027 |
| 85 | 0.0770326 | 0.7528227 | 0.3578818 | 0.3748227 | 0.3321899 | | 0.1111985 | 0.2712974 |
| 86 | 1.3604171 | 2.0296394 | 1.3864687 | 2.649841 | 2.2000255 | | 1.7090872 | 2.5782188 |
| 87 | 1.6290513 | 3.4355131 | 1 | 3.7617141 | 4.6973677 | | 4.3112934 | 4.7885535 |
| 88 | 1.5210852 | 2.2157792 | 1 | 2.2000586 | 1.9374337 | | 2.2743221 | 1.6164604 |
| 89 | 0.5842107 | 2.0141021 | 1 | 1.4449822 | 1.7935668 | | 1.4354138 | 1.9216668 |
| 90 | 1.2088484 | 1.843598 | 1 | 2.0791049 | 1.93243 | | 1.8203393 | 1.7808219 |
| 91 | 1.2974223 | 3.4275692 | 1 | 1.8947907 | 1.9421922 | | 1.7784561 | 2.0153793 |
| 92 | 1.5892155 | 4.530248 | 2.725358 | 3.5818992 | 3.8023499 | | 3.6716364 | 4.24206 |
| 93 | 1 | 0.5217989 | 1 | 0.6715277 | 0.6768552 | | 0.6276578 | 0.3733412 |
| 94 | 1.2383146 | 2.5823099 | 1.6116813 | 2.6456382 | 1.5676941 | | 3.7056823 | 5.2817187 |
| 95 | 5.9547704 | 3.3384221 | 3.769672 | 6.7527453 | 1 | | 4.7475444 | 4.3623186 |
| 96 | 1.3071786 | 2.1187004 | 1.5957115 | 2.4541497 | 2.1095221 | | 1.8213396 | 2.0707934 |
| 97 | 1.6604557 | 3.3966792 | 2.7669818 | 1000 | 1 | | 1 | 1 |
| 98 | 2.639345 | 0.7135338 | 2.8012284 | 1.7597341 | 2.3969827 | | 1 | 2.5359225 |

Table 4

| SEQ ID NO | Patient ID | | | | | | | |
|--------------|------------|-----------|-----------|-----------|-----------|-----|-----------|-----------|
| | 141 | 156 | 228 | 264 | 266 | 267 | 268 | 278 |
| 99 | 1 | 0.4633205 | 0.7667513 | 0.6688876 | 0.788519 | | 0.6098466 | 0.3109924 |
| 100 | 0.8773398 | 0.5611001 | 0.7022909 | 0.7045982 | 0.8904148 | | 0.5971662 | 0.2469489 |
| 101 | 2.7417486 | 2.7820502 | 2.5149176 | 3.1005109 | 3.5758893 | | 2.2876179 | 4.0751966 |
| 102 | 1.3426892 | 1.819379 | 1 | 2.5243098 | 1.7585304 | | 2.0770616 | 2.4547816 |
| 103 | 0.4474353 | 0.4779846 | 0.597857 | 0.5368613 | 0.8094407 | | 0.3485279 | 0.3296542 |
| 104 | 1 | 0.479159 | 1 | 0.6746748 | 0.6536243 | | 0.5719451 | 0.3441876 |
| 105 | 1.6979153 | 2.4381336 | 1 | 1.9798087 | 3.0541962 | | 1.5730167 | 1.7269225 |
| 106 | 1.3613917 | 2.6859306 | 1.3619403 | 2.3547365 | 2.8439924 | | 4.1142381 | 1.3568841 |
| 107 | 0.6557136 | 0.8089155 | 1.8866761 | 1.4851439 | 2.0435453 | | 1.9671358 | 2.6800702 |
| 108 | 2.0715263 | 1.9884444 | 1 | 1.5702741 | 2.2712581 | | 1.2918362 | 1.9671541 |
| 109 | 1.9009814 | 1 | 1.9459605 | 2.2870773 | 1 | | 2.506722 | 2.3911727 |
| 110 | 1.8861553 | 1.1966463 | 1.1800995 | 1.2384229 | 2.2866327 | | 2.2089696 | 2.3979147 |
| 111 | 1.2000775 | 1.878835 | 1.4096258 | 2.1463341 | 2.8265488 | | 1.5410952 | 1.4703261 |
| 112 | 2.4316908 | 1 | 0.5458493 | 1 | 1 | | 1 | 1.2547409 |
| 113 | 1 | 0.4842131 | 0.787 | 0.645008 | 0.756551 | | 0.5551696 | 0.2996004 |
| 114 | 1 | 0.4694813 | 0.7434041 | 0.673071 | 0.7072261 | | 0.5731377 | 0.2981788 |
| 115 | 1 | 3.6283548 | 1 | 1.3753373 | 1 | | 1.7870859 | 1.529726 |
| 116 | 0.9115583 | 0.5238771 | 0.744616 | 0.6327062 | 0.8095819 | | 0.5988735 | 0.2979056 |
| 117 | 1 | 0.5318578 | 0.6976557 | 0.6929223 | 0.6330908 | | 0.5248713 | 0.3303682 |
| 118 | 0.5369837 | 0.4669665 | 0.5238625 | 0.4142943 | 1 | | 0.3346117 | 0.2238483 |
| 119 | 0.7793929 | 0.5143284 | 0.6430526 | 0.5768024 | 0.8255054 | | 0.5095502 | 0.2719554 |
| 120 | 0.7314432 | 0.5029353 | 0.6171001 | 0.5487677 | 0.8352354 | | 0.4435606 | 0.2807648 |
| 121 | 1 | 5.5218294 | 1.385271 | 2.2056872 | 2.1065207 | | 1 | 1.5221147 |
| 122 | 0.2777774 | 1 | 0.4137001 | 0.1917251 | 0.2186291 | | 0.2568164 | 0.2336013 |
| 123 | 1.6809648 | 1.6248096 | 2.6786697 | 4.6996659 | 4.0351873 | | 1.804079 | 3.9164225 |
| 124 | 9.9735087 | 10.560436 | 1.7620652 | 6.6537847 | 5.2289454 | | 4.2811582 | 1 |
| 125 | 1 | 2.0627306 | 1.9694536 | 1.8289423 | 1.4254334 | | 1.421437 | 2.2152267 |
| 126 | 0.5896747 | 0.776267 | 1.9860089 | 1.5259007 | 2.0363095 | | 1.6807936 | 2.9946882 |
| 127 | 1 | 0.4499782 | 0.7169484 | 0.6442336 | 0.8272818 | | 0.5488108 | 0.3217015 |
| 128 | 1 | 0.4919172 | 0.7171531 | 0.6237872 | 0.9164479 | | 0.5740251 | 0.265083 |
| 129 | 1 | 1 | 1 | 1 | 1.8162714 | | 1 | 1000 |
| 130 | 1 | 1 | 1.9891014 | 1000 | 1000 | | 1 | 1000 |
| 131 | 1 | 1 | 1.937556 | 1 | 1000 | | 1 | 1 |
| 132 | 1.8116301 | 2.4782895 | 2.4496068 | 3.7843482 | 3.833139 | | 2.514328 | 1 |
| 133 | 1 | 2.3248352 | 1.4417969 | 3.3132452 | 3.5017515 | | 1.8673318 | 1.6995072 |
| 134 | 1 | 0.4728998 | 0.8227754 | 0.6444284 | 0.7282764 | | 0.5237151 | 0.3684367 |
| 135 | 0.8272111 | 0.5696158 | 0.7046481 | 0.7227974 | 1 | | 0.6437928 | 0.3387182 |
| 136 | 0.3771369 | 5.7797468 | 1.7189821 | 0.4140931 | 0.4935724 | | 0.1575211 | 1 |
| 137 | 1.5053064 | 1 | 1 | 3.2623914 | 3.0370011 | | 1 | 2.2752846 |
| 138 | 0.2832523 | 1.5445532 | 0.3786395 | 0.5483716 | 0.3221969 | | 0.3898424 | 1.277854 |
| 139 | 1.5834887 | 4.8524664 | 1.7901487 | 2.6410851 | 2.6562891 | | 1 | 4.0939329 |
| 140 | 1 | 3.4275754 | 1 | 1.8144111 | 1 | | 1 | 1.66476 |
| 141 | 1.7244141 | 3.9531433 | 1.4316089 | 2.4368472 | 2.3547241 | | 1.954445 | 1.7917669 |
| 142 | 2.4398047 | 2.9177292 | 1.3644553 | 2.5102707 | 2.249016 | | 2.7621865 | 1.2472973 |
| 143 | 1.4992511 | 2.2330872 | 0.7063719 | 1.7733584 | 2.3893286 | | 1.6473792 | 2.6512084 |
| 144 | 1.2156593 | 1.2718425 | 1 | 1.6409282 | 1.6784892 | | 1 | 2.531136 |
| 145 | 1.9933987 | 2.7627931 | 2.4132902 | 2.6010659 | 3.1770445 | | 3.543046 | 2.770455 |
| 146 | 1.397603 | 2.0129831 | 1.4136977 | 1.9957201 | 1.6774372 | | 2.1955427 | 2.2231235 |
| 147 | 1 | 3.3234197 | 1 | 1.5777974 | 1 | | 2.0602027 | 2.2063118 |

Table 4

| SEQ ID NO | Patient ID | | | | | | | |
|--------------|------------|-----------|-----------|-----------|-----------|-----|-----------|-----------|
| | 141 | 156 | 228 | 264 | 266 | 267 | 268 | 278 |
| 148 | 1.3630013 | 1.7550103 | 1.7474392 | 2.3302795 | 2.8138619 | | 2.4025157 | 1.7019967 |
| 149 | 1 | 0.4789561 | 0.6913711 | 0.5566583 | 0.7236113 | | 0.5255027 | 0.2262136 |
| 150 | 0.5318263 | 1.4497248 | 1 | 1.072867 | 0.6488462 | | 0.4005673 | 0.828264 |
| 151 | 2.6274534 | 1 | 1.4007965 | 6.9021719 | 4.0351873 | | 1 | 2.1920329 |
| 152 | 1.4462316 | 1.4247189 | 1 | 1.9995165 | 1.8488444 | | 1 | 1.3152458 |
| 153 | 1.8586491 | 1 | 1.8201524 | 2.1052884 | 2.2797407 | | 2.484835 | 1 |
| 154 | 1.9890187 | 2.3080559 | 1.5385113 | 4.0081198 | 1.9232438 | | 1.9005229 | 2.2764455 |
| 155 | 1.3684105 | 1 | 1.3077292 | 3.5573224 | 1 | | 1 | 2.3677554 |
| 156 | 1.7382 | 3.8781193 | 1 | 1.9637469 | 1.8878678 | | 1.8741013 | 2.3889439 |
| 157 | 1.2457496 | 3.5414457 | 1.4108132 | 2.1561044 | 1.6043807 | | 1 | 1.7278413 |
| 158 | 1.255725 | 1 | 5.4499278 | 5.2113179 | 5.335184 | | 2.0945879 | 5.2879393 |
| 159 | 0.7936277 | 0.4543436 | 0.791887 | 0.7046629 | 0.6919929 | | 0.534419 | 0.3722982 |
| 160 | 0.8262366 | 0.4968974 | 0.6893664 | 0.6917292 | 1 | | 0.6390977 | 0.3077207 |
| 161 | 0.8363434 | 0.509588 | 1 | 0.6199569 | 1 | | 0.6055799 | 0.3164246 |
| 162 | 0.5619495 | 0.4503779 | 1 | 0.6310307 | 1 | | 1 | 0.7153372 |
| 163 | 1 | 1.9720894 | 2.4056641 | 2.2988629 | 1.4656333 | | 1.3070889 | 2.8826803 |
| 164 | 2.7408178 | 1 | 2.752129 | 1.7320868 | 2.4175516 | | 1 | 2.5061171 |
| 165 | 0.5726914 | 1 | 1 | 0.379346 | 0.6716614 | | 0.7538376 | 2.1338437 |
| 166 | 3.2920145 | 1.867571 | 1.8691761 | 3.090645 | 2.5016827 | | 1.8357584 | 3.9973399 |
| 167 | 1 | 0.3215667 | 1.117592 | 0.3849738 | 0.2886365 | | 0.1956019 | 0.6023546 |
| 168 | 1 | 0.3057405 | 1 | 0.755945 | 2.0573812 | | 1 | 1 |
| 169 | 1.4995795 | 1.4364871 | 1 | 1.6342878 | 1.4011801 | | 1.3912205 | 1.2415424 |
| 170 | 1.274734 | 2.8108621 | 2.0292144 | 2.7607197 | 1.6876484 | | 1 | 3.1415302 |
| 171 | 1.7028975 | 2.4199464 | 1.8785875 | 5.0637791 | 2.6189005 | | 2.7730612 | 3.2988765 |
| 172 | 2.8236758 | 2.0099457 | 1.5488184 | 1.7731535 | 1.9574898 | | 1.6744504 | 1.5714077 |
| 173 | 1.6615726 | 2.2449969 | 1.901144 | 3.376967 | 2.7973471 | | 1.8113281 | 2.3166124 |
| 174 | 1.7110662 | 1.9245861 | 1 | 1.754022 | 1.1819013 | | 2.1911033 | 2.6080553 |
| 175 | 1.1324947 | 2.2960294 | 0.7410796 | 2.6015069 | 1.7571982 | | 1.2814656 | 1.6600418 |
| 176 | 1.4356649 | 3.6041973 | 2.213748 | 3.3005611 | 2.0463096 | | 5.8085356 | 3.2306176 |
| 177 | 0.2115523 | 1 | 0.4717015 | 0.324132 | 0.4863727 | | 0.4518806 | 0.3036233 |
| 178 | 0.6881691 | 3.4827705 | 1.6205877 | 2.07108 | 1.7533904 | | 2.4915372 | 2.0131009 |
| 179 | 2.1570999 | 1.5194058 | 1.6231006 | 3.0728223 | 3.1577259 | | 1.7864626 | 1.7501908 |
| 180 | 1.3081313 | 1.4034881 | 1.3251583 | 1.5935256 | 1.7910279 | | 1.3541106 | 1.3702379 |
| 181 | 1 | 1 | 1 | 4.41569 | 1.9854715 | | 1 | 2.3597717 |
| 182 | 1.3656402 | 1.6893505 | 1.3772715 | 1.9943195 | 1.8274326 | | 1.9023837 | 1.4787072 |
| 183 | 2.4840862 | 0.5716632 | 2.8592531 | 1.6659743 | 2.1581319 | | 0.586305 | 2.5574587 |
| 184 | 0.3832469 | 1.8703563 | 1.5389197 | 1.3802357 | 1.4656333 | | 1.6435352 | 1.468712 |
| 185 | 1.6567655 | 1.4557873 | 1.3374809 | 2.1403471 | 1.1841136 | | 2.5945577 | 3.2642286 |
| 186 | 1.4581451 | 1.7587117 | 1.5320375 | 1.8820565 | 1.7611117 | | 1.5411795 | 1.5974013 |
| 187 | 0.8263023 | 1.664074 | 1.3102756 | 1.7501812 | 1.2528908 | | 1.2566874 | 1.5376538 |
| 188 | 1.9496209 | 3.728311 | 1.7398553 | 2.5612151 | 2.5336539 | | 2.5709999 | 1.6709558 |
| 189 | 1.4440744 | 2.9486193 | 1.4959123 | 2.5321402 | 3.1770445 | | 3.0982902 | 1.8083427 |
| 190 | 1.2937212 | 1 | 0.6444052 | 0.5358753 | 1 | | 1 | 0.6793298 |
| 191 | 1 | 3.6231408 | 1.8977452 | 3.0438115 | 2.0370845 | | 1 | 1 |
| 192 | 0.8896585 | 0.5276154 | 0.7959262 | 0.6401542 | 1 | | 0.5858296 | 0.3199012 |
| 193 | 1.6704091 | 1.9843925 | 1 | 1.9954087 | 2.7991474 | | 2.4282958 | 2.1324717 |
| 194 | 0.3552918 | 0.2644533 | 0.291124 | 0.6809254 | 0.8794986 | | 0.5395774 | 0.5123485 |
| 195 | 0.8905126 | 0.5263488 | 0.7578767 | 0.6185675 | 0.7827801 | | 0.5932244 | 0.2846263 |
| 196 | 2.4808231 | 1.3536176 | 1.8007993 | 2.9646644 | 3.7352016 | | 2.7047763 | 3.3263477 |

Table 4

| SEQ ID | Patient ID | | | | | | | |
|--------|------------|-----------|-----------|-----------|-----------|-----|-----------|-----------|
| NO | 141 | 156 | 228 | 264 | 266 | 267 | 268 | 278 |
| 197 | 1 | 0.5255741 | 0.8404747 | 0.6810342 | 0.8681422 | | 0.5600195 | 0.3128176 |
| 198 | 1 | 2.5868598 | 1.6989101 | 2.4071855 | 2.0100755 | | 1.9248029 | 3.2282709 |
| 199 | 1.4780192 | 1.6272137 | 1 | 1 | 1 | | 1 | 2.3858336 |
| 200 | 2.1934317 | 1 | 1 | 1 | 1 | | 1 | 1 |
| 201 | 2.0593719 | 1.4362719 | 1.5050834 | 3.7297159 | 3.3791485 | | 1.9273705 | 2.2652646 |
| 202 | 1 | 3.9445354 | 2.3536023 | 2.7201051 | 1 | | 1 | 2.5892011 |
| 203 | 1.5957636 | 2.8455212 | 1.8503155 | 1 | 3.1654827 | | 1 | |
| 204 | 2.8454114 | 1 | 1.3302572 | 1 | 4.5148125 | | 2.7211032 | 1.9831278 |
| 205 | 1.4886953 | 1.2672742 | 2.0087167 | 2.5289689 | 2.1082439 | | 2.9724431 | 1.3731061 |
| 206 | 2.4844585 | 2.1704708 | 1.3819435 | 2.355821 | 2.3426746 | | 1 | 2.5983333 |
| 207 | 1.1729875 | 1 | 1.2075731 | 3.2582354 | 2.6850905 | | 2.031532 | 1.5574827 |
| 208 | 2.6792684 | 1 | 1 | 1 | 1000 | | 1 | 1000 |
| 209 | 0.1715961 | 0.3191995 | 0.2107102 | 0.3568207 | 0.2781458 | | 0.3041694 | 0.2821679 |
| 210 | 0.8801868 | 0.6391738 | 0.7405989 | 0.6413957 | 0.8241074 | | 0.6726425 | 0.3575414 |
| 211 | 1 | 1.6544516 | 1.6645034 | 3.5827354 | 3.4580731 | | 3.8225768 | 3.2918923 |
| 212 | 1.2012492 | 3.3128873 | 2.2947676 | 1.4495682 | 1.8331131 | | 1.2546727 | 0.8448398 |
| 213 | 0.8670579 | 0.4899004 | 0.7061667 | 0.6065008 | 0.7745465 | | 0.5322434 | 0.2315091 |
| 214 | 2.2160433 | 1.1737677 | 1 | 1.4062135 | 1.8697586 | | 1.43919 | 2.1173051 |
| 215 | 2.3584907 | 2.5417052 | 1.7143291 | 4.7170003 | 3.670771 | | 2.4242215 | 2.9973888 |
| 216 | 1 | 0.4559115 | 0.8231169 | 0.5857675 | 1 | | 0.5337609 | 0.2493204 |
| 217 | 1 | 3.837865 | 3.1828646 | 3.3558471 | 2.9157297 | | 1.2375877 | 4.2489449 |
| 218 | 2.3011131 | 3.1682868 | 1 | 1.9554893 | 1.8708645 | | 1 | 1.2215396 |
| 219 | 2.019569 | 3.8063908 | 1 | 1.7734814 | 1.9512325 | | 1.9426534 | 1.4138379 |
| 220 | 1.3398094 | 1.8373449 | 1.614374 | 2.8036921 | 1.9883081 | | 1 | 3.208144 |
| 221 | 1 | 0.4787102 | 0.7414879 | 0.6041465 | 0.786914 | | 0.5112097 | 0.2597626 |
| 222 | 0.8485963 | 0.5142547 | 0.7469036 | 0.6273265 | 0.7972915 | | 0.5635086 | 0.2792997 |
| 223 | 1 | 0.5043064 | 0.7471924 | 0.6051423 | 0.7425523 | | 0.4905552 | 0.2506427 |
| 224 | 0.8337701 | 0.4610763 | 0.7359129 | 0.5939242 | 0.7159873 | | 0.5165521 | 0.3394507 |
| 225 | 1 | 0.4979919 | 0.8324172 | 0.7308174 | 0.7485752 | | 0.5157106 | 0.4110869 |
| 226 | 1.7307212 | 1 | 1.7174153 | 3.6575359 | 2.9453486 | | 1 | 2.5845946 |
| 227 | 1.6027168 | 1.5508554 | 1 | 1.9287981 | 2.2101574 | | 1 | 2.5962474 |
| 228 | 1.1152157 | 2.7167469 | 1.3581117 | 1 | 1.4401541 | | 1 | 1 |
| 229 | 3.7054613 | 1 | 1 | 1 | 1.8015535 | | 1 | 1 |
| 230 | 2.2105464 | 1.3594033 | 1 | 1.4128159 | 1.8029538 | | 1 | 2.6028963 |
| 231 | 1 | 0.4955386 | 0.814286 | 0.6049277 | 0.8756692 | | 0.5676926 | 0.283962 |
| 232 | 1 | 1 | 2.3797616 | 1 | 1 | | 1 | 1000 |
| 233 | 1 | 1 | 1 | 1000 | 1 | | 1 | 1 |
| 234 | 1000 | 1 | 1 | 1000 | 1 | | 1 | 1000 |
| 235 | 0.2928664 | 1 | 0.3131395 | 0.1827727 | 0.1604832 | | 0.1003212 | 0.2511394 |
| 236 | 1.1384733 | 2.956766 | 1.4599793 | 2.5620703 | 3.2508084 | | 3.9983399 | 1.6323968 |
| 237 | 1 | 2.700644 | 1 | 1 | 1 | | 4.8799346 | 1.3472987 |
| 238 | 0.4052563 | 0.3056974 | 0.2305804 | 0.1979655 | 0.1740562 | | 0.2053678 | 0.1420245 |
| 239 | 0.9077258 | 0.4436944 | 0.7011867 | 0.5677418 | 0.8514856 | | 0.5493727 | 0.2395798 |
| 240 | 0.23043 | 0.3836666 | 0.3813196 | 0.2599515 | 0.8530722 | | 0.7146938 | 0.69377 |
| 241 | 0.3629896 | 0.4365376 | 0.4414865 | 0.3774501 | 1 | | 0.7141684 | 0.7966457 |
| 242 | 2.4134373 | 1.1588822 | 2.5078046 | 4.4169609 | 9.9395523 | | 1.816935 | 2.7278421 |
| 243 | 1.1365681 | 2.6301145 | 1.2706024 | 2.3146042 | 2.0010584 | | 1.4725502 | 2.1105568 |
| 244 | 1.2525933 | 1 | 1.4862365 | 2.7182742 | 2.2697764 | | 3.3912256 | 1.9308425 |
| 245 | 1.2218131 | 1.1162177 | 2.7071498 | 3.398806 | 1.5638539 | | 0.8377231 | 3.4885611 |

Table 4

| SEQ ID NO | Patient ID | | | | | | | |
|--------------|------------|-----------|-----------|-----------|-----------|-----|-----------|-----------|
| | 141 | 156 | 228 | 264 | 266 | 267 | 268 | 278 |
| 246 | 1 | 2.4051592 | 1 | 1 | 1 | | 1.5024692 | 1.8394954 |
| 247 | 1.9511539 | 2.4502216 | 1 | 2.180552 | 2.8008374 | | 2.4033355 | 3.2316109 |
| 248 | 2.8197229 | 6.7274033 | 1 | 1 | 1 | | 1.6632801 | 1 |
| 249 | 0.2499208 | 0.7329508 | 0.6679522 | 0.8328967 | 0.6765262 | | 0.2601565 | 0.4192755 |
| 250 | 1 | 3.0563841 | 1.4694584 | 2.5828546 | 2.8796526 | | 4.3385128 | 1 |
| 251 | 1 | 3.0050564 | 1.3698119 | 2.0538395 | 1.5462017 | | 0.7707268 | 5.3245613 |
| 252 | 1.6182875 | 1 | 3.1955502 | 6.4605073 | 1 | | 4.2001047 | 4.1906874 |
| 253 | 1.5151613 | 1 | 1 | 1.9230939 | 1 | | 1.8028669 | 4.3666768 |
| 254 | 1 | 0.4495909 | 0.737425 | 0.6023302 | 0.815292 | | 0.495782 | 0.2704406 |
| 255 | 1 | 1 | 0.5918894 | 1 | 0.4114616 | | 0.4368414 | 1 |
| 256 | 1 | 1 | 1 | 1000 | 1 | | 1000 | 1000 |
| 257 | 1 | 0.440528 | 0.6936618 | 0.5650327 | 0.8204733 | | 0.5147496 | 0.2393314 |
| 258 | 1 | 2.3379438 | 1.9337281 | 3.8782636 | 2.4752536 | | 1.8278385 | 3.7750313 |
| 259 | 2.0732236 | 1 | 2.4678144 | 2.7088698 | 1 | | 3.4867028 | 5.426183 |
| 260 | 0.1830497 | 1 | 0.2975794 | 0.5216526 | 0.2212821 | | 0.1504853 | 0.5034211 |
| 261 | 1 | 2.2201692 | 1.2638481 | 2.4193292 | 2.4626395 | | 2.7950697 | 1.4845801 |
| 262 | 1 | 1 | 1 | 1000 | 1 | | 1 | 1000 |
| 263 | 2.5363939 | 2.7040257 | 5.3225319 | 2.0844705 | 1 | | 1 | 2.2529972 |
| 264 | 4.6278272 | 1 | 1.933232 | 4.2280937 | 1 | | 1 | 3.3531856 |
| 265 | 0.7820208 | 0.4958645 | 0.6480066 | 0.5982725 | 0.8339842 | | 0.4620291 | 0.2920265 |
| 266 | 0.001 | 1 | 0.04573 | 0.0156661 | 0.012556 | | 0.0113324 | 0.0381306 |
| 267 | 1.4131519 | 2.7183517 | 1.2715027 | 2.3747043 | 2.8120426 | | 3.9136411 | 1.6718746 |
| 268 | 1.7335025 | 1.9766823 | 1.5303576 | 3.3935449 | 1.9676188 | | 5.8241452 | 4.9774373 |
| 269 | 3.1048586 | 3.9044717 | 2.3426287 | 4.1579844 | 2.6886178 | | 4.8580571 | 6.1287003 |
| 270 | 1.6801436 | 2.0225932 | 1.3639614 | 2.3478916 | 2.3385806 | | 1 | 2.2993847 |
| 271 | 1 | 0.4581742 | 0.790616 | 0.5799106 | 0.7786111 | | 0.5426222 | 0.2249409 |
| 272 | 1 | 0.5533468 | 0.8106512 | 0.665517 | 0.7279564 | | 0.5644682 | 0.3811945 |
| 273 | 0.806899 | 1.6450075 | 1 | 1 | 1 | | 1 | 1.4232619 |
| 274 | 0.5026338 | 1 | 0.3970699 | 0.5701845 | 1 | | 0.5570521 | 1 |
| 275 | 1 | 0.5341082 | 0.7374611 | 0.6234223 | 1 | | 0.5413866 | 0.2914118 |
| 276 | 0.001 | 1 | 3.5639595 | 5.9357503 | 1 | | 1 | 0.3249236 |
| 277 | 3.7000301 | 1 | 2.0706941 | 3.9646298 | 1 | | 1 | 1000 |
| 278 | 1.3548546 | 1 | 1.4636937 | 1.8345394 | 1 | | 1 | 2.8321333 |
| 279 | 1.9298345 | 2.5334293 | 1.7457796 | 2.9292401 | 2.6579124 | | 2.0737746 | 2.3847286 |
| 280 | 0.2104573 | 0.5146728 | 1.3159264 | 2.6430865 | 0.6106463 | | 0.1717825 | 1.2530709 |
| 281 | 1 | 0.4937556 | 0.7191924 | 0.5951403 | 1 | | 0.4797872 | 0.2846698 |
| 282 | 0.7141971 | 1.9205895 | 1.1646534 | 3.3457506 | 2.1893659 | | 1.6101441 | 2.1686529 |
| 283 | 1.3394918 | 1 | 2.5808866 | 3.7344354 | 1 | | 0.4318364 | 2.1277907 |
| 284 | 0.8673645 | 1.1965172 | 2.222889 | 1.8965704 | 1.9367327 | | 1.3712792 | 4.8655908 |
| 285 | 0.2060664 | 0.4327194 | 0.3179052 | 0.4170119 | 0.4169671 | | 0.150801 | 0.6334638 |
| 286 | 1 | 4.102927 | 1 | 1.8147973 | 1.5351837 | | 2.0779808 | 2.2923757 |
| 287 | 1 | 1 | 1 | 2.2663392 | 2.1344991 | | 1 | 1 |
| 288 | 1.600921 | 1 | 1.4001199 | 4.1485426 | 1 | | 3.6023913 | 2.8972322 |
| 289 | 1.1971539 | 2.6334839 | 1.2460041 | 2.2089891 | 2.1815413 | | 2.2296852 | 1.6562486 |
| 290 | 1.2647696 | 2.3413869 | 1.137822 | 2.1088178 | 2.4439576 | | 1.8267126 | 1.6025417 |
| 291 | 1.9108473 | 2.3065249 | 1.2728986 | 2.2834021 | 2.4434427 | | 2.5171359 | 1 |
| 292 | 1.3212164 | 1 | 1.4833114 | 3.6300239 | 1 | | 1 | 3.0491898 |
| 293 | 1 | 0.2074382 | 0.7157637 | 0.6576568 | 0.5311564 | | 0.4790896 | 0.7097313 |
| 294 | 2.0239599 | 1.9815704 | 1 | 1.8296837 | 1 | | 1 | 1 |

Table 4

| SEQ ID | Patient ID | | | | | | | |
|--------|------------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|
| | 141 | 156 | 228 | 264 | 266 | 267 | 268 | 278 |
| 295 | 1.3626399 | 2.3276635 | 1.4260558 | 3.0663141 | 2.5730959 | | 1 | 2.954453 |
| 296 | 1 | 0.5263488 | 0.7095507 | 0.6319558 | 1 | | 0.5071836 | 0.293535 |
| 297 | 0.8986922 | 0.4930731 | 0.7279028 | 0.6088009 | 0.8353056 | 0.5624758 | 0.5416625 | 0.220949 |
| 298 | 2.3162678 | 1.9775923 | 1.6563095 | 2.0630615 | 1.324101 | 1.2795378 | 2.0825118 | 4.2614047 |
| 299 | 1 | 0.4081807 | 0.6960642 | 0.6662682 | 1 | 0.4871285 | 0.6409733 | 0.2073655 |
| 300 | 0.7303482 | 2.1351846 | 1.6277278 | 1 | 1 | 2.6949833 | 1 | 4.0240289 |
| 301 | 0.1662197 | 0.1301638 | 1 | 1 | 1 | 1.1478659 | 0.5008676 | 0.276028 |
| 302 | 1 | 1.935721 | 1.7178459 | 3.183349 | 2.3908883 | 2.2884072 | 2.6800763 | 3.5357309 |
| 303 | 0.2204217 | 1 | 0.447585 | 1 | 0.8294611 | 0.5598273 | 0.6029297 | 1.5844572 |
| 304 | 0.3409693 | 5.8830171 | 2.3260718 | 0.6706415 | 0.3870858 | 0.6351475 | 0.2257882 | 0.8832312 |
| 305 | 1 | 1.5320041 | 2.0643983 | 2.9026459 | 2.2988703 | 3.6087525 | 1 | 1.7450193 |
| 306 | 0.3836959 | 0.2494632 | 0.565496 | 0.2471445 | 1 | 1.1378357 | 0.1456409 | 0.1987113 |
| 307 | 2.5254221 | 3.0262933 | 1 | 3.1683642 | 3.3128686 | 2.5901323 | 3.7535708 | 4.9786789 |
| 308 | 1 | 0.258606 | 1 | 0.2271142 | 1 | 0.4941777 | 1 | 1 |
| 309 | 0.2640243 | 3.0587513 | 0.3109882 | 0.2120772 | 0.2502861 | 0.2982521 | 0.1226284 | 0.3133019 |
| 310 | 0.3158721 | 1 | 1.4162746 | 0.819903 | 1.4083262 | 3.7861297 | 0.3087104 | 5.1106399 |
| 311 | 1 | 1.8124927 | 1 | 2.2030274 | 1 | 1.7047143 | 1 | 0.2866874 |
| 312 | 1 | 1.8366194 | 1 | 2.4075631 | 2.6778575 | 2.146204 | 1.8982181 | 2.2113528 |
| 313 | 1.4562179 | 2.1590408 | 1 | 1 | 1 | 1.901093 | 1 | 1.2323543 |
| 314 | 2.3927529 | 0.3916658 | 1 | 0.3861751 | 0.6719727 | 1.316261 | 1 | 0.7549827 |
| 315 | 0.3821738 | 0.2471637 | 0.1638835 | 0.1441627 | 0.1406735 | 0.4723221 | 0.2587303 | 0.0642112 |
| 316 | 1.1208111 | 1.2614884 | 0.665528 | 3.4481393 | 2.4233608 | 1.484243 | 2.1143148 | 1.9515095 |
| 317 | 1.6017751 | 1.8095414 | 1 | 3.1036462 | 1.9352246 | 1.4644703 | 4.6650057 | 2.3114845 |
| 318 | 1 | 0.0631882 | 1 | 1 | 1 | 3.9437998 | 1 | 2.0635858 |
| 319 | 1 | 1.4956911 | 1 | 1.7922464 | 1.9259052 | 1.9642511 | 1.4432817 | 1.7448641 |
| 320 | 0.1016261 | 0.2461984 | 0.1771184 | 0.5383869 | 0.0818073 | 0.0240783 | 0.0714113 | 0.2344891 |
| 321 | 1 | 0.7595554 | 0.7164441 | 0.6632505 | 1 | 0.6584157 | 1 | 0.3791582 |
| 322 | 1 | 1.8673004 | 1.4486699 | 2.5994798 | 1.9248397 | 1.2888857 | 1.9928068 | 1.854575 |
| 323 | 0.9345312 | 0.494807 | 0.7176242 | 0.6273573 | 1 | 0.5500417 | 0.6695573 | 0.2543118 |
| 324 | 0.252286 | 0.0269366 | 0.3869899 | 1 | 1 | 1.1376464 | 1 | 0.7164485 |
| 325 | 1 | 0.4761216 | 1 | 0.4179364 | 0.4713595 | 0.5298428 | 0.4380231 | 0.4274206 |
| 326 | 1.1009918 | 0.5888545 | 0.7768438 | 0.5613455 | 1 | 0.5272429 | 0.8362684 | 0.2341538 |
| 327 | 1 | 1.6663981 | 1 | 7.4402642 | 5.1480954 | 1.3415749 | 2.3987316 | 3.3927441 |
| 328 | 0.5927188 | 0.3936026 | 0.3449182 | 0.5759797 | 0.607554 | 2.5205385 | 1 | 1.1598738 |
| 329 | 1 | 0.4585677 | 0.6704001 | 0.4944674 | 0.5607001 | 0.4485082 | 0.4724378 | 0.3316595 |
| 330 | 1 | 1.4173899 | 1 | 1.7539418 | 1.644806 | 2.502947 | 1 | 1 |
| 331 | 4.030827 | 4.4685416 | 1 | 2.9628328 | 2.9861737 | 1.2875052 | 4.9268693 | 2.960655 |
| 332 | 1 | 1.4645858 | 1 | 3.1168838 | 3.2239995 | 1.5685728 | 1.5049973 | 1.3581319 |
| 333 | 1 | 1.7753188 | 1 | 2.6776746 | 2.534023 | 1.2952962 | 3.5938902 | 2.4366165 |
| 334 | 0.883636 | 0.5418676 | 0.6831428 | 0.5416019 | 0.8410095 | 0.4638082 | 0.574148 | 0.2582974 |
| 335 | 0.6764527 | 0.795604 | 0.6682187 | 1 | 1 | 0.6157088 | 0.4499358 | 0.4707599 |
| 336 | 2.0948496 | 0.5419598 | 1.7726333 | 1 | 1 | 3.1845024 | 2.1124125 | 1 |
| 337 | 0.878172 | 0.5301608 | 0.6802203 | 0.632508 | 1 | 0.5493373 | 0.5857687 | 0.2536537 |
| 338 | 0.3008379 | 1 | 1.4667131 | 1 | 1.4095529 | 3.4428028 | 0.3097507 | 5.1103854 |
| 339 | 2.2978501 | 2.2530944 | 1.8757822 | 3.0894007 | 1.2753011 | 2.4407294 | 1.5909595 | 4.0337633 |
| 340 | 0.2084863 | 29.452603 | 1 | 1 | 1 | 2.3887071 | 1.5135675 | 1 |
| 341 | 0.5142079 | 2.9697332 | 1.4940737 | 1.4813592 | 1.7166668 | 0.9310868 | 1 | 1.1630337 |
| 342 | 2.257193 | 1.4365117 | 1 | 2.0960867 | 1.5151941 | 2.2099016 | 1.3957002 | 3.6339753 |
| 343 | 1 | 1 | 1.3909209 | 4.029378 | 6.2443293 | 1.6183058 | 1.7926005 | 2.0088669 |

Table 4

| SEQ ID NO | Patient ID | | | | | | | |
|--------------|------------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|
| | 141 | 156 | 228 | 264 | 266 | 267 | 268 | 278 |
| 344 | 0.3229896 | 0.6325519 | 0.6304914 | 1 | 0.3499585 | 0.2329983 | 0.3526173 | 0.7075149 |
| 345 | 0.6550019 | 0.2483319 | 1 | 0.4543387 | 0.400023 | 0.6732772 | 1 | 0.6262313 |
| 346 | 0.8174548 | 0.545526 | 0.6949795 | 0.5694483 | 0.7980138 | 0.4404019 | 0.5767749 | 0.3042566 |
| 347 | 0.8983527 | 0.4568399 | 0.6372619 | 0.6224867 | 0.8075713 | 0.5092002 | 0.5965593 | 0.2301309 |
| 348 | 1.5490841 | 1 | 1.3964361 | 3.3483786 | 2.829422 | 2.4774362 | 2.5843242 | 2.3655701 |
| 349 | 0.7592231 | 1.0962474 | 1 | 5.7567293 | 6.498581 | 1.4597991 | 3.9082123 | 1.9219959 |
| 350 | 0.377323 | 0.6824162 | 1 | 0.595741 | 0.4485304 | 0.9795398 | 0.6502487 | 1.162326 |
| 351 | 3.6631289 | 2.7452452 | 1 | 2.3541586 | 1.7227868 | 1.6459947 | 2.8853809 | 2.963132 |
| 352 | 1 | 1.6440852 | 1 | 4.2723522 | 3.8058852 | 1.0326881 | 3.2935066 | 2.5124866 |
| 353 | 1.4486734 | 1.7259341 | 1 | 1.4940214 | 2.0692499 | 1.790758 | 2.4632193 | 2.0600285 |
| 354 | 0.3129156 | 0.3117783 | 0.7287826 | 1 | 0.3904282 | 1.0313055 | 0.3708658 | 1.2957832 |
| 355 | 1 | 0.5906744 | 1 | 1 | 0.2258557 | 0.125463 | 0.2159745 | 1 |
| 356 | 1 | 7.1848212 | 1 | 1 | 1 | 1.7424339 | 4.4717566 | 2.3327289 |
| 357 | 0.5638 | 0.5378711 | 0.6784202 | 0.3221384 | 0.3309843 | 0.4237647 | 0.647447 | 0.7158463 |
| 358 | 0.001 | 3.7698994 | 1 | 1 | 1 | 5.2388183 | 0.7172866 | 1 |
| 359 | 0.8865816 | 0.495016 | 0.729919 | 0.5811359 | 1 | 0.4212968 | 0.7008184 | 0.2620968 |
| 360 | 0.3078568 | 0.4140218 | 0.6159351 | 0.4431988 | 0.215919 | 0.2106703 | 0.6296989 | 0.8514702 |
| 361 | 1 | 0.3525244 | 0.7223702 | 0.3005117 | 0.3432859 | 2.2828193 | 0.6091741 | 1 |
| 362 | 1 | 4.8727934 | 1 | 1000 | 1 | 4.9585787 | 2.4906561 | 2.2533822 |
| 363 | 1.357592 | 1.2887632 | 1 | 5.5369783 | 2.9323166 | 2.9841569 | 1.5942454 | 2.2432877 |
| 364 | 1.1943836 | 2.3902245 | 1.7104385 | 6.8848313 | 3.0752521 | 1.1643863 | 1.7813234 | 3.5078065 |
| 365 | 1000 | 0.1667904 | 1 | 1 | 1 | 1.7697806 | 1 | 1 |
| 366 | 3.1191592 | 2.4240105 | 1 | 2.0376409 | 1 | 1.3736191 | 3.1844365 | 4.1337522 |
| 367 | 5.8729745 | 2.1379637 | 1.4163544 | 0.3859672 | 0.744945 | 2.150804 | 2.9187094 | 0.6442847 |
| 368 | 0.7068168 | 2.8971133 | 1 | 1 | 1 | 3.3956689 | 2.8235007 | 1.7781524 |
| 369 | 0.1522257 | 5.5578535 | 1 | 1.6826333 | 2.2046955 | 0.6424406 | 1 | 0.3754519 |
| 370 | 1 | 0.3794057 | 0.484389 | 0.5255722 | 0.4668188 | 0.7279759 | 0.3657741 | 0.5225175 |
| 371 | 1 | 1.8621787 | 1 | 3.1665337 | 2.1129169 | 1.3941736 | 1.8188117 | 0.6383372 |
| 372 | 1 | 0.6128459 | 0.0696741 | 0.0928352 | 2.8232232 | 11.776624 | 1 | 0.0982941 |
| 373 | 0.7826231 | 1.1352658 | 2.3406644 | 2.0770226 | 2.2319917 | 2.495068 | 1.6520642 | 3.8981084 |
| 374 | 3.8095183 | 1.6719563 | 1 | 2.4928994 | 2.8677851 | 3.5476546 | 2.1859184 | 2.1210549 |
| 375 | 1.1617529 | 1.8730124 | 1 | 1.1488807 | 2.0942849 | 1.9620314 | 1 | 1 |
| 376 | 1 | 1.6366516 | 0.5727502 | 1.8738295 | 2.6151605 | 1.3864511 | 2.7284817 | 1 |
| 377 | 0.426083 | 0.7045201 | 2.0317307 | 0.5943797 | 0.4640358 | 0.4421822 | 0.1002138 | 0.6315703 |
| 378 | 1 | 0.5994053 | 0.4711236 | 0.4391882 | 0.5855454 | 0.395548 | 0.2786183 | 0.5608281 |
| 379 | 0.8177504 | 0.5346185 | 0.6741058 | 0.6436122 | 0.8365005 | 0.6386147 | 0.5933806 | 0.2408773 |
| 380 | 0.4991518 | 0.4805486 | 1 | 0.505384 | 0.3776166 | 0.6948682 | 0.4064178 | 1 |
| 381 | 1 | 1 | 0.651671 | 0.6325706 | 0.7839 | 0.5365168 | 0.7114453 | 0.2745753 |
| 382 | 1 | 2.1012879 | 1 | 3.0601996 | 2.1397499 | 2.679141 | 6.6922333 | 1 |
| 383 | 0.5752427 | 0.5758934 | 0.6121828 | 0.4344019 | 0.7429566 | 0.446303 | 0.4197727 | 1 |
| 384 | 1.2300694 | 1.2912902 | 1.9196417 | 3.1829529 | 3.1090522 | 2.4974037 | 1.4919274 | 2.7307724 |
| 385 | 2.1115154 | 2.8340665 | 1 | 5.1859587 | 4.1349341 | 2.2378887 | 5.1441121 | 2.0782681 |
| 386 | 0.8924069 | 1 | 0.6817278 | 0.664422 | 1 | 0.5214866 | 0.6772994 | 0.2547712 |
| 387 | 0.9333596 | 0.3858616 | 0.6442675 | 0.5387839 | 0.7677951 | 0.5291687 | 0.576474 | 0.1775166 |
| 388 | 1 | 0.3662786 | 1 | 1 | 1 | 0.9621435 | 0.4472537 | 0.6555649 |
| 389 | 1 | 2.2612043 | 1 | 2.5084653 | 2.4325097 | 1.9017541 | 1 | 2.3223923 |
| 390 | 0.2222723 | 0.3643726 | 0.7912551 | 0.2824124 | 0.2692477 | 0.389683 | 0.3573242 | 0.5851393 |
| 391 | 1 | 0.7343465 | 1 | 0.8211402 | 0.3711474 | 0.4707163 | 0.2550692 | 1 |
| 392 | 2.03007 | 2.1883261 | 1 | 3.4444245 | 2.8936629 | 2.4016091 | 2.0171328 | 3.1483716 |

Table 4

| SEQ ID | Patient ID | | | | | | | |
|--------|------------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|
| | 141 | 156 | 228 | 264 | 266 | 267 | 268 | 278 |
| 393 | 1 | 0.5763607 | 1 | 0.4465804 | 0.4331147 | 0.3984311 | 1 | 1 |
| 394 | 0.9011778 | 0.4830756 | 0.6298065 | 0.6375797 | 0.7906064 | 0.568303 | 0.6718485 | 0.2185589 |
| 395 | 2.3747403 | 1.4409263 | 1.4990364 | 2.3297135 | 1.2628726 | 1.6361463 | 2.5366257 | 1.9202017 |
| 396 | 1 | 1 | 1 | 1 | 2.1053735 | 7.6399586 | 1 | 1 |
| 397 | 1 | 1.6528038 | 1.6568557 | 1.9359517 | 2.4273338 | 1.3903989 | 2.5326354 | 1.791562 |
| 398 | 0.792051 | 1.3286116 | 1 | 3.3786026 | 2.4652569 | 1.578966 | 2.2839091 | 1.8270418 |
| 399 | 1 | 0.6035432 | 1 | 1 | 0.1393431 | 0.2939551 | 0.292603 | 0.4410413 |
| 400 | 1 | 0.1403703 | 0.2971746 | 1 | 0.1270799 | 0.4015127 | 0.1941342 | 1 |
| 401 | 0.1086669 | 1.3412775 | 0.5345181 | 1 | 0.4906664 | 0.3390616 | 0.2093086 | 0.4361245 |
| 402 | 0.001 | 0.5572511 | 1 | 0.001 | 1 | 0.3588142 | 0.1806555 | 1 |
| 403 | 1 | 0.6025656 | 1 | 0.823131 | 0.1952623 | 0.1836036 | 1 | 0.4432825 |
| 404 | 0.1801589 | 0.4202932 | 0.4189432 | 0.2026507 | 0.2661521 | 0.7726577 | 0.2617554 | 0.5556505 |
| 405 | 0.0972133 | 0.076678 | 0.5170591 | 0.5250472 | 0.3390146 | 0.3803945 | 0.1774524 | 0.4053319 |
| 406 | 3.3341388 | 1.9959271 | 2.0437414 | 6.4697677 | 2.5947798 | 1.5035229 | 5.2174634 | 4.5252398 |
| 407 | 0.0989434 | 0.5877477 | 0.452017 | 0.4008895 | 0.2373227 | 0.2826945 | 0.1053763 | 0.4284946 |
| 408 | 1.4094727 | 2.0821599 | 1.4294367 | 2.0802322 | 2.0067135 | 2.2524513 | 1.7879364 | 2.0109404 |
| 409 | 0.001 | 0.5546688 | 1 | 1 | 1 | 0.1747193 | 0.1742694 | 1 |
| 410 | 2.2359064 | 1.9701956 | 4.0110192 | 8.1438595 | 3.5836237 | 1.4047555 | 5.5017188 | 4.7671415 |
| 411 | 0.4882128 | 2.1361315 | 0.54233 | 0.2998693 | 0.3806531 | 0.3864189 | 0.2516877 | 0.650586 |
| 412 | 0.7911969 | 0.4183872 | 0.6375314 | 0.487766 | 0.6321648 | 0.5900032 | 0.5025024 | 0.2422679 |
| 413 | 0.6414678 | 0.4469654 | 1.6127159 | 5.2776288 | 2.0644003 | 2.8088978 | 1.3721808 | 2.6080615 |
| 414 | 0.179491 | 0.7915768 | 0.0498214 | 0.0654134 | 1.8248926 | 15.062144 | 0.7460328 | 0.1895481 |
| 415 | 0.0705722 | 0.5423226 | 0.0031644 | 0.0214556 | 1.904505 | 14.863608 | 0.7299893 | 0.0535642 |
| 416 | 3.1268022 | 3.1109029 | 1.5595872 | 3.3202702 | 3.2723633 | 1.5494417 | 2.1379801 | 2.1325896 |
| 417 | 1.1944274 | 1.8092893 | 1.4033003 | 3.3663001 | 1.4435599 | 1.5969936 | 3.643857 | 3.2336782 |
| 418 | 1 | 1 | 1 | 1 | 1 | 2.3120609 | 2.0434671 | 1 |
| 419 | 1 | 1.4224931 | 1 | 2.6893118 | 1.944852 | 2.5198417 | 2.6024665 | 4.0208006 |
| 420 | 3.2206868 | 0.0550783 | 0.5820793 | 1.2175536 | 0.1057936 | 2.9331033 | 6.7073687 | 1.3326225 |
| 421 | 1 | 0.8289965 | 1 | 1 | 0.2399504 | 0.3613282 | 1 | 1 |
| 422 | 0.2865702 | 0.3517128 | 0.4408822 | 1 | 0.3715081 | 0.601267 | 1 | 1 |
| 423 | 1 | 1.1553837 | 1 | 2.7167343 | 1.8788456 | 1.6960969 | 1.4571659 | 1.8418793 |
| 424 | 0.4290942 | 0.3065275 | 0.4788371 | 0.4606531 | 0.8582381 | 0.6442265 | 0.4764243 | 0.6416958 |
| 425 | 1.6829358 | 1.6487335 | 2.0762273 | 2.0303621 | 1 | 1.7681785 | 1 | 2.2370484 |
| 426 | 0.451651 | 0.1108514 | 0.3806974 | 1 | 1 | 0.4832076 | 0.4731996 | 1 |
| 427 | 2.676279 | 2.6065596 | 1 | 3.7974584 | 2.1339754 | 2.1013849 | 1.8261798 | 2.6102034 |
| 428 | 1 | 0.5227335 | 0.651733 | 0.5707062 | 0.7715066 | 0.496148 | 0.6692074 | 0.234247 |
| 429 | 1.3364806 | 1.5601274 | 1.3533076 | 2.467487 | 1.37393 | 2.2034909 | 2.2133078 | 4.9388721 |
| 430 | 0.4562828 | 2.3558851 | 1 | 1.5536141 | 3.4291039 | 2.0317122 | 1.7754302 | 1 |
| 431 | 0.3062581 | 0.3155904 | 1 | 1 | 1 | 1.1859107 | 0.2114132 | 0.3106634 |
| 432 | 0.0400986 | 0.0131271 | 0.2138703 | 0.2506753 | 0.0258824 | 0.3261083 | 0.0222292 | 0.3589568 |
| 433 | 1.6265438 | 1.9354382 | 1 | 4.3689258 | 2.4141129 | 1.2869295 | 2.5859846 | 1.8093733 |
| 434 | 1 | 0.4178707 | 0.7029853 | 0.5280062 | 0.6726092 | 0.4996884 | 0.5825229 | 0.2344829 |
| 435 | 1 | 1000 | 1000 | 1 | 1000 | 1.3366403 | 1000 | 1 |
| 436 | 1 | 0.8352988 | 0.5741902 | 1 | 0.2638062 | 1.0553252 | 1 | 0.7876749 |
| 437 | 0.7876381 | 0.486611 | 0.6883464 | 0.5493846 | 0.6284879 | 1.1081411 | 0.5167748 | 0.279039 |
| 438 | 0.4823436 | 3.8103873 | 1 | 1 | 3.1211844 | 2.4911471 | 2.1312684 | 1 |
| 439 | 2.0067685 | 2.9694566 | 1 | 5.0180789 | 3.2608625 | 1.2986025 | 3.1330889 | 3.3649563 |
| 440 | 1.2799024 | 2.0473286 | 1 | 1.6946365 | 1.6222591 | 1.5203459 | 2.3377284 | 1.7277482 |
| 441 | 1.2456511 | 1.457515 | 1.687385 | 2.2089255 | 1 | 1.9057634 | 4.2788826 | 3.4617046 |

Table 4

| SEQ ID | Patient ID | | | | | | | |
|--------|------------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|
| | 141 | 156 | 228 | 264 | 266 | 267 | 268 | 278 |
| 442 | 0.2079388 | 4.1400701 | 1 | 0.4863192 | 1 | 0.5239747 | 0.5996765 | 1 |
| 443 | 0.8432637 | 0.5570175 | 0.718185 | 0.571484 | 0.7899961 | 0.3770429 | 0.6562312 | 0.3203606 |
| 444 | 1 | 0.4970942 | 0.6687701 | 0.6298291 | 0.7718232 | 0.5870866 | 0.7438072 | 0.2595949 |
| 445 | 1 | 2.2147462 | 1.3249253 | 1 | 1 | 1.3659002 | 1 | 1.4447298 |
| 446 | 0.2782701 | 0.2978274 | 0.5111051 | 0.8458052 | 0.7010347 | 0.9347789 | 0.4332542 | 0.5670922 |
| 447 | 3.015573 | 2.4978971 | 1.8471864 | 1 | 1 | 1.6542594 | 2.4782779 | 2.3072878 |
| 448 | 1.4412384 | 2.1654906 | 1 | 5.5857498 | 2.1540568 | 1.1019896 | 2.1736076 | 2.8448166 |
| 449 | 0.8556152 | 1.8220967 | 1 | 4.0751736 | 2.3955799 | 1.2917473 | 3.2898531 | 1.7148662 |
| 450 | 0.2587355 | 0.4770931 | 0.4880622 | 1.5021818 | 1 | 0.7368721 | 0.3691892 | 0.367313 |
| 451 | 1.3010138 | 1.6976202 | 1 | 3.3717733 | 1 | 0.9749473 | 2.0458412 | 2.1055034 |
| 452 | 1 | 1.3108609 | 1.3102528 | 1 | 1 | 0.8734501 | 1.5820261 | 3.4839671 |
| 453 | 0.3013306 | 0.5068765 | 0.4995397 | 0.5998768 | 0.4283636 | 0.5698278 | 0.4145962 | 0.7620414 |
| 454 | 1 | 1.2877179 | 1 | 1 | 1 | 1.785438 | 3.2386117 | 1.4828232 |
| 455 | 0.8771975 | 0.5098708 | 0.6855352 | 0.6085547 | 0.78768 | 0.5456242 | 0.68081 | 0.2630219 |
| 456 | 0.2221299 | 0.7269683 | 1 | 0.446791 | 0.3667115 | 0.6469662 | 0.4929628 | 1 |
| 457 | 1 | 0.5559415 | 0.5063289 | 1 | 0.4988301 | 0.5269559 | 0.4282134 | 0.3172627 |
| 458 | 1 | 2.8686149 | 1 | 1 | 2.1859958 | 2.1425046 | 2.9688411 | 1 |
| 459 | 2.1964648 | 2.1936446 | 1.8837524 | 3.548439 | 2.1543903 | 1.3738951 | 1 | 2.7040462 |
| 460 | 1 | 0.6606936 | 1000 | 1 | 1000 | 3.60103 | 38.647877 | 1 |
| 461 | 0.8814679 | 0.4865987 | 0.7314349 | 0.5805336 | 0.8253586 | 0.4862169 | 0.6533929 | 0.2672993 |
| 462 | 1.3709947 | 0.4029053 | 1 | 1 | 1.5718017 | 4.1321177 | 2.6455986 | 1 |
| 463 | 2.1984906 | 1.9897356 | 1.5414376 | 2.9499613 | 3.3279199 | 1.9329756 | 1.8543045 | 1.2124695 |
| 464 | 1.6559881 | 1.406132 | 1.0963278 | 1.7145159 | 1.9774035 | 2.5631834 | 1.6561429 | 1.7956781 |
| 465 | 1 | 1.8654559 | 1 | 1 | 1 | 2.5507506 | 1.9311356 | 1 |
| 466 | 0.1827431 | 0.1094003 | 1 | 1 | 1 | 2.0930612 | 0.4930965 | 0.3916553 |
| 467 | 1 | 5.9987073 | 1.621564 | 2.8073849 | 1 | 1.9309622 | 2.9877309 | 4.483285 |
| 468 | 1.4605431 | 2.1216394 | 1 | 4.5138799 | 2.8412055 | 1.2142413 | 1.8824282 | 1.8619752 |
| 469 | 2.1587643 | 1 | 1 | 1.9652557 | 1.755248 | 1.24208 | 2.291898 | 2.6688644 |
| 470 | 0.8352155 | 0.4886707 | 0.6648704 | 0.5747717 | 0.697689 | 0.6044935 | 0.6412213 | 0.2507545 |
| 471 | 1 | 0.1405486 | 0.3678469 | 0.2451327 | 0.17866 | 0.580149 | 0.1870965 | 0.3285057 |
| 472 | 0.9143067 | 0.405918 | 0.6727099 | 0.5204814 | 0.6816489 | 0.5296222 | 0.6008018 | 0.1910505 |
| 473 | 1 | 1.9124919 | 1 | 1.9552402 | 2.9341713 | 1.8761799 | 3.0033368 | 1.7803935 |
| 474 | 0.4619221 | 0.4719899 | 0.7044637 | 1.2553818 | 1 | 0.8760315 | 0.4116703 | 1.3631792 |
| 475 | 3.6602272 | 2.9936202 | 1 | 1 | 1 | 1.4466511 | 3.3934721 | 3.5023619 |
| 476 | 1.3635488 | 2.1668371 | 1 | 2.1160874 | 1.6066032 | 1.478685 | 2.6602117 | 1.7170887 |
| 477 | 1 | 2.2849437 | 1 | 2.3744103 | 1 | 1.445122 | 2.6950739 | 2.9986925 |
| 478 | 0.3209091 | 9.9754731 | 0.1516546 | 1 | 1 | 2.687633 | 1 | 1.3304993 |
| 479 | 2.3849019 | 2.175488 | 1 | 2.2459079 | 1.4685408 | 0.9305007 | 2.8315882 | 3.4021868 |
| 480 | 1 | 0.1136981 | 1 | 0.1133242 | 1 | 0.3170343 | 0.2424357 | 1 |
| 481 | 0.3288149 | 0.1600886 | 0.7146235 | 1 | 1 | 0.6736753 | 1 | 1 |
| 482 | 1.5938583 | 8.2193438 | 3.9969798 | 2.1320805 | 2.5242792 | 1.113715 | 2.4532459 | 2.4809926 |
| 483 | 0.8597433 | 1 | 0.6718583 | 0.5887835 | 0.752054 | 0.5643098 | 0.6987934 | 0.2380712 |
| 484 | 0.3011335 | 0.6610317 | 0.5176166 | 0.4744856 | 0.4108276 | 0.6182808 | 0.3968631 | 1 |
| 485 | 1 | 2.0784032 | 1 | 3.5301548 | 1 | 2.0853995 | 1.9278321 | 3.1260222 |
| 486 | 0.1034986 | 0.0983576 | 0.1121737 | 0.0812822 | 0.060551 | 0.1548744 | 0.0474864 | 0.2654306 |
| 487 | 2.0760267 | 1.685563 | 1.937556 | 1.7095881 | 1 | 1.1170132 | 5.1677003 | 1.7153194 |
| 488 | 0.8512243 | 0.4834076 | 0.7091634 | 0.6834424 | 0.7366411 | 0.5710057 | 0.6908006 | 0.2205393 |
| 489 | 1.2093193 | 2.7108935 | 1.8341945 | 4.5513639 | 2.970241 | 2.8425491 | 2.6854408 | 5.0957465 |
| 490 | 2.9876836 | 1.9397421 | 1 | 1 | 1.5982637 | 1.4449502 | 3.1111199 | 3.6555239 |

Table 4

| SEQ ID | Patient ID | | | | | | | |
|--------|------------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|
| | 141 | 156 | 228 | 264 | 266 | 267 | 268 | 278 |
| 491 | 0.30628 | 0.3953979 | 0.6351673 | 0.7861265 | 0.43153 | 0.6365817 | 0.2899963 | 1 |
| 492 | 1.0331242 | 2.1877112 | 1.4020212 | 3.6603275 | 2.895951 | 2.3980288 | 2.2882682 | 1.9332078 |
| 493 | 0.2445444 | 0.6620155 | 0.7123136 | 0.6781391 | 0.3948815 | 0.9670603 | 0.6585551 | 1.9943149 |
| 494 | 1 | 2.9607564 | 1 | 1 | 1 | 2.306357 | 1.9961247 | 1.6660017 |
| 495 | 0.1453491 | 1 | 0.1412267 | 1 | 0.100256 | 0.0512912 | 0.1172464 | 0.2550009 |
| 496 | 0.4165128 | 1.6569417 | 0.6337893 | 0.7397798 | 0.4812698 | 0.7799801 | 0.6962979 | 0.6949993 |
| 497 | 0.6483553 | 0.263322 | 0.3850798 | 1 | 1 | 0.7878226 | 0.4080128 | 0.4241241 |
| 498 | 1 | 2.6797268 | 1 | 1 | 1 | 0.8129234 | 1.9625454 | 2.4674712 |
| 499 | 1.5524786 | 1.5983096 | 1 | 2.2658707 | 1 | 1.155603 | 2.3922142 | 2.0700733 |
| 500 | 1 | 3.2261197 | 1.7554165 | 1 | 1 | 0.5386224 | 0.6835602 | 2.8789554 |
| 501 | 0.4899867 | 2.2663875 | 0.7927783 | 1.7802293 | 1 | 1.9679619 | 1.6144807 | 2.4582023 |
| 502 | 0.1352424 | 0.299137 | 1 | 0.468123 | 0.2073616 | 0.8100937 | 0.1833333 | 1.1631269 |
| 503 | 1.2273866 | 2.4187966 | 1.8941204 | 1 | 1.8009008 | 1.2204736 | 2.5806551 | 4.3770196 |
| 504 | 2.304639 | 2.7544557 | 1.7843423 | 3.3832207 | 2.2855061 | 1.4487588 | 1.6381837 | 2.9160244 |
| 505 | 0.4438547 | 0.0289226 | 0.3993633 | 1 | 0.3369005 | 1.377546 | 1 | 0.3999742 |
| 506 | 1.3715641 | 1 | 1 | 2.5473556 | 1 | 2.1503812 | 1 | 1.9254352 |
| 507 | 1 | 2.5292791 | 2.2122535 | 2.228557 | 1.2866907 | 1.1815041 | 2.4434588 | 4.2424201 |
| 508 | 1 | 2.3951495 | 2.0842082 | 1 | 1 | 1.6457718 | 3.1006771 | 2.3077906 |
| 509 | 1 | 4.2958609 | 1 | 1 | 1 | 1.1166825 | 2.1346594 | 1 |
| 510 | 1 | 1.3915108 | 0.3575033 | 1 | 1 | 0.4993303 | 0.2190618 | 0.510964 |
| 511 | 1 | 2.7571733 | 5.2034694 | 11.905577 | 11.780397 | 11.903503 | 9.7035654 | 10.836634 |
| 512 | 0.1155435 | 0.4323812 | 1 | 0.3732256 | 1 | 0.9565315 | 0.8250282 | 1 |
| 513 | 1 | 0.5522217 | 0.6389637 | 0.6442823 | 1 | 0.4327836 | 0.6738732 | 0.2926535 |
| 514 | 2.40805 | 2.7252872 | 2.6876489 | 5.9578729 | 2.2289175 | 2.0266678 | 8.1759438 | 5.4341853 |
| 515 | 1 | 0.7112712 | 1.3193357 | 2.6253616 | 1.5367432 | 1.6663308 | 2.3701777 | 1.4214305 |
| 516 | 1 | 2.0956251 | 1 | 1 | 2.162424 | 0.7164932 | 3.3249899 | 2.6673745 |
| 517 | 0.067342 | 0.444629 | 0.1817694 | 0.173544 | 0.3037028 | 0.9115107 | 0.2040854 | 0.2822982 |
| 518 | 0.4765292 | 2.3743245 | 1 | 1 | 5.0044448 | 4.4388153 | 3.415688 | 4.9359046 |
| 519 | 0.4241668 | 1 | 0.6823759 | 1 | 0.4681787 | 0.9190469 | 0.4823334 | 1.5823589 |
| 520 | 0.2207064 | 0.3410636 | 0.2259861 | 1 | 1 | 1.1474444 | 0.1996783 | 0.5453139 |
| 521 | 1 | 1.9035766 | 1.4326975 | 2.0493962 | 1 | 1.7291844 | 2.3654019 | 1.6801936 |
| 522 | 1 | 2.2694372 | 1.3703848 | 1.8961954 | 1 | 1.4396253 | 1.6508058 | 0.7847881 |
| 523 | 1.5119201 | 3.393113 | 1 | 1 | 1.7504793 | 1.8086128 | 2.0176384 | 2.1835464 |
| 524 | 1.1945697 | 1 | 0.7184178 | 1 | 1 | 0.5336167 | 1 | 0.2521327 |
| 525 | 2.0311978 | 2.471809 | 1.9962138 | 3.4563714 | 1 | 5.3794958 | 1.8059292 | 4.1969142 |
| 526 | 1.4869433 | 3.9594455 | 1.4341697 | 2.2589998 | 1 | 1.3996863 | 2.0812042 | 2.7020161 |
| 527 | 1.7787476 | 3.0617579 | 1.8527718 | 1.3725819 | 1.3536972 | 0.8855709 | 2.1341743 | 1.186271 |
| 528 | 1.1969897 | 3.4165511 | 1.8805093 | 1.8556128 | 1.3344866 | 1.3307212 | 3.6559141 | 3.7885713 |
| 529 | 0.001 | 0.6316419 | 1 | 0.001 | 1 | 0.9060968 | 1 | 0.2253693 |
| 530 | 1 | 1.2120729 | 1 | 0.3612728 | 0.2379418 | 0.8012812 | 0.3639409 | 1 |
| 531 | 2.3273491 | 2.7070384 | 1 | 1 | 1 | 1.8767271 | 4.0959951 | 1 |
| 532 | 1.424715 | 1 | 1 | 1 | 5.1461918 | 1.763816 | 2.4121834 | 5.6705617 |
| 533 | 0.1331728 | 0.0105631 | 0.1134528 | 0.3441875 | 0.3076408 | 0.4191512 | 0.1977234 | 0.2028522 |
| 534 | 2.1725612 | 1.864798 | 1.2813603 | 2.041979 | 1 | 1.7640721 | 3.9027985 | 1.8741991 |
| 535 | 1 | 0.6027255 | 1 | 1 | 0.8104966 | 2.0161334 | 3.6957175 | 1 |
| 536 | 1 | 0.5219218 | 0.6866844 | 0.6135423 | 1 | 0.5816143 | 0.6249152 | 0.2267785 |
| 537 | 0.4978159 | 8.4610968 | 1.4686852 | 2.1602321 | 4.2130414 | 1.8024436 | 2.3281661 | 1.7846523 |
| 538 | 1 | 3.350922 | 1.9298164 | 1 | 1 | 2.9429679 | 2.3648063 | 9.2403071 |
| 539 | 1.5502448 | 2.4379738 | 1.9483753 | 3.6226545 | 1 | 5.4567866 | 1.9830584 | 3.7274828 |

Table 4

| SEQ ID | Patient ID | | | | | | | |
|--------|------------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|
| | 141 | 156 | 228 | 264 | 266 | 267 | 268 | 278 |
| 540 | 1 | 2.791691 | 1.5028026 | 2.6606833 | 1 | 1.2101574 | 2.3561049 | 2.6820692 |
| 541 | 2.1121833 | 2.8670901 | 1 | 2.1775817 | 2.0242845 | 0.9834678 | 3.495571 | 3.8633612 |
| 542 | 1.5098834 | 1.6717534 | 1.4606018 | 2.8599122 | 1.7809435 | 1.3747413 | 2.7697898 | 2.7773275 |
| 543 | 0.8653278 | 0.4700408 | 0.6814874 | 0.5820793 | 0.6889578 | 0.5234682 | 0.6277137 | 0.2267537 |
| 544 | 0.1369177 | 0.1054468 | 0.4669582 | 1 | 0.2324838 | 0.6372159 | 0.1551756 | 0.5918814 |
| 545 | 1.2849722 | 2.3422662 | 1 | 1 | 1.7134543 | 1.3083573 | 1.7922014 | 3.6899792 |
| 546 | 0.7301292 | 1.5080434 | 1.5686436 | 1 | 3.3994531 | 1.3417889 | 3.3558814 | 5.0576966 |
| 547 | 1.3707757 | 1.7655181 | 1.7759332 | 2.5907906 | 1 | 1.0757087 | 3.3206791 | 3.9677331 |
| 548 | 1 | 1.7424612 | 1 | 2.9965027 | 1 | 2.3377065 | 2.038514 | 4.3845625 |
| 549 | 1.2658646 | 1.6038678 | 1.8156798 | 2.2497272 | 1 | 1.0345341 | 2.9638441 | 3.3673775 |
| 550 | 1 | 2.075458 | 2.6914882 | 2.6469159 | 1 | 1.468284 | 1.9818727 | 1 |
| 551 | 0.0507638 | 0.5596368 | 0.122339 | 0.1192141 | 0.0843743 | 0.5516562 | 0.0775135 | 0.0871256 |
| 552 | 1.637428 | 12.520775 | 1000 | 1 | 2.2819835 | 0.7248738 | 2.4861506 | 1 |
| 553 | 0.6782814 | 0.6725233 | 0.2799543 | 0.5458749 | 0.3538126 | 0.6513815 | 0.47839 | 0.5277013 |
| 554 | 1 | 0.4339737 | 0.578048 | 0.603638 | 1 | 0.5519513 | 0.5060812 | 0.1941173 |
| 555 | 1 | 2.4930029 | 0.0239998 | 0.086991 | 9.2033865 | | 2.1621812 | 0.0862192 |
| 556 | 1 | 2.9655031 | 0.5785805 | 2.6045976 | 1 | | 1 | 1.3486024 |
| 557 | 0.5842873 | 0.0991016 | 0.4826797 | 0.8139108 | 0.4511066 | | 1 | 0.5135715 |
| 558 | 1 | 0.6626795 | 1 | 1.6721098 | 1 | | 2.2273936 | 2.5496488 |
| 559 | 1 | 1.1967877 | 1 | 2.2478818 | 1.8873045 | | 2.0175661 | 1 |
| 560 | 1 | 1 | 1 | 1.7242246 | 1.5148643 | | 1 | 1 |
| 561 | 1.3581943 | 1.7850888 | 1.338431 | 1.3384403 | 1.4622149 | | 2.6333585 | 3.212738 |
| 562 | 0.5641395 | 0.4838257 | 1.4135651 | 3.097007 | 1.475422 | | 1 | 3.882203 |
| 563 | 1 | 0.4481091 | 0.7078181 | 0.5218229 | 0.782877 | | 0.5119436 | 0.2325335 |
| 564 | 0.7649828 | 2.1241542 | 1 | 1.3801861 | 1.2725492 | | 2.6739716 | 2.404067 |
| 565 | 1 | 0.4971495 | 0.6904716 | 0.5885396 | 0.8039141 | | 0.5411683 | 0.297111 |
| 566 | 1.2555389 | 2.8262702 | 1.4350162 | 2.7592306 | 2.7102943 | | 1.928888 | 2.0130077 |
| 567 | 0.788755 | 2.16613 | 4.3963747 | 2.870182 | 6.8329542 | | 1.63008 | 1 |
| 568 | 1 | 0.507356 | 0.7527597 | 0.6704247 | 0.7465274 | | 0.5691031 | 0.2905675 |
| 569 | 1.395424 | 0.7906729 | 1 | 0.415589 | 0.7270209 | | 0.361341 | 1 |
| 570 | 0.3830279 | 0.3489952 | 0.4277795 | 0.2933204 | 0.7503187 | | 0.2785797 | 0.1296578 |
| 571 | 0.8277258 | 0.4874042 | 1 | 0.4985605 | 0.6776659 | | 0.5065225 | 0.2782691 |
| 572 | 1.2611233 | 2.7683329 | 1 | 2.3490416 | 2.4031912 | | 2.6968797 | 0.9298484 |
| 573 | 2.0846443 | 2.7706877 | 1 | 2.3441617 | 2.0869989 | | 2.438489 | 2.0761759 |
| 574 | 1 | 0.3064721 | 0.4908595 | 0.499141 | 0.5168591 | | 0.784723 | 2.2756261 |
| 575 | 1 | 0.5462084 | 1 | 0.723902 | 1 | | 0.6096552 | 0.3147111 |
| 576 | 0.879705 | 0.4852091 | 0.7291986 | 0.6244014 | 0.7863893 | | 0.5384276 | 0.3613904 |
| 577 | 0.4717222 | 1.8435918 | 1 | 0.2467495 | 0.7616353 | | 1 | 1 |
| 578 | 1.4750079 | 1.7043221 | 1.9248385 | 2.0763481 | 1.54476 | | 1 | 1 |
| 579 | 0.843844 | 0.4391077 | 0.7264994 | 0.5626999 | 0.7917578 | | 0.5492923 | 0.2479794 |
| 580 | 0.5267784 | 0.1599902 | 0.8016577 | 0.5871795 | 0.6170411 | | 0.508465 | 0.6497168 |
| 581 | 1.4011398 | 2.0131306 | 1.3661123 | 4.9719073 | 2.9989142 | | 2.2507931 | 1.7633397 |
| 582 | 1.7023829 | 1.5078712 | 1.4604603 | 2.5845946 | 2.0428254 | | 1.4040816 | 2.0342149 |
| 583 | 3.4082259 | 2.1307823 | 1.5242603 | 3.4847834 | 2.4812553 | | 1.630882 | 2.3830275 |
| 584 | 1.7931357 | 2.9775172 | 1.3895362 | 2.6640088 | 1.5807998 | | 1.2207766 | 2.3902352 |
| 585 | 0.7916349 | 1.8203628 | 1.6067678 | 2.895417 | 1.9526013 | | 1.5439666 | 3.3380873 |
| 586 | 1.4304199 | 1.3909083 | 1 | 1.6368327 | 1.3981115 | | 1.9581125 | 1 |
| 587 | 0.374717 | 0.3722365 | 1 | 0.4423709 | 0.505494 | | 0.4378665 | 0.4577041 |
| 588 | 1 | 0.2668696 | 0.8155195 | 0.4186524 | 0.6920273 | | 1 | 0.7144122 |

Table 4

| SEQ ID NO | Patient ID | | | | | | | |
|--------------|------------|-----------|-----------|-----------|-----------|-----|-----------|-----------|
| | 141 | 156 | 228 | 264 | 266 | 267 | 268 | 278 |
| 589 | 0.4475777 | 0.9211503 | 0.2420343 | 0.3894147 | 1.5348451 | | 1 | 0.2998426 |
| 590 | 1 | 0.5319009 | 1 | 0.4986317 | 0.7952414 | | 0.5895439 | 0.2601288 |
| 591 | 1 | 0.6620278 | 1 | 0.477334 | 0.6582304 | | 0.514632 | 0.3039089 |
| 592 | 1 | 0.3905406 | 0.7547271 | 0.5031339 | 0.7834852 | | 0.4983295 | 0.2339055 |
| 593 | 0.7728996 | 0.3423856 | 1.4857677 | 1.377337 | 1.1331879 | | 0.6285539 | 2.4006525 |
| 594 | 0.3999565 | 0.6510527 | 0.7730826 | 0.4793708 | 0.5244591 | | 0.5551587 | 0.7736631 |
| 595 | 1.4054541 | 2.1969156 | 1.4441176 | 1.6681474 | 1.6134948 | | 2.0091494 | 2.4861391 |
| 596 | 0.8453332 | 0.5772215 | 1 | 0.5219933 | 0.84218 | | 0.6269734 | 0.44106 |
| 597 | 1 | 1 | 1 | 1 | 1000 | | 1 | 1 |
| 598 | 1 | 3.277392 | 1 | 1.6253563 | 2.2378057 | | 2.637179 | 1 |
| 599 | 1 | 1 | 1 | 1 | 1.7926889 | | 3.4897259 | 1 |
| 600 | 1 | 3.306745 | 1 | 4.3432074 | 32.932705 | | 1 | 1.9434886 |
| 601 | 0.6880049 | 0.1902962 | 0.509526 | 0.4422256 | 0.3070205 | | 0.2562873 | 0.4591258 |
| 602 | 1.4748327 | 1.5266549 | 1 | 1.9095024 | 1.5196944 | | 2.7359004 | 3.0886117 |
| 603 | 1.2715476 | 1.341505 | 1 | 2.1217045 | 1 | | 1.7264723 | 2.0640327 |
| 604 | 1 | 0.50106 | 1 | 2.3519217 | 2.9205022 | | 1 | 1 |
| 605 | 1 | 0.585442 | 0.7495182 | 1 | 0.6540789 | | 0.6143144 | 0.2978373 |
| 606 | 1.286111 | 2.0664874 | 1.4465845 | 3.3920448 | 2.658928 | | 1.4550963 | 1.6610475 |
| 607 | 1.34339 | 2.0483247 | 1.8136699 | 2.2267461 | 1.5450344 | | 2.3576822 | 2.7723485 |
| 608 | 0.8137975 | 2.4963046 | 1 | 1.3306415 | 1 | | 3.1343088 | 1.9011053 |
| 609 | 1 | 0.5123794 | 1 | 0.5103352 | 0.5261842 | | 1 | 0.4856968 |
| 610 | 0.6557574 | 2.4877398 | 1 | 1 | 0.7669996 | | 0.4094507 | 1 |
| 611 | 0.6034716 | 0.5510412 | 1 | 1 | 0.4156843 | | 0.285077 | 1 |
| 612 | 1 | 0.4484841 | 0.7486992 | 0.5781192 | 0.803877 | | 0.5800583 | 0.2416409 |
| 613 | 0.8999733 | 0.4132102 | 0.6755863 | 0.5284862 | 0.6621702 | | 0.5006495 | 0.2290259 |
| 614 | 0.6665102 | 0.4504394 | 0.7175354 | 0.4836706 | 0.6694515 | | 0.5008053 | 0.261805 |
| 615 | 1 | 0.5066182 | 0.6729261 | 0.483436 | 1 | | 0.6332798 | 0.3514325 |
| 616 | 1.3754404 | 1.1557342 | 1.247035 | 1.8311246 | 1.5353869 | | 1.2694272 | 2.2687226 |
| 617 | 0.0584068 | 0.2912362 | 0.4001691 | 2.0269295 | 1 | | 0.1974152 | 1 |
| 618 | 0.0584616 | 0.2806484 | 0.3812713 | 1.9872949 | 1 | | 0.18399 | 1 |
| 619 | 0.3787575 | 0.4785933 | 1.3646776 | 0.4914965 | 0.705255 | | 0.4242766 | 0.5913475 |
| 620 | 0.6784675 | 1.350365 | 0.6633256 | 1 | 1 | | 0.4856424 | 0.5319477 |
| 621 | 0.001 | 0.001 | 1 | 0.5948635 | 1.9944628 | | 0.5695978 | 1 |
| 622 | 0.7686072 | 1 | 2.0170494 | 3.171114 | 2.0456479 | | 4.3660781 | 2.0722027 |
| 623 | 2.4574779 | 1.331815 | 1 | 3.0830699 | 3.3057865 | | 2.1942603 | 2.6412877 |
| 624 | 2.0868452 | 1.5912204 | 1 | 1.5055418 | 1 | | 1 | 1 |
| 625 | 1 | 3.0524368 | 1 | 1.2871812 | 1 | | 1 | 1 |
| 626 | 0.3296581 | 1.8970961 | 0.5433387 | 0.4189999 | 0.4959363 | | 0.260231 | 0.3792948 |
| 627 | 0.6934032 | 0.1814792 | 0.6057666 | 0.4886015 | 0.3003665 | | 0.1785766 | 0.4017995 |
| 628 | 0.7221905 | 0.3720336 | 0.6169233 | 0.3652209 | 0.2825195 | | 0.157068 | 0.7524621 |
| 629 | 1 | 2.138554 | 1 | 2.223842 | 2.2030204 | | 1 | 1.7058333 |
| 630 | 1.4389827 | 1.7509154 | 1 | 5.9188094 | 2.8788187 | | 1 | 1 |
| 631 | 0.001 | 0.2900987 | 1 | 0.4063219 | 0.2238468 | | 0.188595 | 1 |
| 632 | 0.3452836 | 0.5574909 | 1 | 0.4834025 | 0.3051625 | | 0.28916 | 1 |
| 633 | 1.6255473 | 2.5205359 | 1 | 2.5346495 | 1.8426757 | | 2.2039584 | 2.2036857 |
| 634 | 0.6818401 | 1.6929289 | 1 | 2.4194818 | 1.6850737 | | 1 | 2.8581021 |
| 635 | 0.7627271 | 0.1856356 | 1 | 0.3637285 | 0.3066633 | | 0.2819291 | 0.4708716 |
| 636 | 1.1286075 | 2.4596595 | 1.4774087 | 1.7649962 | 2.0427655 | | 3.1770751 | 1.5775475 |
| 637 | 1.2934803 | 2.1451206 | 1 | 2.06723 | 2.180926 | | 1.8630101 | 2.5190052 |

Table 4

| SEQ ID | Patient ID | | | | | | | |
|--------|------------|-----------|-----------|-----------|-----------|-----|-----------|-----------|
| | 141 | 156 | 228 | 264 | 266 | 267 | 268 | 278 |
| 638 | 0.2190749 | 0.6024058 | 1 | 0.5996846 | 0.3989223 | | 0.407995 | 0.811384 |
| 639 | 1 | 1.4580622 | 1.4596117 | 2.4004081 | 1.3136774 | | 3.4778795 | 4.4046212 |
| 640 | 1.1543179 | 3.4223184 | 1 | 1.8525216 | 1.594784 | | 2.0427263 | 3.0991346 |
| 641 | 0.3947115 | 1 | 0.6227807 | 0.5796959 | 0.3850191 | | 0.4684981 | 0.4949345 |
| 642 | 1 | 0.4491789 | 0.7129133 | 0.5890095 | 0.8117067 | | 0.5729279 | 0.2860728 |
| 643 | 0.9176136 | 0.4075474 | 0.7877979 | 0.5208099 | 0.6959516 | | 0.4968312 | 0.2311242 |
| 644 | 1 | 2.8844289 | 1 | 2.2166468 | 1 | | 1.8237565 | 1 |
| 645 | 0.7302606 | 1 | 2.0128476 | 3.1837453 | 2.1786045 | | 4.5512159 | 2.3871187 |
| 646 | 1 | 0.484416 | 0.6704419 | 0.509177 | 0.6823105 | | 0.57085 | 0.2827018 |
| 647 | 0.8520127 | 0.4760233 | 0.7782797 | 0.4886731 | 0.6773559 | | 0.5384482 | 0.3756816 |
| 648 | 1 | 3.7511896 | 1 | 2.2403996 | 1 | | 1 | 2.6361039 |
| 649 | 1 | 3.1319246 | 2.326359 | 2.6100019 | 2.0595734 | | 2.0768319 | 3.0576515 |
| 650 | 1.3252241 | 5.1978955 | 1.9519075 | 1.5577142 | 1.2687441 | | 1 | 1.6474516 |
| 651 | 1 | 2.3379684 | 1 | 1.7851164 | 2.3722235 | | 1 | 1 |
| 652 | 1 | 2.0032623 | 1 | 1.8756617 | 1 | | 1 | 1 |
| 653 | 0.001 | 2.287981 | 1 | 1 | 1 | | 1 | 1 |
| 654 | 0.2162717 | 0.7769864 | 1 | 0.1387815 | 0.575031 | | 0.6474693 | 1 |
| 655 | 1 | 0.2776972 | 1 | 2.1106741 | 0.6586229 | | 1 | 1 |
| 656 | 1 | 0.5176548 | 1 | 1 | 0.3114939 | | 0.6791443 | 1 |
| 657 | 1 | 1 | 0.7905911 | 1 | 1 | | 0.5410488 | 1 |
| 658 | 1.2651091 | 2.3177029 | 1 | 1.7085223 | 2.0741224 | | 3.0637562 | 2.3089764 |
| 659 | 0.372954 | 0.6218781 | 0.3404343 | 0.1554883 | 0.2475359 | | 0.192046 | 0.197507 |
| 660 | 1 | 2.6728405 | 1 | 1.1676042 | 1.5539706 | | 1 | 1 |
| 661 | 0.6699485 | 1 | 0.7692242 | 0.444521 | 0.47802 | | 0.4012005 | 1 |
| 662 | 1.4314163 | 0.46032 | 1 | 0.3884232 | 1 | | 0.5367096 | 0.2612649 |
| 663 | 1 | 0.5682816 | 1 | 1 | 0.1280299 | | 1 | 1 |
| 664 | 1.6090568 | 2.0214742 | 1 | 2.1374257 | 1.4626144 | | 1.4319485 | 4.0982787 |
| 665 | 1.8594594 | 0.2236887 | 1 | 1.9917829 | 1 | | 4.4073996 | 3.9886609 |
| 666 | 1 | 1.5471294 | 1 | 2.4878074 | 1.4238875 | | 2.4485554 | 2.3418052 |
| 667 | 1 | 1.5957641 | 4.3549666 | 4.1975626 | 3.2634622 | | 1 | 2.2644079 |
| 668 | 1.7256843 | 2.0848529 | 1.4451975 | 2.649841 | 2.2025323 | | 1 | 3.4908271 |
| 669 | 1 | 1.7110547 | 1 | 2.6041556 | 2.824713 | | 1 | 1 |
| 670 | 1 | 1 | 1 | 2.9157716 | 1 | | 1 | 1 |
| 671 | 0.3559269 | 2.1504698 | 0.6895809 | 1.7577185 | 0.4056996 | | 1 | 1.7546606 |
| 672 | 1 | 3.8216883 | 1 | 2.0093604 | 5.4543663 | | 1 | 4.5441437 |
| 673 | 1 | 1 | 1 | 1.4900178 | 1.5121649 | | 1 | 2.2614528 |
| 674 | 1 | 1.2080333 | 1 | 4.0079104 | 4.0810982 | | 1 | 2.1598498 |
| 675 | 1 | 1 | 1 | 3.9474969 | 1 | | 1 | 1 |
| 676 | 1.3516134 | 1.8752689 | 1 | 1 | 1 | | 1.4350848 | 2.7158976 |
| 677 | 1.6075347 | 1.3660806 | 1 | 1 | 1.4073009 | | 2.1584542 | 1 |
| 678 | 1 | 0.4301923 | 0.7759879 | 0.5364672 | 0.7302941 | | 0.5558158 | 0.2371338 |
| 679 | 1 | 1.748536 | 1 | 2.3232241 | 1.3806906 | | 2.531725 | 3.1947157 |
| 680 | 1 | 3.7097671 | 1 | 2.8316276 | 1.6085344 | | 1 | 1 |
| 681 | 1 | 2.1713931 | 0.3026072 | 1 | 2.1223901 | | 1 | 1 |
| 682 | 0.4952207 | 2.5576667 | 0.2793245 | 0.2638896 | 4.79909 | | 1 | 0.2921568 |
| 683 | 1 | 2.560538 | 1 | 2.7797219 | 3.2714402 | | 3.964582 | 4.7514658 |
| 684 | 1 | 0.2449687 | 0.6119343 | 0.2496687 | 0.2258886 | | 0.6209144 | 1.610693 |
| 685 | 0.740236 | 1 | 1 | 0.6929098 | 0.8176967 | | 0.7322756 | 0.6064893 |
| 686 | 1 | 0.6824162 | 0.5803894 | 0.2748202 | 0.2901481 | | 0.5185438 | 1 |

Table 4

| SEQ ID NO | Patient ID | | | | | | | |
|--------------|------------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|
| | 141 | 156 | 228 | 264 | 266 | 267 | 268 | 278 |
| 687 | 1 | 0.1716662 | 1 | 1 | 0.3625805 | | 0.1576626 | 1 |
| 688 | 0.8364857 | 0.6000201 | 0.7351664 | 0.6058973 | 0.7528025 | | 0.5649719 | 0.4052077 |
| 689 | 0.5836851 | 0.1474165 | 1 | 0.3903458 | 0.2457387 | | 0.4209927 | 1 |
| 690 | 0.4809421 | 2.8523583 | 1 | 1 | 2.125372 | | 1 | 1 |
| 691 | 1 | 1 | 1 | 2.6967787 | 3.8663632 | | 1 | 1 |
| 692 | 1.3520076 | 1.6431199 | 1 | 1.4812734 | 1.541919 | | 3.0039772 | 2.6495508 |
| 693 | 1 | 0.4953111 | 1 | 0.6482503 | 0.8015805 | | 0.6290662 | 0.4096652 |
| 694 | 1.4886734 | 1.4639894 | 1 | 1.8674449 | 1.9776845 | | 2.9929678 | 3.7996529 |
| 695 | 1 | 2.9058933 | 1 | 1.7553461 | 1.3959519 | | 1.2501632 | 2.4568428 |
| 696 | 0.123745 | 0.0472328 | 0.1340669 | 0.3110692 | 0.4349366 | | 0.1603633 | 0.2593156 |
| 697 | 1 | 3.1322566 | 1 | 3.8702433 | 2.0698654 | | 1 | 1.3844174 |
| 698 | 1.897138 | 0.8707941 | 1 | 1.7914514 | 1.4986498 | | 2.043393 | 4.9230164 |
| 699 | 1 | 0.4317848 | 1 | 0.600473 | 0.7091143 | | 0.5399703 | 0.279039 |
| 700 | 1 | 1.5079819 | 1 | 2.6417216 | 2.0939068 | | 1 | 1 |
| 701 | 1 | 0.4686574 | 1 | 0.5432199 | 0.7400096 | | 0.5268391 | 0.2776359 |
| 702 | 1 | 1.3804189 | 1.423766 | 2.6070754 | 2.560692 | | 2.3622287 | 5.0010097 |
| 703 | 0.8537866 | 0.4863036 | 1 | 0.4873571 | 0.7462072 | | 0.5256056 | 0.2992962 |
| 704 | 1 | 2.2805721 | 1 | 1 | 2.5208957 | | 1.7369565 | 2.5948505 |
| 705 | 0.7494777 | 0.3449126 | 0.5860944 | 1 | 0.5039674 | | 0.2299155 | 0.6956635 |
| 706 | 1 | 0.4417392 | 0.8223086 | 0.5598424 | 0.771652 | | 0.5190358 | 0.2457942 |
| 707 | 0.792051 | 0.5397095 | 1 | 0.5137796 | 0.6336846 | | 0.5419438 | 0.3104585 |
| 708 | 1 | 1 | 0.1714076 | 0.001 | 1 | | 0.6831127 | 1 |
| 709 | 2.3561583 | 2.7371599 | 1.5418476 | 2.451014 | 2.6091791 | | 2.9167454 | 2.5810746 |
| 710 | 1.7454927 | 1.6551217 | 1 | 3.0448986 | 1.692986 | | 6.8119686 | 7.2378719 |
| 711 | 1 | 2.3892284 | 1 | 1 | 3.1342584 | | 1 | 1 |
| 712 | 1 | 1 | 1.6906023 | 3.3909954 | 1 | | 2.691598 | 1 |
| 713 | 1 | 1 | 1 | 6.0926985 | 2.5681579 | | 1 | 4.2711702 |
| 714 | 1 | 5.7254125 | 1 | 3.0925135 | 2.6512289 | | 1 | 1 |
| 715 | 1 | 0.4441617 | 0.7732809 | 0.5458516 | 0.7041132 | | 0.615146 | 0.2439193 |
| 716 | 1 | 0.6820965 | 1 | 0.001 | 0.367624 | | 0.1720799 | 1 |
| 717 | 1 | 0.4533599 | 0.7175969 | 0.5259829 | 0.8463489 | 0.4644818 | 0.5363009 | 0.2831239 |
| 718 | 1 | 0.7006097 | 1 | 1.4317705 | 1.185445 | 2.5973283 | 1 | 1 |
| 719 | 1 | 1.7058162 | 5.0268159 | 8.0863573 | 8.1483379 | 9.4318606 | 3.9017175 | 7.2283424 |
| 720 | 1 | 1.2414689 | 4.0305391 | 1 | 4.2201956 | 7.6298331 | 2.6246497 | 5.1433136 |
| 721 | 1 | 2.3498042 | 1 | 2.9814829 | 1 | 2.9528991 | 1 | 2.1596387 |
| 722 | 1.2452678 | 2.903354 | 1.2550716 | 2.5457498 | 4.4123268 | 1.7349716 | 2.9494166 | 1.9889076 |
| 723 | 1.5862262 | 2.1895988 | 1.8232788 | 1 | 1.6967012 | 1.0689178 | 1.9326589 | 1.3684748 |
| 724 | 1 | 1.494984 | 1.5457688 | 1.9018352 | 2.256162 | 1.3495199 | 1.55004 | 1.7135687 |
| 725 | 0.525103 | 0.22126 | 0.2067337 | 0.2608112 | 0.3569799 | 0.4756618 | 0.2041202 | 0.3892527 |
| 726 | 0.2754779 | 1.9446794 | 2.8354797 | 1 | 2.0452271 | 2.1620701 | 1.3199486 | 0.6191539 |
| 727 | 1.6114329 | 1.5630049 | 1.4293012 | 1.9263285 | 2.0048634 | 1.790758 | 3.1463847 | 1.8815992 |
| 728 | 0.2803287 | 0.7163437 | 0.7175149 | 0.7424642 | 1 | 0.2617241 | 1 | 0.4453746 |
| 729 | 0.3215989 | 0.7557802 | 0.6779503 | 0.6731832 | 0.6855438 | 0.4067444 | 0.6269036 | 0.4274703 |
| 730 | 0.1604929 | 2.0817172 | 1.3171453 | 0.3218452 | 0.4810735 | 0.7126652 | 0.2821211 | 0.7796043 |
| 731 | 0.4013471 | 0.5214054 | 1.3262076 | 1 | 1 | 0.8098478 | 0.4481965 | 2.0059304 |
| 732 | 1.5520844 | 1.5656426 | 1.2226178 | 2.052521 | 2.0854978 | 1.7103386 | 1.6061055 | 2.0803603 |
| 733 | 1.3365792 | 0.3588389 | 0.7939726 | 1 | 1 | 18.681689 | 3.1918321 | 1 |
| 734 | 1.5601545 | 0.8423757 | 1.5620762 | 1.7577588 | 1.4700299 | 1.563662 | 1.4732817 | 1 |
| 735 | 0.5148649 | 0.4978013 | 0.437842 | 0.6749122 | 0.4028226 | 0.5860675 | 0.5112747 | 0.4180276 |

Table 4

| SEQ ID NO | Patient ID | | | | | | | |
|--------------|------------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|
| | 141 | 156 | 228 | 264 | 266 | 267 | 268 | 278 |
| 736 | 1 | 4.5100747 | 2.2611698 | 1 | 1 | 2.3934636 | 1.5072114 | 2.4710533 |
| 737 | 0.5898827 | 0.2701652 | 1 | 0.8410861 | 0.594444 | 9.4891375 | 0.5299209 | 1.4145829 |
| 738 | 1.9322872 | 2.5287749 | 2.4965071 | 3.2398009 | 4.691667 | 1.6864733 | 3.2975541 | 4.691737 |
| 739 | 0.6780186 | 0.2093504 | 0.575633 | 0.3682055 | 0.239171 | 1.4219027 | 0.4298926 | 1.2733096 |
| 740 | 1 | 0.7584363 | 1.7892562 | 2.1442349 | 2.2170582 | 1.789264 | 1 | 1.5142117 |
| 741 | 1 | 1.6873215 | 1.6826383 | 1 | 2.6634059 | 1.623229 | 2.6494548 | 3.0561802 |
| 742 | 1.6871187 | 1.3385845 | 1 | 1.4542386 | 1.7375416 | 2.4585037 | 1 | 1.8640673 |
| 743 | 0.2153081 | 0.1674791 | 0.1228205 | 0.1370204 | 0.053761 | 0.160897 | 0.0645644 | 0.1955762 |
| 744 | 1 | 2.9000891 | 2.2715972 | 3.6369061 | 3.210612 | 1.8396705 | 1.3700123 | 4.1096707 |
| 745 | 2.5262871 | 1.6403346 | 1.4555806 | 2.8180045 | 2.5513971 | 1.6903044 | 2.0099377 | 2.7016746 |
| 746 | 0.0849604 | 0.1154935 | 0.0147767 | 0.1201439 | 8.8319337 | 20.40315 | 1 | 0.0980209 |
| 747 | 1.8721722 | 2.4114061 | 2.589755 | 1.796821 | 2.140869 | 1.6329952 | 1.3133342 | 1.9929119 |
| 748 | 0.7405864 | 0.2812633 | 0.4148569 | 0.4495395 | 0.2513983 | 0.4715381 | 0.4359997 | 0.3999742 |
| 749 | 0.0564139 | 1 | 0.033588 | 0.1864228 | 0.0254522 | 0.0445886 | 0.0167 | 0.0800048 |
| 750 | 0.5521603 | 1 | 0.4155156 | 0.1964114 | 0.2495913 | 0.4720265 | 0.1775492 | 0.3279842 |
| 751 | 2.5076504 | 1.5525893 | 2.6533023 | 2.949281 | 2.6269085 | 1.3089209 | 2.144163 | 4.1681517 |
| 752 | 1 | 0.152034 | 2.6292361 | 0.2929978 | 1 | 5.768751 | 0.4960483 | 1.3789914 |
| 753 | 1.9125993 | 1.7325867 | 4.1838043 | 5.9357503 | 3.2628502 | 1.4045391 | 4.1542763 | 4.5769043 |
| 754 | 1 | 0.4096133 | 0.7203059 | 0.5738647 | 1 | 0.4733871 | 0.5788963 | 0.2579622 |
| 755 | 0.0895374 | 0.1006387 | 0.0149024 | 0.1506893 | 7.9555054 | 12.877477 | 1 | 0.1064578 |
| 756 | 1 | 1 | 3.4090398 | 1 | 1 | 6.1727589 | 1 | 1 |
| 757 | 1.6942361 | 1.7371797 | 1.1873502 | 1.5602482 | 1.7247083 | 1.3542819 | 1.2982951 | 1.0932725 |
| 758 | 1.1923469 | 1.3822204 | 1.8772773 | 2.5632686 | 2.3267732 | 1.6939955 | 2.1442446 | 4.3499457 |
| 759 | 1 | 2.8045475 | 1.3331279 | 1.9668173 | 1.8803687 | 0.9281714 | 2.10712 | 2.6468316 |
| 760 | 2.5392628 | 2.0383703 | 1.3962033 | 2.2242288 | 2.6344668 | 1.894606 | 2.9156889 | 1 |
| 761 | 1 | 1.8517263 | 1 | 2.3136272 | 2.1309694 | 2.3589313 | 1 | 2.6214588 |
| 762 | 0.8139617 | 1.8194221 | 3.6119549 | 2.0024909 | 4.7280069 | 0.8814248 | 1.7019634 | 1.5097605 |
| 763 | 0.3077692 | 0.4951451 | 0.3318526 | 1 | 0.3682679 | 0.6265755 | 0.3340028 | 0.6164658 |
| 764 | 1 | 1 | 2.2930919 | 1.703402 | 1 | 1.2133927 | 2.787465 | 2.485003 |
| 765 | 1 | 1 | 3.1080478 | 1 | 3.4117869 | 1.4592733 | 1 | 1 |
| 766 | 1.2417858 | 1.4379443 | 1.4135386 | 1.990956 | 2.9397493 | 1.5015002 | 1.5445167 | 1.5609034 |
| 767 | 1.1601323 | 1.2503965 | 1.2766719 | 2.3470298 | 1.693769 | 1.7909046 | 1.4574297 | 1.874137 |
| 768 | 1.3249722 | 1.613398 | 1.2537354 | 1 | 1.9238818 | 1.8856242 | 1 | 1.5974385 |
| 769 | 1.7416164 | 1.4453902 | 1.8570174 | 2.3501208 | 2.6780636 | 1.6719854 | 1.6297499 | 1.5407765 |
| 770 | 0.6193051 | 0.2310731 | 0.4695503 | 0.2585648 | 0.2308548 | 0.8829046 | 0.225463 | 0.7012012 |
| 771 | 1 | 0.8157281 | 1.6110611 | 1 | 4.2379297 | 1.0695031 | 1 | 1.1531938 |
| 772 | 1 | 1.2239887 | 1 | 2.4567427 | 1 | 1.5297868 | 1.6993457 | 1.809932 |
| 773 | 0.7435866 | 0.1753984 | 0.7064778 | 0.3247301 | 0.2815422 | 0.5191476 | 0.2594522 | 0.659265 |
| 774 | 1 | 0.1713957 | 0.4916792 | 0.3426138 | 0.316763 | 0.752646 | 0.2554612 | 0.5448855 |
| 775 | 1 | 1 | 1.4940737 | 1 | 1 | 0.8878712 | 1 | 3.2045122 |
| 776 | 1 | 2.120336 | 1.4367944 | 3.2703169 | 3.9248057 | 2.3605604 | 2.136764 | 2.203605 |
| 777 | 1 | 0.551533 | 0.7494735 | 0.5800245 | 1 | 0.4386534 | 0.6175596 | 0.3297163 |
| 778 | 1.5738638 | 0.819866 | 1.1119857 | 2.3742634 | 2.0775902 | 5.1707142 | 1 | 2.0964829 |
| 779 | 1.2853774 | 1 | 0.7641935 | 1 | 1.7414987 | 1.8880979 | 0.5843048 | 1.3218327 |
| 780 | 0.3067399 | 0.1398047 | 0.265263 | 0.3028267 | 0.1432962 | 0.261302 | 0.1301462 | 0.3201185 |
| 781 | 2.9755182 | 1.4316728 | 1.6625207 | 6.9991284 | 2.6665698 | 1.6078863 | 2.2364995 | 2.7820768 |
| 782 | 0.1458747 | 1 | 0.0214886 | 0.1079651 | 4.7428302 | 10.524515 | 1 | 0.0974932 |
| 783 | 2.201228 | 1.2929257 | 2.9540647 | 4.3059172 | 5.6787013 | 0.8514283 | 4.7063062 | 4.7790426 |
| 784 | 1.8716685 | 1.4653175 | 1 | 1.6504935 | 1 | 1.3159126 | 2.2746893 | 2.9439364 |

Table 4

| SEQ ID NO | Patient ID | | | | | | | |
|--------------|------------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|
| | 141 | 156 | 228 | 264 | 266 | 267 | 268 | 278 |
| 785 | 0.0851575 | 1 | 0.165263 | 0.2766503 | 1 | 0.2814586 | 0.0349685 | 0.1433903 |
| 786 | 1 | 1.8772364 | 1.9425499 | 2.3280171 | 1.7525073 | 1.4389245 | 2.0346864 | 4.1133211 |
| 787 | 2.0711869 | 1.9640471 | 1.9989139 | 1.7899887 | 1 | 0.8550557 | 1 | 2.2799345 |
| 788 | 1.2984297 | 1 | 2.1402582 | 1.6505645 | 1.6813687 | 1.18167 | 3.0210489 | 1.6930259 |
| 789 | 0.1870026 | 0.1324142 | 0.0931874 | 0.0391534 | 0.0543813 | 0.1808897 | 0.0332399 | 0.082724 |
| 790 | 1.3983695 | 1 | 1.5218903 | 2.1899493 | 2.2347155 | 1.4751155 | 2.1508743 | 3.2032892 |
| 791 | 1 | 1.2297621 | 2.1231351 | 1.785158 | 1.923935 | 1.1730274 | 1.7211987 | 1.6320864 |
| 792 | 0.8732993 | 0.2515537 | 0.5086285 | 0.5207357 | 0.5015808 | 0.8208296 | 0.3987898 | 0.5667942 |
| 793 | 0.4558777 | 0.1839632 | 0.2150371 | 0.1843168 | 0.1459684 | 0.5429969 | 0.2442347 | 0.2839248 |
| 794 | 1.7212058 | 2.0862855 | 1 | 2.4521106 | 2.6485044 | 2.2735666 | 1.7939702 | 2.4795585 |
| 795 | 0.2517056 | 1 | 0.6160559 | 0.5694694 | 0.6213607 | 0.4762147 | 0.6625818 | 0.3481235 |
| 796 | 1 | 0.2408246 | 1 | 0.1993921 | 0.152937 | 0.7232299 | 0.1530925 | 0.6187815 |
| 797 | 1.1594753 | 1.3072271 | 1 | 1.7426687 | 1.9804988 | 1.3994356 | 1 | 2.0217426 |
| 798 | 1.7612496 | 2.8054944 | 3.4065744 | 2.3527149 | 2.6296881 | 1.3897452 | 1.9737505 | 2.6490169 |
| 799 | 0.7779694 | 1 | 2.9125112 | 1.9203024 | 2.4443869 | 2.4423644 | 1.5662832 | 5.6203561 |
| 800 | 1.4119255 | 1 | 1 | 1.4422391 | 2.096367 | 1.2773114 | 2.2431769 | 2.1484391 |
| 801 | 0.7755823 | 0.2232706 | 0.3923426 | 0.3698311 | 0.3473297 | 0.6569092 | 0.2217558 | 0.5471888 |
| 802 | 1.5857992 | 1.9264368 | 1.5102407 | 2.2081627 | 2.5627667 | 2.0012311 | 2.7481762 | 2.6394997 |
| 803 | 0.6721823 | 0.1780914 | 0.4872072 | 0.2006875 | 0.2031613 | 0.7463905 | 0.1131223 | 0.5967673 |
| 804 | 0.6231267 | 1.1446054 | 0.553921 | 0.879383 | 1 | 0.9371496 | 0.4518588 | 0.3617691 |
| 805 | 1.3135734 | 1.4100055 | 1.6025314 | 3.1889055 | 1.9883649 | 1.4426633 | 1.5261939 | 1.7694299 |
| 806 | 2.3653782 | 1.6590629 | 1.9256254 | 4.5974502 | 5.0878705 | 1.5303861 | 2.1124125 | 3.0967444 |
| 807 | 1 | 1 | 1 | 1.7759031 | 1.3416393 | 2.2483307 | 0.8012485 | 1.2910091 |
| 808 | 1.7358677 | 1.5258802 | 1.5049331 | 1.5998049 | 2.0355352 | 1.3992924 | 1.9580445 | 2.0415033 |
| 809 | 0.7958834 | 0.6376244 | 1.4077038 | 2.9148855 | 2.026997 | 2.2651388 | 1.5414746 | 4.3917144 |
| 810 | 1 | 1.4419839 | 1.3746589 | 1.8534165 | 1.814661 | 1.6456233 | 1.7486533 | 1.7761223 |
| 811 | 1 | 2.2682997 | 1 | 2.6748743 | 2.9180528 | 1.5475564 | 2.4210967 | 2.474176 |
| 812 | 1.3769405 | 1.8663105 | 1 | 2.1640704 | 2.2098065 | 1.6519859 | 2.4596711 | 2.1593531 |
| 813 | 1.2606306 | 1.4990112 | 1.2369855 | 2.7476704 | 2.0756691 | 1.2101708 | 1.7929998 | 2.0171672 |
| 814 | 1 | 2.1297063 | 1.308842 | 1.7692694 | 1.8536215 | 1.6633155 | 1.8830572 | 1.990857 |
| 815 | 1.163023 | 1.6781294 | 1.2561385 | 2.0820949 | 1.7832711 | 2.0149079 | 1.2814073 | 1.3898433 |
| 816 | 1 | 0.4065083 | 0.7107082 | 0.5780277 | 0.9144728 | 0.6439193 | 0.5528275 | 0.2513939 |
| 817 | 1 | 0.4592317 | 0.7006261 | 0.5834603 | 0.8863545 | 0.5850424 | 0.6147903 | 0.2575214 |
| 818 | 1 | 0.4403988 | 0.7242514 | 0.6125432 | 1 | 0.6693467 | 0.612618 | 0.2896673 |
| 819 | 0.6677695 | 0.3515837 | 0.5228631 | 0.4654848 | 0.5348635 | 0.7072965 | 0.4145322 | 0.4304626 |
| 820 | 1 | 0.5081 | 1 | 0.5605213 | 0.6705999 | 0.4552811 | 0.6743974 | 0.308801 |
| 821 | 2.3875408 | 1.2467074 | 1 | 2.8685725 | 1.7294663 | 2.2155865 | 1 | 2.6816471 |
| 822 | 1.5315423 | 1.4221857 | 1 | 2.5546492 | 1 | 2.1230016 | 1 | 2.1538837 |
| 823 | 1.2786103 | 1 | 1 | 3.015936 | 4.3176029 | 1.9577821 | 2.2896629 | 1.2114886 |
| 824 | 0.2779088 | 0.1518865 | 1 | 1 | 0.2149658 | 1.6544096 | 0.2272304 | 1 |
| 825 | 0.4922971 | 0.3849701 | 0.2840588 | 0.4548747 | 0.3354971 | 0.5892785 | 0.2566924 | 0.4605412 |
| 826 | 1.7522926 | 1.1188862 | 1.6781424 | 4.8038217 | 3.9625765 | 1.5430373 | 2.177808 | 2.7137992 |
| 827 | 1 | 0.4958706 | 0.7213055 | 0.5577062 | 1 | 0.5172964 | 0.5943946 | 0.2956582 |
| 828 | 0.3679718 | 0.3712097 | 0.258771 | 0.4055637 | 0.4415154 | 0.4434335 | 0.3732684 | 0.3794624 |
| 829 | 1.2939402 | 1.9981467 | 1 | 2.2005634 | 2.8503996 | 1.5653852 | 3.3717451 | 1.5582215 |
| 830 | 0.2455299 | 0.0722265 | 0.053719 | 0.0533398 | 0.0490913 | 0.7457849 | 0.0847053 | 0.184327 |
| 831 | 0.1924009 | 0.2083174 | 0.1516821 | 0.2009508 | 0.2900792 | 0.2005315 | 0.1525202 | 0.2494694 |
| 832 | 2.2654712 | 1.6317451 | 1.872706 | 2.1731413 | 1.4674569 | 1.3684293 | 2.3998554 | 6.7572721 |
| 833 | 0.1353957 | 0.049311 | 0.0398611 | 0.0238928 | 0.0383087 | 0.7746386 | 0.0556621 | 0.1719603 |

Table 4

| SEQ ID | Patient ID | | | | | | | |
|--------|------------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|
| | 141 | 156 | 228 | 264 | 266 | 267 | 268 | 278 |
| 834 | 0.8337373 | 0.4142185 | 0.7533466 | 0.5894167 | 1 | 0.5581931 | 0.5714521 | 0.2536972 |
| 835 | 0.478336 | 0.2816137 | 0.5280319 | 0.5833671 | 0.1905804 | 0.8211747 | 0.2356874 | 0.8059021 |
| 836 | 1 | 0.4395381 | 0.6968043 | 0.5940208 | 1 | 0.7236126 | 0.5644513 | 0.2564722 |
| 837 | 1 | 0.4275731 | 0.7028738 | 0.5779624 | 1 | 0.7249555 | 0.5940249 | 0.2828508 |
| 838 | 1.4098012 | 2.4634163 | 2.1116542 | 3.3132452 | 2.2545539 | 1.0333905 | 4.4481058 | 1.8885089 |
| 839 | 1.4440635 | 1.1556973 | 3.2927193 | 3.8490817 | 1.882658 | 1.2575886 | 2.2012893 | 2.9396651 |
| 840 | 2.2715265 | 1.580399 | 1.5822777 | 1.5066652 | 1.7975049 | 0.798835 | 2.6790569 | 1.5310669 |
| 841 | 2.0355449 | 1 | 2.3539698 | 2.2940518 | 1.1261276 | 1.0859398 | 1.6354735 | 2.9069542 |
| 842 | 1 | 1.9361145 | 1.6705171 | 2.2499251 | 2.5571163 | 1.8163916 | 2.3183956 | 3.2491552 |
| 843 | 0.431536 | 0.1528579 | 0.5096087 | 0.5699093 | 0.4092619 | 0.2835328 | 0.4716983 | 0.5179544 |
| 844 | 2.0162731 | 1 | 1.5617525 | 1.7287697 | 2.2252824 | 1.41159 | 1.5976808 | 2.4487597 |
| 845 | 1.763341 | 1.2463139 | 1.4562837 | 4.2322915 | 2.6777545 | 1.8225355 | 1 | 3.0372701 |
| 846 | 0.2538956 | 0.431834 | 0.1141199 | 0.3973746 | 0.3194004 | 0.3705604 | 0.4730844 | 0.1530688 |
| 847 | 1 | 0.7316104 | 1 | 1 | 1 | 1.608501 | 1 | 2.0919447 |
| 848 | 0.3305888 | 0.0854642 | 1.4384123 | 1.3238233 | 0.6394906 | 2.9214307 | 0.5661583 | 1 |
| 849 | 1 | 0.4507714 | 0.6959871 | 0.5849726 | 1 | 0.5903854 | 0.5929185 | 0.2731101 |
| 850 | 1 | 1.6561055 | 1 | 2.063006 | 2.3693158 | 2.2098123 | 1 | 1.2031075 |
| 851 | 0.6518921 | 0.4742279 | 0.280613 | 0.2467003 | 0.1714163 | 0.2314208 | 0.2490535 | 0.2421065 |
| 852 | 0.4052563 | 0.52143 | 0.7656141 | 2.123231 | 0.7080032 | 1.8312008 | 0.6319233 | 2.4839228 |
| 853 | 1.4259085 | 1.5070965 | 1.9260683 | 1 | 1.6323818 | 1.3656785 | 1.6448305 | 2.8091072 |
| 854 | 1.3668885 | 1.1919304 | 2.0251794 | 2.3375204 | 2.2625441 | 2.3890202 | 3.40331 | 2.5698937 |
| 855 | 0.5772356 | 0.3699063 | 1 | 1 | 0.4255163 | 0.591602 | 0.2817487 | 0.6830609 |
| 856 | 1.2183858 | 1.3661728 | 1.6955467 | 1.8347149 | 1.256919 | 1.4108071 | 1 | 1.8834369 |
| 857 | 0.3809037 | 0.6094396 | 0.5500161 | 0.5546223 | 0.4409531 | 0.3792825 | 0.6153744 | 0.3241972 |
| 858 | 1 | 0.1544688 | 0.1010109 | 0.1167542 | 0.2429486 | 1.3505864 | 0.2451901 | 0.4371302 |
| 859 | 0.4349524 | 0.4503287 | 0.7870822 | 0.4288997 | 0.4270544 | 0.5665047 | 0.4368481 | 0.5834631 |
| 860 | 0.2319301 | 0.1518496 | 0.3716636 | 0.5032461 | 0.1198533 | 0.7505132 | 0.1152375 | 1.1391943 |
| 861 | 1.8185614 | 1 | 2.0258326 | 1.808808 | 1.7039719 | 1.5014796 | 1.7813234 | 2.3786632 |
| 862 | 1.8185614 | 1 | 2.0258326 | 1.808808 | 1.7039719 | 1.5014796 | 1.7813234 | 2.3786632 |
| 863 | 1 | 0.457215 | 0.6916375 | 0.5781148 | 1 | 0.6021806 | 0.5677098 | 0.2847132 |
| 864 | 0.2910158 | 0.0623704 | 0.5506188 | 1 | 0.2721818 | 0.9240782 | 0.4276739 | 0.7138162 |
| 865 | 0.7522261 | 0.360622 | 0.3713687 | 0.3543916 | 0.5845911 | 0.7560535 | 0.4323632 | 0.3345649 |
| 866 | 1.2458701 | 1.7966726 | 1.4748068 | 3.0377863 | 2.8591834 | 2.3588296 | 1.7886175 | 3.0871404 |
| 867 | 1.3154787 | 1.8569156 | 1.1949557 | 1 | 2.0734425 | 2.2848698 | 1.9665865 | 2.0472024 |
| 868 | 1 | 0.3950106 | 0.709337 | 0.5395947 | 0.8413247 | 0.578382 | 0.5496192 | 0.2452168 |
| 869 | 1.813634 | 2.5181195 | 1.8605014 | 3.5114152 | 3.5045732 | 1.3611918 | 4.6538325 | 3.7729019 |
| 870 | 1.7415945 | 1.7645651 | 1 | 1.789446 | 2.4289436 | 2.2713476 | 2.1009136 | 2.2595779 |
| 871 | 1.4124182 | 1.3773262 | 1.4393463 | 1.9317601 | 2.4309801 | 2.0429063 | 2.4613901 | 2.365477 |
| 872 | 1.5215998 | 1.5540158 | 1 | 1.8080834 | 2.0936548 | 2.3435165 | 1.7145475 | 1.9674397 |
| 873 | 1.2440414 | 1.6590506 | 1.2213102 | 2.0586887 | 2.3406258 | 2.4378463 | 1.9080524 | 1.9779315 |
| 874 | 1.3231436 | 1.3584257 | 1.318897 | 1.7360841 | 2.0400705 | 1.7154082 | 1.5630681 | 1.711669 |
| 875 | 1.2489799 | 2.2600607 | 1.6165555 | 1.5186226 | 1.4056805 | 1.18428 | 1.9042481 | 2.2670029 |
| 876 | 1.2773292 | 0.8519674 | 1.3170762 | 1.5981722 | 1 | 1.8805345 | 1 | 1.2130034 |
| 877 | 0.1775419 | 0.2129042 | 0.1609922 | 0.1461827 | 0.1515065 | 0.5409185 | 0.0956259 | 0.0949727 |
| 878 | 1 | 0.1965676 | 0.406629 | 0.3533243 | 0.3548211 | 0.7665659 | 0.2313988 | 0.5241005 |
| 879 | 1 | 1.2712461 | 0.8779025 | 2.3938181 | 1.7601762 | 1.5332822 | 1 | 1.1792992 |
| 880 | 1 | 0.5021483 | 0.735482 | 0.6249965 | 0.6768025 | 0.5267224 | 0.4921705 | 0.311756 |
| 881 | 0.2646594 | 0.1756812 | 0.1100617 | 0.2035376 | 0.3495419 | 0.2358184 | 0.1669514 | 0.2648408 |
| 882 | 0.6636961 | 0.2572042 | 0.3630712 | 0.2840264 | 0.3137396 | 0.4989795 | 0.2377689 | 0.5233556 |

Table 4

| SEQ ID NO | Patient ID | | | | | | | |
|--------------|------------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|
| | 141 | 156 | 228 | 264 | 266 | 267 | 268 | 278 |
| 883 | 0.1266357 | 0.0754852 | 0.087369 | 0.1018631 | 0.3332717 | 0.1310775 | 0.080998 | 0.2158211 |
| 884 | 1.367436 | 2.2585359 | 1.5928786 | 2.9602039 | 2.9434798 | 2.6421877 | 2.8458891 | 2.4114051 |
| 885 | 1 | 2.0180617 | 1.4296265 | 1.838055 | 3.4989343 | 1.2501147 | 1.8049458 | 1.6752705 |
| 886 | 0.8010846 | 1.7318551 | 1 | 2.0793302 | 2.4934358 | 2.1753567 | 1.9367109 | 1.9950475 |
| 887 | 1.5564424 | 2.2592798 | 1.323111 | 1.9208793 | 3.0335588 | 1.776622 | 4.0080094 | 1.5594755 |
| 888 | 1.5578769 | 1.2617897 | 1.2355052 | 2.4265977 | 2.2424932 | 1.9085566 | 1.5079374 | 2.8826058 |
| 889 | 0.5173834 | 0.5976468 | 0.442643 | 1.3579585 | 0.2791624 | 0.6720032 | 0.3203354 | 0.7879481 |
| 890 | 1.5549204 | 1.5389765 | 1 | 2.0371541 | 2.166396 | 1.603126 | 1.6987309 | 1.9089897 |
| 891 | 1 | 0.5870161 | 0.6640152 | 0.5627123 | 1 | 0.5687847 | 0.6160337 | 0.2773317 |
| 892 | 1 | 0.4248985 | 0.7317687 | 0.6045273 | 0.828296 | 0.5929554 | 0.5515181 | 0.2352775 |
| 893 | 1.5677647 | 0.658185 | 1 | 1.5297642 | 1.3627904 | 1.5586487 | 1 | 2.5523183 |
| 894 | 1 | 1 | 1.2837393 | 2.3667205 | 2.2277045 | 1.8054484 | 1.5041537 | 2.4359212 |
| 895 | 1 | 2.1366479 | 1.3418864 | 2.2433471 | 8.5814287 | 1.030499 | 2.4471729 | 1.7868687 |
| 896 | 1.3923033 | 1 | 1.3235525 | 2.743348 | 1 | 2.4451488 | 1.8924169 | 2.424076 |
| 897 | 1.6016327 | 1 | 1.1054291 | 1.7353773 | 1 | 1.3893569 | 1.8690041 | 2.528423 |
| 898 | 0.8800554 | 1.352929 | 1 | 2.0035366 | 1.7884501 | 2.01424 | 1.3926991 | 1.4354299 |
| 899 | 1.3669761 | 1.2941308 | 1.3071169 | 1.7198576 | 2.1300562 | 1.7735109 | 1.5460847 | 2.2820515 |
| 900 | 1.6202038 | 1.166408 | 1 | 1.6186703 | 1 | 1.3504363 | 1.7819994 | 2.5431364 |
| 901 | 1.2770445 | 1 | 1 | 2.0857171 | 2.0498661 | 1.9964096 | 1.372816 | 1.4929922 |
| 902 | 1.7599794 | 1.4003032 | 1 | 1.7673948 | 1 | 1.2220554 | 2.8087232 | 3.165233 |
| 903 | 1 | 0.4285814 | 0.6682009 | 0.5191116 | 1 | 0.5507535 | 0.5693101 | 0.2609173 |
| 904 | 1.3744549 | 1.2430552 | 0.8562005 | 2.4421988 | 2.0525265 | 2.1202033 | 1.3635806 | 2.1347315 |
| 905 | 0.7282787 | 0.1830778 | 0.2980396 | 0.3364706 | 0.2892136 | 0.6228045 | 0.1836087 | 0.5090581 |
| 906 | 1.3359879 | 2.1535379 | 1 | 1.8758451 | 2.255577 | 2.1726777 | 1.2422532 | 1.7302253 |
| 907 | 0.122201 | 0.1631382 | 0.5189425 | 0.2408735 | 0.1202264 | 0.1896985 | 0.0744597 | 1 |
| 908 | 0.5627379 | 0.7452724 | 0.7649381 | 0.3044089 | 0.4222244 | 0.829419 | 0.3305815 | 0.5751752 |
| 909 | 0.3845171 | 0.4727338 | 0.4250533 | 0.5463218 | 0.518577 | 0.6150994 | 0.4230725 | 0.4482552 |
| 910 | 0.4359817 | 0.1805938 | 0.2297433 | 0.234321 | 0.3389221 | 0.3660159 | 0.2037703 | 0.3177035 |
| 911 | 0.3334905 | 0.1407454 | 0.2371331 | 0.2997474 | 0.490117 | 0.4364306 | 0.2482547 | 0.3854906 |
| 912 | 0.8070961 | 0.2836919 | 0.475346 | 0.4192242 | 0.505527 | 0.9027838 | 0.3353445 | 0.4090382 |
| 913 | 1 | 0.5081308 | 0.7836938 | 1 | 1.1552937 | 0.5188324 | 0.5928998 | 0.2902447 |
| 914 | 1 | 0.457258 | 0.7475333 | 0.6049897 | 1 | 0.6871331 | 0.6165527 | 0.2800571 |
| 915 | 0.2725762 | 1 | 0.0386995 | 0.1122772 | 7.4036393 | 12.941468 | 1.8691901 | 0.1298254 |
| 916 | 0.7404878 | 0.2011729 | 0.6578483 | 0.2524991 | 0.1871715 | 0.735643 | 0.2056721 | 0.684346 |
| 917 | 1.6281644 | 2.0966581 | 1.316501 | 1.9279742 | 3.2085395 | 1.787568 | 3.568174 | 1.6103391 |
| 918 | 1 | 0.4346315 | 0.6848437 | 0.5748277 | 0.8657983 | 0.5469119 | 0.5723518 | 0.2594708 |
| 919 | 2.2135795 | 2.0919422 | 1 | 2.5755721 | 3.3628186 | 1.7350542 | 2.9666529 | 2.028522 |
| 920 | 1.8369354 | 1.691441 | 3.8425131 | 7.2163495 | 2.8280422 | 1.7947835 | 2.5259371 | 5.1923768 |
| 921 | 0.4038109 | 0.3895446 | 0.7393131 | 0.402551 | 0.3730216 | 0.5206971 | 0.4035306 | 0.6224195 |
| 922 | 1 | 1.7354458 | 1.748899 | 2.1844629 | 1.8259461 | 1.4577563 | 1.9853641 | 3.0179254 |
| 923 | 1.3310166 | 1.3049522 | 1.759679 | 2.2965235 | 2.3205658 | 1.4958329 | 2.1806735 | 3.2523834 |
| 924 | 0.1364907 | 1.9767008 | 0.0162573 | 0.0773106 | 8.7574636 | 12.990652 | 2.4408128 | 0.1048561 |
| 925 | 1.6654379 | 1.3081617 | 1.919495 | 1.8497082 | 1 | 1.3705554 | 1.9501836 | 4.8016776 |
| 926 | 1 | 0.4617772 | 0.6846135 | 0.5654033 | 1 | 0.6076232 | 0.573091 | 0.2862529 |
| 927 | 1 | 1.1465667 | 1 | 2.2495293 | 1.9846221 | 2.4798514 | 1.783974 | 3.4242382 |
| 928 | 0.5870467 | 1 | 0.7060344 | 1 | 0.3434147 | 2.333816 | 0.6239741 | 0.3207517 |
| 929 | 1 | 0.4067542 | 0.4673781 | 0.4346184 | 0.8051699 | 0.7129904 | 0.471801 | 0.2780332 |
| 930 | 1 | 1 | 0.195459 | 0.2708965 | 0.2779758 | 0.6195801 | 1 | 0.226226 |
| 931 | 1.4830342 | 1.7539774 | 1 | 2.194647 | 3.3853955 | 2.1539382 | 2.4581688 | 2.1563918 |

Table 4

| SEQ ID NO | Patient ID | | | | | | | |
|--------------|------------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|
| | 141 | 156 | 228 | 264 | 266 | 267 | 268 | 278 |
| 932 | 1.3803679 | 1 | 3.3323187 | 3.3416708 | 5.3643852 | 11.041923 | 2.4813336 | 2.0154413 |
| 933 | 2.4497253 | 1 | 1 | 1.7537814 | 2.204486 | 1.7600413 | 2.2566522 | 1.9548185 |
| 934 | 1 | 1.414457 | 1.130178 | 2.1579235 | 2.1027651 | 1.4333057 | 1.7164277 | 2.1411631 |
| 935 | 1 | 2.1956428 | 1 | 2.7043825 | 1 | 1.6221457 | 1 | 1 |
| 936 | 0.3138135 | 1.3428454 | 0.3582118 | 0.7488552 | 0.3726022 | 1.8037514 | 0.2436538 | 0.4557485 |
| 937 | 0.4159105 | 0.3069763 | 0.4881033 | 0.5912424 | 0.3822758 | 0.2506698 | 0.2867862 | 0.5395962 |
| 938 | 1.1925002 | 2.0796636 | 1.3089557 | 1.989717 | 2.501323 | 1.7174552 | 1.8278385 | 1.9247709 |
| 939 | 1.521775 | 1 | 1 | 1 | 2.4599408 | 2.256913 | 1 | 1.8457719 |
| 940 | 1 | 0.4781445 | 0.6992545 | 0.5214895 | 1 | 0.5858885 | 0.615603 | 0.2638413 |
| 941 | 1.5321993 | 4.1425418 | 0.1439762 | 0.2775931 | 0.2415227 | 1.0543588 | 1 | 0.1657708 |
| 942 | 0.0873256 | 0.0331035 | 0.0594765 | 0.1562644 | 0.0781512 | 0.2080066 | 0.0422187 | 0.2148588 |
| 943 | 0.2796389 | 0.1330782 | 0.41698 | 0.4715783 | 0.2277234 | 0.3793536 | 0.16834 | 0.421529 |
| 944 | 2.021759 | 1 | 1 | 1.5389997 | 1.8618543 | 1.6771127 | 1.4804814 | 1.582899 |
| 945 | 1.7660895 | 2.1126934 | 0.7404752 | 2.5603605 | 2.6700486 | 2.3109374 | 2.0369665 | 2.2586343 |
| 946 | 0.122201 | 1.913156 | 0.0205971 | 0.0930781 | 8.1056267 | 12.05702 | 1 | 0.105061 |
| 947 | 1.744989 | 1.7539958 | 1.2844394 | 3.2694808 | 2.8180782 | 2.4717259 | 2.1474316 | 2.6101227 |
| 948 | 1 | 1.7817317 | 1.7743026 | 1 | 2.7970097 | 2.0653956 | 2.8348646 | 1 |
| 949 | 1.3444193 | 2.179005 | 2.429941 | 1.820049 | 2.4051016 | 1.3261874 | 1.3949746 | 1.9204873 |
| 950 | 1.3830287 | 1.259982 | 2.1695228 | 3.4895377 | 4.075362 | 1.3493368 | 2.3281661 | 2.3170594 |
| 951 | 1 | 0.3895077 | 0.6926609 | 0.5315874 | 0.7808565 | 0.5897646 | 0.5421576 | 0.2226377 |
| 952 | 2.9097093 | 1.6482047 | 2.0815027 | 1.9849301 | 1.8157974 | 1.4458097 | 1 | 2.281052 |
| 953 | 1.4259742 | 1.2407618 | 1.4849773 | 1.9993081 | 1.9508496 | 1.8452568 | 1.4920854 | 1.379606 |
| 954 | 0.7674356 | 0.7909681 | 1.5192213 | 0.4400597 | 0.494235 | 0.3735508 | 0.258404 | 1.1766731 |
| 955 | 1 | 0.4361195 | 0.4879611 | 0.3428373 | 0.246655 | 0.4728754 | 0.3736447 | 0.4526879 |
| 956 | 1 | 1.1956502 | 2.6698449 | 1 | 1.380225 | 1.0545417 | 1 | 3.6647678 |
| 957 | 1 | 1.8843564 | 1.4779302 | 2.6739422 | 1.9679526 | 3.2113352 | 1 | 1.4571399 |
| 958 | 1.5524457 | 1.2991972 | 1.2496402 | 1.8199195 | 1.4307086 | 2.1598501 | 1 | 1 |
| 959 | 1.3359331 | 1.3195918 | 1 | 1.6751762 | 2.1987742 | 2.3862058 | 1 | 1.4045877 |
| 960 | 1.8213318 | 1.2533908 | 1.3628022 | 2.3264643 | 2.172958 | 1.6440403 | 1.2207237 | 1.6893941 |
| 961 | 1.8978607 | 1.9550642 | 1 | 1.6606381 | 2.7186594 | 2.5854793 | 1 | 1.7736018 |
| 962 | 1.5727359 | 1.2810591 | 1.240467 | 1.8720009 | 2.0244023 | 1.4931376 | 2.0676869 | 2.292562 |
| 963 | 0.8845887 | 1.2842809 | 1.1557059 | 1.9852896 | 1.8192153 | 2.0279077 | 1.3645382 | 1.5075379 |
| 964 | 1 | 1.8892875 | 1 | 1 | 2.1941983 | 1.6185452 | 1.3073315 | 1 |
| 965 | 1 | 1.3503466 | 1 | 2.5368283 | 1 | 2.1772186 | 1.4422474 | 1 |
| 966 | 1.3700092 | 2.5622473 | 1.5911635 | 2.8067688 | 3.2362945 | 1.4322546 | 2.1943457 | 1.945202 |
| 967 | 0.4386973 | 0.6742264 | 0.4184478 | 0.7249211 | 0.4191168 | 0.629529 | 0.447826 | 0.4703626 |
| 968 | 1.3309399 | 1 | 1 | 1.7999401 | 1 | 2.7500009 | 1 | 1.3457094 |
| 969 | 0.79204 | 0.4685282 | 0.7147726 | 0.6120692 | 0.8635956 | 0.5720569 | 0.6016293 | 0.2438572 |
| 970 | 1 | 1.27472 | 1.1456745 | 4.044031 | 6.3008697 | 1.3119824 | 2.6653708 | 1.136947 |
| 971 | 1.956826 | 1.0747461 | 1.8574293 | 1.8371748 | 1 | 1.741158 | 1 | 2.9339164 |
| 972 | 0.4916401 | 0.3197099 | 0.3606769 | 0.459445 | 0.206141 | 0.4723914 | 0.2147317 | 0.3313366 |
| 973 | 0.6937536 | 0.2294744 | 0.4943723 | 0.3513859 | 0.3147927 | 0.5392039 | 0.2793393 | 0.542514 |
| 974 | 0.8002962 | 0.4297496 | 0.7214713 | 0.6410099 | 1 | 0.5623861 | 0.5919406 | 0.3046104 |
| 975 | 0.719464 | 0.2624735 | 1 | 0.5894122 | 0.3235181 | 0.5458638 | 0.2857971 | 0.5836928 |
| 976 | 0.5687932 | 0.2030851 | 0.4892662 | 0.5207922 | 0.4797436 | 0.819962 | 0.3627227 | 0.5124913 |
| 977 | 2.3356601 | 1.8285218 | 1.4035094 | 2.79257 | 2.323355 | 1.8154872 | 4.9866022 | 2.8427182 |
| 978 | 1.8638503 | 1.3227214 | 1 | 1.8315617 | 2.1670032 | 2.9290975 | 1.7218299 | 1.122395 |
| 979 | 1 | 1 | 1.3351589 | 1 | 1.6181096 | 0.8891486 | 1 | 2.075729 |
| 980 | 1.438917 | 1 | 1 | 1 | 1.9611861 | 4.3822631 | 2.0176384 | 1.818996 |

Table 4

| SEQ ID NO | Patient ID | | | | | | | |
|--------------|------------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|
| | 141 | 156 | 228 | 264 | 266 | 267 | 268 | 278 |
| 981 | 0.4735399 | 1.2332914 | 0.7027886 | 1 | 0.6660044 | 1.5542634 | 0.2776135 | 0.3930583 |
| 982 | 1.3184461 | 0.8174005 | 1.8778386 | 1.7307194 | 1.5655779 | 2.0090236 | 1.5221536 | 1.9034955 |
| 983 | 1.3640415 | 2.0161065 | 1 | 1.7913259 | 3.4225263 | 1.1831783 | 1.814244 | 1.5143793 |
| 984 | 1 | 2.2456117 | 1.4448097 | 3.3992577 | 4.3063807 | 2.95873 | 1 | 2.4758584 |
| 985 | 0.350441 | 1.7717712 | 0.0251445 | 0.1130683 | 6.6071786 | 12.101039 | 1 | 0.1142305 |
| 986 | 1.5023389 | 1.8347011 | 1.5324424 | 2.9328229 | 2.9535996 | 1.422809 | 1.7358328 | 1.8328278 |
| 987 | 0.4801537 | 0.1373883 | 0.3379779 | 0.2216973 | 0.1910618 | 0.6298734 | 0.2785894 | 0.2760776 |
| 988 | 0.8143669 | 0.454233 | 0.7454777 | 0.5698585 | 1 | 0.5213673 | 0.5480209 | 0.2570496 |
| 989 | 0.6984511 | 0.1878737 | 0.4556874 | 0.1262234 | 0.1531039 | 0.779069 | 0.100562 | 0.5800859 |
| 990 | 1 | 1.3465837 | 1.7907017 | 1.8154843 | 1.3220634 | 1.3317581 | 1.3995828 | 1.2156791 |
| 991 | 0.2597538 | 0.2497829 | 1 | 1 | 1 | 0.492265 | 0.6477596 | 0.831784 |
| 992 | 1 | 0.4312991 | 0.8026139 | 0.5239179 | 1 | 0.6510985 | 0.6223477 | 0.2630653 |
| 993 | 1 | 1 | 1 | 1 | 1 | 0.4461374 | 1 | 1 |
| 994 | 1 | 1.2564221 | 1.6691113 | 1 | 1 | 2.2276794 | 1 | 1 |
| 995 | 1 | 1 | 0.7327149 | 1 | 1 | 0.5357022 | 0.5598915 | 0.2829874 |
| 996 | 1.1561465 | 1.2583404 | 1.263615 | 1.7441343 | 1 | 2.2301321 | 1 | 1.1994757 |
| 997 | 1.509763 | 0.0711566 | 1 | 1 | 0.2319266 | 3.1910055 | 1 | 1.4959659 |
| 998 | 1.2777781 | 1.6787627 | 1.2651847 | 2.0668403 | 2.7249405 | 2.8504753 | 1 | 3.2373907 |
| 999 | 0.4722697 | 0.3082429 | 0.5852797 | 0.4571375 | 0.4579073 | 0.6429277 | 1 | 0.8042756 |
| 1000 | 0.6240903 | 1 | 1 | 0.5239465 | 0.1810794 | 0.7570425 | 0.3597745 | 0.6590229 |
| 1001 | 0.1665263 | 0.0611469 | 0.1055548 | 0.2357406 | 0.4333952 | 0.2797282 | 0.1752417 | 0.2821058 |
| 1002 | 0.5305452 | 0.2653633 | 0.3604751 | 0.3563948 | 0.5266342 | 0.6379852 | 0.3301437 | 0.4005889 |
| 1003 | 1 | 1.3056839 | 1 | 2.4252171 | 1.6450393 | 1.4527611 | 1 | 1.7093472 |
| 1004 | 1.7404886 | 1.6304048 | 1.3158345 | 1.7714751 | 1.7100857 | 1.8154269 | 2.9638441 | 1.7027354 |
| 1005 | 1 | 0.4961781 | 0.7184588 | 0.5638452 | 1 | 0.6418675 | 0.607002 | 0.2890403 |
| 1006 | 0.7705672 | 0.1499866 | 0.3947883 | 1.5172113 | 1 | 0.4917847 | 1 | 0.4563942 |
| 1007 | 0.5473642 | 0.1980187 | 0.1567691 | 0.1759294 | 0.2266575 | 0.4898708 | 1 | 0.2141759 |
| 1008 | 1 | 0.4568399 | 0.702376 | 0.563241 | 1 | 0.5928397 | 0.5647511 | 0.2664301 |
| 1009 | 0.9122043 | 0.4586722 | 0.7467112 | 0.5668234 | 1 | 0.5213921 | 0.5480209 | 0.2689382 |
| 1010 | 1.4283723 | 1.7910959 | 1.686743 | 1.700759 | 1.6864214 | 1.7014527 | 2.312117 | 1.8332127 |
| 1011 | 1 | 0.499818 | 0.7772443 | 0.6152938 | 0.9105003 | 0.6540222 | 0.5783971 | 0.2669268 |
| 1012 | 1.7729989 | 1.3463009 | 1.839971 | 2.4524241 | 2.0042283 | 2.0278701 | 1.9331231 | 2.3886025 |
| 1013 | 1.374214 | 0.615373 | 1.7472771 | 1.9901298 | 1 | 1.4002597 | 3.0272163 | 2.2816356 |
| 1014 | 0.7501018 | 0.5365122 | 0.7380244 | 0.6313163 | 1 | 0.6067367 | 0.5053822 | 0.26923 |
| 1015 | 3.2260522 | 2.1890209 | 1.1874811 | 3.0620314 | 2.9104858 | 2.4293996 | 1.6442546 | 3.0877922 |
| 1016 | 1 | 0.5193579 | 0.7409339 | 0.5872424 | 1 | 0.4727855 | 0.6389745 | 0.3105268 |
| 1017 | 1 | 1 | 1 | 1.9435523 | 1 | 1.3933212 | 1 | 1.2810698 |
| 1018 | 1 | 0.2357275 | 0.3978875 | 0.4130076 | 0.3394843 | 0.7656537 | 0.2661305 | 0.4861437 |
| 1019 | 1.5056677 | 0.1731541 | 1.4079404 | 3.4482943 | 1.7482804 | 2.156231 | 2.822228 | 0.8224718 |
| 1020 | 1.7343238 | 0.3197714 | 1.2189201 | 2.2785878 | 1 | 8.3990853 | 1.7487619 | 1.6346566 |
| 1021 | 1.7122378 | 1.7253745 | 1.3376709 | 2.5736716 | 2.5960383 | 1.7796571 | 2.1646731 | 1.6941123 |
| 1022 | 1.1788128 | 1 | 1 | 1.7518595 | 1 | 0.9956606 | 0.5453531 | 0.759943 |
| 1023 | 0.9020866 | 0.484084 | 0.7388927 | 0.6115716 | 0.8792652 | 0.6422444 | 0.5571512 | 0.2648471 |
| 1024 | 0.5407943 | 0.4359227 | 0.4962342 | 0.5254931 | 0.4117904 | 0.5071697 | 0.3537619 | 0.5958733 |
| 1025 | 2.5791424 | 2.4189811 | 3.0864102 | 2.7017163 | 2.2565278 | 1.2725117 | 1 | 2.7427604 |
| 1026 | 1.7127415 | 2.3313587 | 1.5828094 | 2.8251636 | 3.5096992 | 1.707242 | 2.073851 | 2.06574 |
| 1027 | 1.6862208 | 1.9425766 | 1.495111 | 5.5119205 | 4.1263523 | 1.6196477 | 1.703404 | 2.3344485 |
| 1028 | 1 | 1.8339633 | 1 | 2.7569504 | 2.777362 | 1.5052402 | 1 | 1.7627002 |
| 1029 | 1.5929166 | 2.1463441 | 1.4213226 | 1.8960549 | 1.5971999 | 1.734779 | 2.5231095 | 2.8041841 |

Table 4

| SEQ ID NO | Patient ID | | | | | | | |
|--------------|------------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|
| | 141 | 156 | 228 | 264 | 266 | 267 | 268 | 278 |
| 1030 | 0.3097183 | 1 | 0.4150077 | 0.5566906 | 0.4469173 | 0.4993257 | 0.4499501 | 0.6657277 |
| 1031 | 2.101551 | 2.3073488 | 1.4765115 | 4.6425124 | 4.2633749 | 1.7787021 | 1.9605652 | 3.4835139 |
| 1032 | 0.2736712 | 0.0924366 | 0.5514286 | 1 | 0.3547488 | 0.6709562 | 0.1748979 | 0.51472 |
| 1033 | 3.5741609 | 2.1423968 | 1.2899353 | 3.2286226 | 2.9809289 | 1.6579705 | 2.2453221 | 2.4359522 |
| 1034 | 2.2336398 | 2.8928954 | 1 | 2.842853 | 3.047108 | 2.9447109 | 2.5670176 | 2.1329249 |
| 1035 | 1.2743727 | 1 | 1.1858556 | 1.9689875 | 1.5970166 | 1.335449 | 1.2306951 | 1 |
| 1036 | 0.6547829 | 0.2424109 | 0.7798178 | 0.3504823 | 0.7266186 | 1.052411 | 1 | 1.1725633 |
| 1037 | 1 | 0.3236449 | 0.4013091 | 0.3918628 | 0.3981895 | 0.698324 | 0.3843461 | 0.4586726 |
| 1038 | 1 | 1.6936237 | 1.9805811 | 2.5904407 | 1.3995737 | 1.2651086 | 1.2964431 | 2.1861166 |
| 1039 | 1 | 3.3890612 | 2.5904672 | 4.6764654 | 4.0379972 | 3.5300228 | 3.4845467 | 6.212132 |
| 1040 | 1 | 2.9809051 | 1 | 3.7398959 | 2.929354 | 2.064577 | 3.5726987 | 4.3971155 |
| 1041 | 1 | 2.5074396 | 1 | 1 | 1 | 1.578328 | 1 | 2.1729738 |
| 1042 | 2.4634346 | 1.587273 | 1.2802285 | 3.0843092 | 1.8115903 | 2.6830841 | 1.3527777 | 2.6416664 |
| 1043 | 1 | 1.6292304 | 1 | 2.9650081 | 2.1950981 | 1.5302791 | 2.1982836 | 1.9058794 |
| 1044 | 1.2178712 | 1.506039 | 1.3863157 | 2.0032751 | 2.3880167 | 1.6440156 | 1 | 1.402688 |
| 1045 | 1 | 1 | 2.6126478 | 6.1014189 | 2.0764743 | 5.1687595 | 1 | 3.9136102 |
| 1046 | 0.6496802 | 0.3293999 | 0.3069353 | 0.3817447 | 0.5281651 | 0.4935043 | 0.3767222 | 0.2593714 |
| 1047 | 0.3106271 | 1.5357854 | 0.0710949 | 0.128903 | 4.6307849 | 12.947596 | 1 | 0.1332958 |
| 1048 | 1 | 0.4480906 | 0.1047625 | 0.1248884 | 1 | 5.7757571 | 0.7985347 | 0.1175767 |
| 1049 | 1.9596182 | 1.6905371 | 2.2931617 | 1.706888 | 1.612448 | 2.0032469 | 1 | 1.7256685 |
| 1050 | 1.4523745 | 1.4532787 | 1 | 2.3744103 | 1 | 2.6691383 | 1 | 2.0592649 |
| 1051 | 0.3671396 | 0.1208181 | 0.2857118 | 0.2319937 | 0.1728916 | 0.444069 | 0.1305941 | 0.3447401 |
| 1052 | 1 | 0.4403128 | 0.6998844 | 0.5591326 | 0.8710327 | 0.5354557 | 0.6099126 | 0.2912132 |
| 1053 | 0.7644024 | 0.4219164 | 0.4571246 | 0.5030778 | 0.4719637 | 0.7151254 | 0.3591096 | 0.531749 |
| 1054 | 0.6841615 | 0.2471329 | 0.4606872 | 0.4207414 | 0.4279394 | 0.6790284 | 0.287358 | 0.5049545 |
| 1055 | 0.660444 | 0.3882718 | 0.5769373 | 0.5385192 | 0.4251887 | 0.7713065 | 0.2875486 | 0.510753 |
| 1056 | 0.6920345 | 0.2923798 | 0.5977527 | 0.4799645 | 0.4155031 | 0.5954473 | 0.4848735 | 0.5380007 |
| 1057 | 0.7232527 | 0.329154 | 0.5421505 | 0.5290693 | 0.4032709 | 0.8293938 | 0.3093409 | 0.552981 |
| 1058 | 0.6608929 | 0.3187814 | 1 | 0.5254967 | 0.342674 | 0.5705709 | 0.4427381 | 0.5410737 |
| 1059 | 1.6852025 | 1.8689052 | 1.530513 | 3.0923889 | 2.6688197 | 2.066254 | 1.4663042 | 1 |
| 1060 | 0.5332279 | 0.3706502 | 0.3678649 | 0.6282768 | 0.4510218 | 0.4105889 | 0.3253478 | 0.4196914 |
| 1061 | 1 | 1.2052788 | 1 | 2.2461052 | 1.7942142 | 2.4731231 | 1.9063096 | 3.8608407 |
| 1062 | 1.4497465 | 0.45593 | 0.8549379 | 1.2558543 | 2.4934358 | 2.2738029 | 1.4575428 | 1 |
| 1063 | 1.1987855 | 1.4576072 | 1.5376951 | 2.3435173 | 1.4591488 | 1.3687204 | 1.3394966 | 1.7316655 |
| 1064 | 0.8168635 | 2.4206473 | 1.4540922 | 4.292188 | 3.7396177 | 2.1270474 | 2.2499842 | 2.030701 |
| 1065 | 1.7838612 | 1.306022 | 1.4757598 | 3.5319422 | 2.3875251 | 1.1425662 | 6.5173033 | 3.75704 |
| 1066 | 1 | 0.4923844 | 0.7209536 | 0.5717949 | 1 | 0.5890754 | 0.6108581 | 0.3113028 |
| 1067 | 1 | 1.4192467 | 3.0721935 | 8.3740527 | 4.1589054 | 7.4202081 | 2.5037148 | 5.8539947 |
| 1068 | 2.4954303 | 1.9355796 | 1.6139592 | 2.0586335 | 2.8262044 | 1.7562263 | 2.7042571 | 2.5409573 |
| 1069 | 0.8663571 | 0.380371 | 0.6119045 | 0.5771625 | 0.7287034 | 0.7124656 | 0.5405868 | 0.3044366 |
| 1070 | 2.1871245 | 2.7426875 | 1.6582045 | 1.9180464 | 2.0056724 | 1.5394324 | 1.5639357 | 1.702574 |
| 1071 | 0.8409861 | 0.2575424 | 0.439435 | 0.3872724 | 0.4244159 | 0.7815964 | 0.289962 | 0.444133 |
| 1072 | 1.6427059 | 2.1653983 | 2.2222991 | 2.5095318 | 2.2419874 | 2.3827231 | 1.2895893 | 2.1887302 |
| 1073 | 1.2947833 | 1.4836215 | 1.3980162 | 2.146214 | 2.6837443 | 1.8910684 | 2.1030307 | 1.5647897 |
| 1074 | 0.2311636 | 1 | 0.6580953 | 1 | 0.7166583 | 1.1486494 | 0.5111634 | 0.890383 |
| 1075 | 0.0226116 | 0.0325194 | 1 | 0.0510151 | 0.2690021 | 0.0650246 | 0.0570092 | 0.1099344 |
| 1076 | 1 | 4.1985055 | 1 | 1 | 1 | 1.5616528 | 1 | 1 |
| 1077 | 3.8628882 | 2.3462996 | 1.3724311 | 6.4856263 | 3.6767835 | 1.693235 | 2.6720696 | 2.5049437 |
| 1078 | 1.6618244 | 1.6450628 | 1.2499304 | 2.3820764 | 2.0183544 | 1.8039299 | 1.9558018 | 1.4024273 |

Table 4

| SEQ ID NO | Patient ID | | | | | | | |
|--------------|------------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|
| | 141 | 156 | 228 | 264 | 266 | 267 | 268 | 278 |
| 1079 | 1.4229849 | 1.5972643 | 1 | 2.5515062 | 1 | 2.4545866 | 1 | 2.1678769 |
| 1080 | 1.5447151 | 1.7616569 | 1 | 2.3021045 | 1 | 2.6516676 | 1.8024055 | 2.0775169 |
| 1081 | 0.3599893 | 0.5681401 | 0.2572983 | 0.4010424 | 0.2666141 | 0.6812275 | 0.3098563 | 0.2170379 |
| 1082 | 1.9936067 | 1.4727325 | 1.2973517 | 1.9390828 | 2.0772181 | 1.8692224 | 1.9097338 | 1 |
| 1083 | 1.1137484 | 1.6055587 | 1.1285196 | 1.6217493 | 1.9419754 | 1.3687889 | 1.5140555 | 2.1850736 |
| 1084 | 1.3697793 | 1.7417726 | 2.6932194 | 1 | 1.982643 | 1.9097896 | 2.3538412 | 4.5124696 |
| 1085 | 0.1849769 | 0.2220655 | 0.2124332 | 0.1849971 | 0.1866324 | 0.5446543 | 0.0839694 | 0.1154473 |
| 1086 | 1 | 1.9438555 | 1.4077038 | 2.6728245 | 1.4440692 | 2.2974436 | 1.4870452 | 4.921185 |
| 1087 | 0.1662854 | 0.2853274 | 0.4209627 | 1.8824721 | 1 | 1.5202825 | 0.1810909 | 1 |
| 1088 | 0.4347115 | 0.7338423 | 0.6526642 | 0.6276447 | 0.5550825 | 0.441098 | 0.6130312 | 0.3265812 |
| 1089 | 0.3805423 | 0.1811902 | 0.2425671 | 0.4117753 | 0.5413125 | 0.4069517 | 0.3015665 | 0.3581373 |
| 1090 | 1.9801712 | 1.5176904 | 1.7850185 | 2.5116676 | 1.8016934 | 1.3844681 | 2.2347255 | 3.1354276 |
| 1091 | 0.8509286 | 1 | 0.564302 | 0.6669052 | 0.804072 | 0.4802733 | 0.389215 | 1 |
| 1092 | 1.8311757 | 0.4297496 | 1 | 1.9241548 | 4.2978695 | 1.9105568 | 2.477733 | 1.1439933 |
| 1093 | 1 | 1.113869 | 2.2953966 | 1.7757387 | 2.1485367 | 2.5724668 | 1.6055106 | 4.0769349 |
| 1094 | 1.6798589 | 2.0562255 | 1 | 1.5806576 | 2.7400695 | 1.1739087 | 3.1398977 | 2.2761413 |
| 1095 | 0.8817198 | 0.4857748 | 0.7320174 | 0.5900876 | 0.9342141 | 0.6608862 | 0.5980091 | 0.267678 |
| 1096 | 1.2762342 | 1.389697 | 1 | 2.4215434 | 2.6904889 | 1.2490155 | 2.0437635 | 1.3759494 |
| 1097 | 1 | 0.4943827 | 0.7766997 | 0.5807093 | 1 | 0.5471554 | 0.6057036 | 0.2524866 |
| 1098 | 1 | 1.208931 | 1.2634455 | 2.1610839 | 3.4357068 | 2.3013105 | 1.5544014 | 1.5584884 |
| 1099 | 2.1139682 | 1.4516186 | 1.573392 | 2.876099 | 2.7192968 | 2.4828912 | 1.8119105 | 1.8859201 |
| 1100 | 1.3170883 | 1.3227951 | 1 | 1.8089359 | 1 | 2.8133771 | 1 | 1.4256334 |
| 1101 | 6.2020632 | 4.2752265 | 1.6740421 | 2.2177359 | 1.7994571 | 1.6398994 | 2.6434887 | 2.4636717 |
| 1102 | 1 | 1 | 1 | 1 | 1.5575532 | 2.4076355 | 1 | 1.7480179 |
| 1103 | 0.6511365 | 0.522094 | 1.4530829 | 2.6763671 | 1 | 2.670246 | 1 | 3.1707645 |
| 1104 | 1.4022567 | 2.2251556 | 1.5243528 | 2.161023 | 1.4499366 | 1.8171158 | 1.493232 | 2.3074616 |
| 1105 | 0.8754345 | 0.7027063 | 0.5854934 | 0.6941509 | 0.8478958 | 0.5041425 | 0.5219155 | 1 |
| 1106 | 1.1568035 | 1.872539 | 0.7982191 | 2.4927375 | 2.4761344 | 2.3424625 | 2.0741563 | 1.4041407 |
| 1107 | 1 | 1.3358546 | 0.8410469 | 2.1740648 | 1.9024224 | 0.8817872 | 1 | 1 |
| 1108 | 1 | 1 | 1.8922657 | 1 | 1.3832155 | 2.3470365 | 1 | 1.7446406 |
| 1109 | 0.4526584 | 0.8783813 | 0.5504057 | 0.4973809 | 0.7101781 | 0.349728 | 0.3109832 | 0.2435903 |
| 1110 | 1 | 2.3152927 | 1.2527351 | 2.8989174 | 2.6911132 | 1.7247944 | 2.4457921 | 1.6604826 |
| 1111 | 1.3990922 | 0.8684699 | 1 | 1.6849611 | 1 | 1.9869444 | 1 | 1.8815247 |
| 1112 | 1 | 1.4966625 | 1.3259276 | 1 | 1 | 1.4795451 | 1 | 1.441216 |
| 1113 | 1 | 2.9027084 | 1.4067316 | 3.4965343 | 4.6166527 | 2.9843198 | 3.1571383 | 2.8777386 |
| 1114 | 0.8895599 | 1 | 0.6390017 | 0.7525199 | 1 | 0.5131176 | 0.4511895 | 0.8527615 |
| 1115 | 0.7222453 | 0.1531223 | 0.4013818 | 1.5634591 | 1 | 0.5426332 | 1 | 0.4859761 |
| 1116 | 1.6457499 | 1.6719072 | 1 | 2.4096801 | 2.5255618 | 3.400525 | 1 | 1 |
| 1117 | 1 | 0.4865741 | 0.7094905 | 0.55286 | 1 | 0.6060644 | 0.5699839 | 0.2703289 |
| 1118 | 0.5404658 | 0.5203909 | 0.4763795 | 0.5660665 | 0.5026677 | 0.3836204 | 0.2977155 | 0.446579 |
| 1119 | 0.2697949 | 0.1809627 | 0.3147402 | 0.6264814 | 0.2477086 | 0.5619239 | 0.2272158 | 0.3695728 |
| 1120 | 1.41532 | 1 | 1 | 2.2451851 | 3.7188331 | 2.1630962 | 2.4136299 | 2.1984398 |
| 1121 | 1.44702 | 1.8389374 | 1.3764917 | 2.1348685 | 2.0268198 | 1.6011079 | 1 | 1.828389 |
| 1122 | 1 | 2.8975129 | 0.6777369 | 2.7259999 | 2.234285 | 1.0871054 | 1.5327532 | 1.3607704 |
| 1123 | 1.2412273 | 1.3115372 | 1 | 2.1386171 | 2.6663654 | 0.5733493 | 1 | 1 |
| 1124 | 1.6168312 | 1.5302272 | 1.3044247 | 1.9930245 | 2.7839176 | 2.1170025 | 2.5053846 | 1.8315241 |
| 1125 | 1.2551447 | 1.9314293 | 1.8149802 | 1.6588072 | 1 | 1.0630586 | 1 | 1.8658491 |
| 1126 | 2.8518061 | 2.2526825 | 1 | 3.443497 | 2.6965359 | 1.9258286 | 1.4964044 | 3.0700306 |
| 1127 | 2.5737112 | 1.5721661 | 1.2660773 | 2.9565539 | 2.4665676 | 1.6840845 | 1.4585992 | 3.0036156 |

Table 4

| SEQ ID NO | Patient ID | | | | | | | |
|--------------|------------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|
| | 141 | 156 | 228 | 264 | 266 | 267 | 268 | 278 |
| 1128 | 2.210853 | 2.3429548 | 2.2299264 | 2.5830285 | 2.8245984 | 0.9918416 | 3.3985889 | 2.4788383 |
| 1129 | 1 | 2.6464634 | 1.3672275 | 2.4200922 | 2.6652421 | 0.9403562 | 1 | 1.7899914 |
| 1130 | 1.4856951 | 1.2158296 | 2.1139642 | 1 | 2.0214619 | 12.292795 | 1 | 2.1723903 |
| 1131 | 1.7127962 | 1.8985041 | 1.1642036 | 2.3769111 | 2.1444977 | 1.6835661 | 1.8035016 | 1.9321276 |
| 1132 | 1 | 0.5110267 | 0.7034511 | 0.6514977 | 1 | 0.5154632 | 0.629727 | 0.2901081 |
| 1133 | 1.2201159 | 1.4763602 | 1.3175597 | 1.9265704 | 1 | 1.9042372 | 1.6640169 | 1.7662637 |
| 1134 | 1 | 1.5318012 | 1 | 1 | 1 | 2.9517038 | 1 | 1 |
| 1135 | 1.5477811 | 1.2920711 | 1.185147 | 2.0475915 | 2.2281325 | 2.3336168 | 1.4226931 | 1.5416643 |
| 1136 | 1.1395245 | 1.510841 | 1.1400077 | 2.0256988 | 2.2232917 | 2.5487892 | 1.4872415 | 1.8752234 |
| 1137 | 1.5316299 | 1.2200598 | 1.3993919 | 2.3880814 | 1 | 2.2505049 | 1 | 1.4803834 |
| 1138 | 1.7547235 | 1.5846476 | 1.6527862 | 3.9325259 | 2.4955819 | 1.6553359 | 1.3713459 | 1.8840018 |
| 1139 | 1 | 1.5232302 | 1 | 2.2735243 | 2.0772181 | 2.0777936 | 1 | 1.741698 |
| 1140 | 1.384496 | 0.4853874 | 1 | 1.9957201 | 1 | 5.9663605 | 1 | 1.3231613 |
| 1141 | 1.3355718 | 1.2335066 | 1 | 1.8765791 | 1 | 1.9545287 | 1.7968878 | 2.0122814 |
| 1142 | 1 | 1 | 1 | 3.1669258 | 2.9712556 | 1.9674309 | 1.9458735 | 1 |
| 1143 | 1 | 0.4090784 | 0.4718551 | 0.6826398 | 0.3644242 | 0.638652 | 0.3142261 | 0.7740852 |
| 1144 | 0.7383088 | 0.4767365 | 0.4611778 | 0.455815 | 0.3551942 | 0.6561998 | 0.2994336 | 0.6240087 |
| 1145 | 1 | 1.5782347 | 1 | 1.8652206 | 1 | 2.4017673 | 1 | 1.3923949 |
| 1146 | 1.138539 | 1.1326773 | 1.6947842 | 2.7006703 | 1 | 1.8239943 | 1 | 2.2069077 |
| 1147 | 1.8001765 | 1.3193274 | 1 | 2.1087019 | 1 | 1.5590486 | 2.2126126 | 1 |
| 1148 | 1.2753363 | 2.3950326 | 1.3927716 | 2.6002726 | 4.2519128 | 1.279433 | 2.0073601 | 1.3281216 |
| 1149 | 1.3949641 | 0.8841179 | 1.802867 | 1.8107716 | 1.8477643 | 1.2397009 | 2.1580408 | 2.6092473 |
| 1150 | 0.2014893 | 0.0450808 | 0.1596787 | 0.299915 | 0.5171856 | 0.4283583 | 0.1658976 | 0.2500406 |
| 1151 | 1 | 1.3181284 | 1 | 4.0232511 | 6.6891094 | 1.2673807 | 2.7357676 | 1.2256122 |
| 1152 | 1 | 1.615882 | 1 | 6.5588037 | 2.8200197 | 9.445707 | 1 | 2.7859196 |
| 1153 | 2.1134097 | 1.7768191 | 2.044074 | 1.8972738 | 1.3690105 | 1.8318448 | 1 | 1.9580405 |
| 1154 | 1.3708743 | 1.7690412 | 1 | 2.3786058 | 1 | 2.3366079 | 1 | 1.9412847 |
| 1155 | 1.2119034 | 1 | 1 | 1.3864957 | 1.5361326 | 5.1364775 | 1 | 1.6042365 |
| 1156 | 0.8699924 | 0.4714734 | 0.6931706 | 0.5976947 | 1 | 0.753652 | 0.638258 | 0.2897046 |
| 1157 | 1.0497681 | 1.8005892 | 1.8814012 | 1.7891122 | 1.3457648 | 1.7398563 | 1.3994438 | 1.9994677 |
| 1158 | 0.8033732 | 0.4112918 | 0.592499 | 0.539963 | 0.6636923 | 0.7288296 | 0.4973486 | 0.3900846 |
| 1159 | 0.7101018 | 0.3195808 | 0.533489 | 0.4434293 | 0.4368424 | 0.6925584 | 0.3769616 | 0.5051904 |
| 1160 | 0.1109993 | 1 | 1 | 1.6628333 | 0.4715544 | 0.5768021 | 0.3367272 | 0.7118482 |
| 1161 | 0.6608272 | 0.280052 | 0.4398581 | 0.4387788 | 0.3106803 | 0.8594833 | 0.2688503 | 0.4383718 |
| 1162 | 0.8682405 | 0.3055622 | 0.5205123 | 0.516088 | 0.4904451 | 0.8051267 | 0.3905882 | 0.4428355 |
| 1163 | 0.6892751 | 0.4014173 | 1 | 0.5502237 | 0.5365668 | 0.681185 | 0.4188989 | 0.4664576 |
| 1164 | 1.6869873 | 2.2567897 | 1 | 1.6756152 | 2.2297746 | 1.6348258 | 2.5403996 | 2.2644389 |
| 1165 | 1 | 1.3982065 | 1 | 2.2948751 | 1 | 3.0547459 | 1 | 1.5196439 |
| 1166 | 1.72575 | 1.9216102 | 1.9629903 | 2.4466375 | 2.8095448 | 1.6566647 | 1 | 3.3974437 |
| 1167 | 1.9020764 | 1.6577718 | 1.1555287 | 1.4280931 | 2.4157052 | 2.5051253 | 2.6094565 | 2.6393632 |
| 1168 | 1.6824869 | 1.9055503 | 1 | 2.6861109 | 2.6602495 | 2.067074 | 2.5539865 | 2.3337284 |
| 1169 | 0.0498331 | 0.0275945 | 0.414558 | 0.0401062 | 0.4305049 | 1.4239574 | 0.0273588 | 0.0738214 |
| 1170 | 0.5068933 | 1 | 0.6947745 | 0.7387613 | 0.5444679 | 0.5087123 | 0.6031039 | 0.4233542 |
| 1171 | 0.8461326 | 0.4460555 | 0.6967785 | 0.576499 | 1 | 0.6066257 | 0.5873623 | 0.2371151 |
| 1172 | 0.2201151 | 0.0918033 | 0.2356811 | 0.2656759 | 0.0823898 | 0.4513751 | 1 | 0.2671627 |
| 1173 | 1.2690839 | 1.9345159 | 0.7411014 | 1.1895426 | 2.3507468 | 2.0216858 | 1 | 1.3521659 |
| 1174 | 1.6179262 | 2.2068024 | 2.9128489 | 3.841951 | 3.9540204 | 1.984529 | 3.3330536 | 5.3533052 |
| 1175 | 0.1894773 | 0.2431672 | 0.0266894 | 0.1674409 | 6.5266184 | 17.288018 | 1 | 0.1356673 |
| 1176 | 0.7879776 | 0.2246356 | 0.3808879 | 0.3544292 | 0.3245653 | 0.7590704 | 0.2003591 | 0.5063327 |

Table 4

| SEQ ID NO | Patient ID | | | | | | | |
|--------------|------------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|
| | 141 | 156 | 228 | 264 | 266 | 267 | 268 | 278 |
| 1177 | 0.7460066 | 0.2422387 | 0.3769861 | 0.3896461 | 0.3389056 | 0.7320979 | 0.2561289 | 0.5570473 |
| 1178 | 0.3863786 | 0.2429089 | 1 | 1.583757 | 0.6276432 | 1.2170515 | 0.4344165 | 0.4595665 |
| 1179 | 1.7858979 | 1.77313 | 1.1398353 | 1.7423917 | 2.3281744 | 2.8063034 | 2.1017756 | 1.9698423 |
| 1180 | 1.4306717 | 2.093467 | 1.3119406 | 2.4042439 | 2.1801744 | 3.0243395 | 1.6503223 | 1.7233838 |
| 1181 | 1 | 2.0114583 | 1.4987979 | 3.0813366 | 1.9339875 | 2.9664331 | 2.0368192 | 1.84828 |
| 1182 | 3.3483518 | 2.3843404 | 1.4022821 | 3.673646 | 3.3386175 | 1.9055641 | 2.267367 | 2.4997723 |
| 1183 | 1 | 1.539161 | 1 | 1.76878 | 1.734337 | 2.8605389 | 1 | 1.5235178 |
| 1184 | 1.3881642 | 1.885457 | 0.7705927 | 2.3580653 | 1 | 2.5981303 | 1.7010899 | 1.9795643 |
| 1185 | 1 | 1 | 1.3281942 | 2.1831577 | 1.698026 | 2.7857198 | 1.4104429 | 1.4953016 |
| 1186 | 1 | 1.3211965 | 1 | 1.9311281 | 1 | 2.2259567 | 1 | 1.7624829 |
| 1187 | 2.2378555 | 1.8297454 | 1.2958571 | 1.9461649 | 2.4591584 | 1.6735203 | 2.3669917 | 2.3055495 |
| 1188 | 1.1934309 | 1.4794529 | 1.9042182 | 2.0017073 | 1.6748936 | 1.8568785 | 2.5360549 | 2.2838457 |
| 1189 | 1 | 0.5727331 | 1 | 0.6387421 | 1 | 0.5911192 | 0.5784506 | 0.2903378 |
| 1190 | 0.2542351 | 0.2566262 | 0.9345417 | 1 | 1.3755867 | 0.4880239 | 1 | 1 |
| 1191 | 1 | 1.2099271 | 1 | 2.1961546 | 1.9635657 | 2.6253189 | 1 | 3.2588089 |
| 1192 | 0.210961 | 0.113403 | 0.126825 | 0.1628979 | 0.3583882 | 0.2088119 | 0.1156792 | 0.254914 |
| 1193 | 1 | 0.4566002 | 0.730577 | 0.6157728 | 1 | 0.5867969 | 0.6550792 | 0.2803427 |
| 1194 | 1 | 0.2771438 | 0.6219225 | 0.4038625 | 0.4355709 | 0.6323422 | 1 | 0.4719456 |
| 1195 | 1.4650216 | 1.8738916 | 1 | 2.1550145 | 2.399876 | 1.6079572 | 2.2503436 | 1.8899244 |
| 1196 | 0.6426285 | 0.3396372 | 0.5639052 | 0.485295 | 0.5762882 | 0.7042817 | 0.3825509 | 0.3962121 |
| 1197 | 0.6441176 | 0.2790252 | 0.7571534 | 0.3919769 | 0.7178634 | 1.04265 | 1 | 1 |
| 1198 | 0.6611995 | 0.3517251 | 0.538563 | 0.4798714 | 0.5842819 | 0.7137302 | 0.3819468 | 0.4185305 |
| 1199 | 1 | 0.3949122 | 0.0777443 | 0.1223723 | 1 | 6.1668426 | 0.7459242 | 0.0983996 |
| 1200 | 0.7628913 | 0.3912477 | 0.6356012 | 0.4905413 | 1 | 0.7917058 | 0.4638623 | 0.3401585 |
| 1201 | 1.998797 | 2.517603 | 1.3069582 | 2.4744097 | 3.7700079 | 1.6878786 | 2.9020242 | 1.8176985 |
| 1202 | 1.8405489 | 2.1715284 | 1.736288 | 1.7658085 | 1.7988989 | 1.5032542 | 1.5350079 | 1.7423064 |
| 1203 | 1 | 0.7279766 | 0.2541162 | 0.3811928 | 0.2138638 | 0.7173861 | 0.2526198 | 0.2162929 |
| 1204 | 1.9158076 | 1.427621 | 1.6138209 | 4.4554317 | 3.7779904 | 1.6913237 | 2.4631116 | 2.7005075 |
| 1205 | 1.3797875 | 1.1269346 | 1.4621603 | 1.7938805 | 1.5429105 | 1.5852361 | 1.3523232 | 1.5223879 |
| 1206 | 1.5537159 | 1.6381457 | 1.6570743 | 4.7210635 | 2.5689163 | 1.8759225 | 1.6311181 | 2.032042 |
| 1207 | 1.3883394 | 1.6692326 | 0.9226547 | 2.1804281 | 2.2398946 | 1.5414282 | 2.5255974 | 2.2055295 |
| 1208 | 1.3276112 | 0.1870928 | 0.7755248 | 1 | 1 | 21.642518 | 6.4843043 | 1 |
| 1209 | 1.4266641 | 2.0099027 | 2.0547179 | 2.7064811 | 2.2604861 | 1.2512445 | 2.0843606 | 1.7342854 |
| 1210 | 0.8070195 | 1.1271621 | 2.5103941 | 1.7801054 | 2.0370248 | 2.3329698 | 1 | 4.159752 |
| 1211 | 1.4400668 | 1.7692503 | 1.1679744 | 1.9379564 | 2.7313579 | 1.9051327 | 2.3110739 | 2.3192757 |
| 1212 | 0.833146 | 0.5204585 | 0.7970289 | 0.6166586 | 1 | 0.6145603 | 0.6231254 | 0.2836827 |
| 1213 | 1.895397 | 1.4940679 | 1 | 1.6439517 | 1.2837947 | 1.3317095 | 2.8971005 | 3.3124972 |
| 1214 | 1.5628262 | 1.8510008 | 1.5903241 | 3.0171219 | 3.419331 | 2.2878807 | 1.8127265 | 1 |
| 1215 | 1 | 0.3932644 | 0.7002355 | 0.5849815 | 1 | 0.5408864 | 0.604761 | 0.2981167 |
| 1216 | 1.7007513 | 1.4807317 | 1 | 1.7176631 | 1 | 1.2629175 | 2.4293427 | 3.198931 |
| 1217 | 1 | 2.0051314 | 1.7653257 | 1 | 1 | 2.3779058 | 1 | 2.8807309 |
| 1218 | 1 | 1.4549326 | 0.8531668 | 4.1489913 | 2.7834722 | 1.5267121 | 1 | 1.3913829 |
| 1219 | 0.0423105 | 0.0810619 | 0.3217294 | 0.3474495 | 0.18512 | 0.6120534 | 0.0469629 | 0.1048065 |
| 1220 | 2.2178171 | 1.9949434 | 1.6821125 | 1 | 1.3487383 | 1.2007518 | 1 | 2.875963 |
| 1221 | 1 | 2.2193699 | 1 | 2.0717511 | 3.1296067 | 2.0566578 | 2.4440947 | 2.4823025 |
| 1222 | 0.1844951 | 2.002918 | 0.0242203 | 0.1008242 | 7.4297251 | 12.607341 | 1 | 0.1032296 |
| 1223 | 1 | 0.6680779 | 4.0763184 | 0.7684287 | 1 | 4.6397153 | 2.4022085 | 2.3825433 |
| 1224 | 1 | 1.4176235 | 1 | 2.0690696 | 2.7426614 | 1.7693225 | 2.0568187 | 2.2589012 |
| 1225 | 1.3175263 | 1.8380828 | 1.5728995 | 2.2445283 | 1 | 1.7206161 | 2.9481821 | 2.9614682 |

Table 4

| SEQ ID | Patient ID | | | | | | | | |
|--------|------------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|
| | NO | 141 | 156 | 228 | 264 | 266 | 267 | 268 | 278 |
| 1226 | | 0.0387517 | 0.0265 | 0.0404172 | 0.1185737 | 0.063199 | 0.1861838 | 1 | 0.1210284 |
| 1227 | | 0.4734523 | 0.2035093 | 0.2060549 | 0.3686672 | 0.2461446 | 0.6551661 | 0.2376525 | 0.267051 |
| 1228 | | 1.3053719 | 0.7788002 | 1 | 2.0367755 | 2.6072239 | 1.8156379 | 2.6613425 | 2.2536677 |
| 1229 | | 1.6968641 | 1.9942117 | 1 | 1.5455093 | 2.9007797 | 2.2878807 | 1 | 1.7719752 |
| 1230 | | 1.8356652 | 0.5716018 | 2.0008775 | 1.9097876 | 2.049685 | 1.6741607 | 4.1625622 | 2.2996765 |
| 1231 | | 1 | 1.6688759 | 1.8741962 | 1.5949167 | 1.6550161 | 1.4783053 | 1.6956128 | 2.0078239 |
| 1232 | | 0.5107587 | 0.3330152 | 0.2849157 | 0.555373 | 0.4455751 | 0.661942 | 0.2468161 | 0.4763783 |
| 1233 | | 1.3882627 | 2.2683181 | 1.5766836 | 2.5717739 | 3.3732515 | 1.4259994 | 2.395163 | 2.243536 |
| 1234 | | 1 | 1.5424812 | 4.1177431 | 1 | 2.9252903 | 1.0445917 | 1 | 1.1515362 |
| 1235 | | 0.6496364 | 0.4883695 | 1.3719564 | 2.7812333 | 1.7303694 | 2.5031761 | 1 | 3.1857138 |
| 1236 | | 0.4919905 | 0.6207652 | 0.3863709 | 0.3171219 | 0.4791523 | 1.0507732 | 0.2864319 | 0.3679649 |
| 1237 | | 1.7642608 | 3.2312598 | 1.6844058 | 1.8313431 | 2.1559922 | 0.9433894 | 1 | 1.9867285 |
| 1238 | | 0.7964309 | 0.5021975 | 0.4949599 | 0.5497703 | 1 | 0.6977449 | 0.5063359 | 0.2526542 |
| 1239 | | 1.3343563 | 2.3096299 | 1.5126656 | 1 | 2.4778096 | 2.6749477 | 2.1635925 | 1.8857836 |
| 1240 | | 1 | 1.4291397 | 1.3819688 | 2.1087019 | 1 | 2.3410086 | 1 | 1.3224722 |
| 1241 | | 1 | 2.3891793 | 1 | 1 | 2.9335528 | 1.8155475 | 2.46613 | 1.3384706 |
| 1242 | | 1 | 1.2202504 | 1 | 1.9475975 | 1 | 2.5400294 | 1 | 1.5711035 |
| 1243 | | 1 | 1.4897086 | 1.1362438 | 1.9516099 | 2.363602 | 1.9125612 | 1 | 1.9984558 |
| 1244 | | 1 | 1.6299805 | 1 | 1.7250387 | 2.1785363 | 2.0431734 | 1 | 2.0288758 |
| 1245 | | 1 | 1.5299505 | 1 | 1 | 1 | 1.9207559 | 1.6476682 | 1.6896424 |
| 1246 | | 1.5320132 | 1.7745072 | 1.626393 | 1 | 2.4749015 | 2.9357799 | 1.9831282 | 1.9502865 |
| 1247 | | 1.3517448 | 1.6091494 | 1.6821501 | 2.4321356 | 1.5777532 | 1.5161522 | 1 | 1.4770061 |
| 1248 | | 1.465164 | 1.4512251 | 1.4999015 | 2.438706 | 1 | 2.3470365 | 1 | 1 |
| 1249 | | 1 | 2.5427381 | 1.5780371 | 3.4604241 | 1 | 3.3425403 | 1 | 1.4572082 |
| 1250 | | 1 | 0.4594039 | 0.7193366 | 0.5953712 | 1 | 0.5940212 | 0.5611461 | 0.2719306 |
| 1251 | | 1 | 0.1600209 | 0.373119 | 0.2901658 | 0.2842471 | 0.6918881 | 0.1923187 | 0.5486601 |
| 1252 | | 1 | 0.4751317 | 0.5640022 | 0.5001267 | 1 | 0.7556305 | 0.4134433 | 0.3143076 |
| 1253 | | 1 | 1 | 1.8307193 | 1 | 1 | 2.2089197 | 1 | 1.8596906 |
| 1254 | | 1.642684 | 1.9208355 | 1 | 1.6200373 | 1 | 2.774344 | 1 | 1.5821664 |
| 1255 | | 1.394986 | 1.493951 | 1 | 1.6931407 | 1.7089098 | 1.4270971 | 1.7729723 | 1.5854443 |
| 1256 | | 1.4811727 | 1.5976209 | 1 | 1.4732532 | 1 | 2.932946 | 1 | 1.4496094 |
| 1257 | | 0.4636521 | 0.5755921 | 0.5595718 | 1 | 0.414649 | 1.0285223 | 0.385952 | 0.5358278 |
| 1258 | | 1.9548112 | 0.7432803 | 2.0546058 | 1 | 1 | 1.1667088 | 1 | 1.7366073 |
| 1259 | | 0.7184675 | 0.2915743 | 0.5124849 | 0.5176163 | 0.5133322 | 0.6628205 | 0.3696978 | 0.4235591 |
| 1260 | | 1 | 0.5377051 | 1 | 0.6226786 | 1 | 0.5894627 | 0.4983162 | 0.3092541 |
| 1261 | | 0.7918977 | 0.4284769 | 0.6775663 | 0.5877822 | 1 | 0.5308947 | 0.6223614 | 0.2922686 |
| 1262 | | 1 | 1.3132404 | 1.2068963 | 2.1110805 | 1.4587511 | 1.6100637 | 2.5465994 | 2.107223 |
| 1263 | | 2.1040804 | 1.6176528 | 3.5111601 | 1.9122148 | 1.9053916 | 1.8000409 | 0.7274542 | 2.3631179 |
| 1264 | | 0.8170715 | 0.2974154 | 0.4802835 | 0.4531393 | 0.4702224 | 0.8224033 | 0.3479984 | 0.5009316 |
| 1265 | | 0.7248513 | 0.4249907 | 0.6644074 | 0.5974248 | 1 | 0.5992116 | 0.4981136 | 0.4717718 |
| 1266 | | 1 | 0.2886415 | 0.4933432 | 0.4534661 | 0.5658568 | 0.7771869 | 0.3714574 | 0.4713248 |
| 1267 | | 1 | 2.7765842 | 0.5705519 | 1 | 1 | 2.2025148 | 1 | 1.4087658 |
| 1268 | | 2.4188466 | 1.5806265 | 2.870579 | 2.306672 | 1.8671999 | 1.1957245 | 1 | 2.7872544 |
| 1269 | | 1.448323 | 1.878128 | 1.3626297 | 1 | 2.9776126 | 1.4580478 | 4.8917965 | 5.196201 |
| 1270 | | 1 | 1.7008236 | 1.1817463 | 2.4606819 | 2.3760305 | 2.13794 | 1.9028334 | 2.4785403 |
| 1271 | | 1.4139074 | 1.7668093 | 3.9815654 | 1 | 6.2527456 | 22.873544 | 1 | 3.3516212 |
| 1272 | | 0.7524123 | 0.3819266 | 0.565195 | 0.4790356 | 0.5541145 | 0.6479819 | 0.3818173 | 0.4530914 |
| 1273 | | 1.6460784 | 1 | 1.5272874 | 1.9461649 | 1 | 2.6986403 | 1.8182248 | 2.8404709 |
| 1274 | | 0.0567643 | 0.2368465 | 0.415495 | 2.1309555 | 1 | 1.4795251 | 0.1386599 | 1 |

Table 4

| SEQ ID NO | Patient ID | | | | | | | |
|--------------|------------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|
| | 141 | 156 | 228 | 264 | 266 | 267 | 268 | 278 |
| 1275 | 0.5670193 | 0.3578121 | 0.4958163 | 1 | 1 | 1.725883 | 1 | 0.328276 |
| 1276 | 0.3705888 | 1 | 0.558262 | 0.5504526 | 0.549737 | 0.5682824 | 0.4895366 | 0.4393403 |
| 1277 | 1.3339402 | 1.4429185 | 1 | 1 | 2.2757892 | 1.4315611 | 2.8786005 | 1.9198789 |
| 1278 | 1.2637841 | 1.9310543 | 1.2330997 | 2.9510959 | 2.2619557 | 2.0538001 | 2.1429399 | 2.0843645 |
| 1279 | 1 | 1.8687822 | 1.5857734 | 2.7326013 | 1 | 2.785436 | 1 | 1.9761187 |
| 1280 | 0.290534 | 0.3360034 | 0.5248036 | 1 | 0.4013566 | 1.8672121 | 0.3460239 | 0.3075531 |
| 1281 | 1.4872828 | 11.43158 | 1.2975527 | 1.4666637 | 1 | 1.0218539 | 2.0156897 | 3.0753573 |
| 1282 | 2.1820985 | 2.0550634 | 1.3144805 | 4.1706405 | 2.7154767 | 2.4196188 | 1 | 3.2154634 |
| 1283 | 0.7748267 | 0.5537096 | 1 | 0.6688002 | 1 | 0.5786298 | 0.5344342 | 0.284676 |
| 1284 | 1.2478301 | 2.0169673 | 1 | 1 | 2.147012 | 1.7241691 | 2.4507918 | 1.6532935 |
| 1285 | 1 | 1.3514287 | 1.2837174 | 2.0738228 | 2.6919461 | 1.8410019 | 1 | 1.6783001 |
| 1286 | 1 | 1.5153048 | 1.137925 | 2.5460032 | 2.4603757 | 1.5580714 | 1 | 2.6325528 |
| 1287 | 1 | 1.2420837 | 1.7909144 | 1 | 1.4375954 | 1.7083886 | 1 | 2.8553829 |
| 1288 | 1.5162234 | 2.3515627 | 1.825089 | 1.3441848 | 1.8531279 | 1.3692515 | 2.009866 | 1.287309 |
| 1289 | 1.5018352 | 1.9732638 | 2.3326953 | 1 | 2.6386624 | 2.1621983 | 1 | 2.624029 |
| 1290 | 1 | 1.836976 | 1 | 1 | 1 | 3.5926325 | 1 | 1.9956497 |
| 1291 | 1.5431383 | 2.2319436 | 1.8043777 | 1 | 3.0148956 | 2.3253813 | 1 | 1 |
| 1292 | 0.1989271 | 0.2052555 | 0.0417474 | 0.2057105 | 4.6019976 | 12.235043 | 1 | 0.1398702 |
| 1293 | 1 | 0.4522593 | 0.7637366 | 0.5662169 | 1 | 0.587156 | 0.6224508 | 0.281932 |
| 1294 | 0.8206412 | 1.6466491 | 1.108502 | 1.5212118 | 1.6276854 | 1.7605796 | 1.6389937 | 1.9086172 |
| 1295 | 1 | 0.4400853 | 0.7524365 | 0.5690851 | 1 | 0.5369856 | 0.5787357 | 0.2933674 |
| 1296 | 0.6031102 | 0.2215429 | 0.4020798 | 0.2915162 | 0.3942997 | 0.6044167 | 0.3080606 | 0.4259058 |
| 1297 | 0.2155271 | 0.3737491 | 0.3518865 | 0.3706833 | 0.2800127 | 0.4097537 | 0.1753944 | 0.5794589 |
| 1298 | 1 | 1.8035466 | 1 | 2.8455941 | 1 | 1.4939329 | 2.2669109 | 1.9985613 |
| 1299 | 0.386729 | 10.003713 | 2.6344747 | 1 | 3.5012229 | 2.5054122 | 1 | 1.4283092 |
| 1300 | 1 | 1 | 0.69261 | 1 | 0.5802527 | 0.5168515 | 1 | 0.230671 |
| 1301 | 1 | 1.749489 | 1.935665 | 3.0655791 | 1 | 1.5943167 | 2.3634177 | 4.5398104 |
| 1302 | 1 | 0.3376328 | 0.1248442 | 0.3582284 | 1 | 1.1883329 | 0.3720313 | 0.4500432 |
| 1303 | 0.1216645 | 1 | 0.4501272 | 0.5021166 | 0.420393 | 0.5620307 | 0.1781909 | 1 |

Table 4

| SEQ ID NO | Patient ID | | | | | | | |
|--------------|------------|-----------|-----|-----|-----------|-----------|-----------|-----------|
| | 295 | 296 | 300 | 322 | 339 | 341 | 356 | 360 |
| 1 | 1000 | 1000 | | | 1.243439 | 1000 | 1 | 1 |
| 2 | 1.6933117 | 1.8643873 | | | 0.8354588 | 0.316661 | 1.7321107 | 0.435199 |
| 3 | 1000 | 1000 | | | 1 | 1 | 1000 | 1 |
| 4 | 0.5422463 | 0.5978163 | | | 0.1886367 | 0.3016081 | 1 | 0.2345406 |
| 5 | 0.6674355 | 0.5002344 | | | 0.8375616 | 0.2775426 | 0.242161 | 0.4841635 |
| 6 | 0.7499986 | 0.6201072 | | | 1 | 0.3718346 | 0.276016 | 0.5365668 |
| 7 | 1.7689442 | 1.2572259 | | | 1 | 1.4952663 | 1.6797355 | 0.7400161 |
| 8 | 1 | 1000 | | | 1.2879898 | 1 | 1 | 1 |
| 9 | 1.2608076 | 0.4909874 | | | 0.5277583 | 1 | 0.4009279 | 1 |
| 10 | 1 | 0.3285348 | | | 0.8113925 | 0.2039801 | 0.708386 | 0.3305963 |
| 11 | 1.6196198 | 0.5921192 | | | 0.2103085 | 0.4723454 | 0.8102189 | 0.557351 |
| 12 | 4.4102928 | 1 | | | 1.3322489 | 1 | 3.1896117 | 2.1940344 |
| 13 | 1 | 1.1831883 | | | 0.7377046 | 0.3948293 | 2.0876789 | 1.3558048 |
| 14 | 1 | 1 | | | 1 | 2.3878657 | 1 | 1 |
| 15 | 1 | 0.4040004 | | | 0.6102498 | 0.4298842 | 1 | 0.422064 |
| 16 | 5.0356733 | 6.6562667 | | | 2.0242557 | 3.0673075 | 5.439614 | 1.823374 |
| 17 | 1 | 2.4310982 | | | 1 | 1.4690661 | 1 | 1.1935128 |
| 18 | 5.3365676 | 1 | | | 0.6203411 | 1.7289611 | 1 | 1.4109239 |
| 19 | 1 | 0.7708311 | | | 1 | 0.5315276 | 0.6097758 | 0.671799 |
| 20 | 1000 | 1000 | | | 0.5488364 | 1 | 1000 | 1 |
| 21 | 1 | 1 | | | 1 | 1 | 1 | 1 |
| 22 | 1 | 6.0348442 | | | 1 | 2.6497581 | 1 | 1.9443554 |
| 23 | 1 | 1 | | | 1 | 1 | 1 | 1.5572286 |
| 24 | 3.8040686 | 1 | | | 1 | 2.563504 | 1 | 1.2649478 |
| 25 | 0.8385553 | 0.7091071 | | | 0.7403305 | 0.3840733 | 0.3886578 | 0.5171512 |
| 26 | 1000 | 1000 | | | 1 | 1 | 1000 | 1 |
| 27 | 0.6944816 | 0.5997202 | | | 0.8637005 | 0.3490183 | 0.2581986 | 0.5040152 |
| 28 | 0.3283008 | 0.2815079 | | | 1 | 0.248178 | 1 | 0.4909435 |
| 29 | 1 | 1000 | | | 1 | 2.7125714 | 1 | 3.1794243 |
| 30 | 12.123465 | 8.9972277 | | | 1 | 5.6311753 | 1 | 2.519187 |
| 31 | 1 | 1 | | | 4.9748627 | 1 | 1000 | 3.2600761 |
| 32 | 4.5164533 | 4.3188155 | | | 1.6175835 | 2.9027822 | 6.4527024 | 1.4703037 |
| 33 | 4.983433 | 4.8413734 | | | 1.7669414 | 1.3247761 | 4.7921033 | 1 |
| 34 | 2.46072 | 2.4499591 | | | 1.6469822 | 2.1118949 | 1 | 1.4468366 |
| 35 | 5.9226265 | 6.0968153 | | | 1.8383757 | 5.4977717 | 4.9037674 | 2.0954948 |
| 36 | 3.7938667 | 4.1485621 | | | 1.2470208 | 2.4327637 | 3.747358 | 1.6927074 |
| 37 | 4.8647531 | 1 | | | 1 | 1 | 3.8410872 | 1.7245896 |
| 38 | 2.3544874 | 3.0288673 | | | 0.5784766 | 1.7335258 | 2.1205128 | 1.305205 |
| 39 | 0.6655559 | 0.8171968 | | | 0.2221102 | 0.5661569 | 0.6855774 | 0.4685141 |
| 40 | 5.868357 | 7.9716341 | | | 1.5500328 | 3.5093 | 4.9152815 | 1.7561215 |
| 41 | 4.156 | 10.12351 | | | 0.3449369 | 1.7553947 | 7.1114711 | 2.8524387 |
| 42 | 6.048531 | 1 | | | 1.5147785 | 6.3341061 | 2.506425 | 1 |
| 43 | 0.7675303 | 0.6774566 | | | 1 | 0.3529103 | 0.3080975 | 0.5393162 |
| 44 | 2.5425124 | 1.3561522 | | | 0.3555112 | 1 | 1 | 0.4983107 |
| 45 | 3.569431 | 6.3548842 | | | 1.3107281 | 5.0115883 | 7.8404214 | 1.5655675 |
| 46 | 2.2158473 | 1 | | | 2.4776922 | 2.9208485 | 1 | 1.4653906 |
| 47 | 4.5030744 | 4.3711109 | | | 1.5414909 | 3.7185792 | 1 | 2.4588465 |
| 48 | 1 | 0.2103079 | | | 0.5369844 | 1 | 0.5151932 | 1 |
| 49 | 1000 | 1000 | | | 1 | 1 | 1 | 1 |

Table 4

| SEQ ID NO | Patient ID | | | | | | | |
|--------------|------------|-----------|-----|-----|-----------|-----------|-----------|-----------|
| | 295 | 296 | 300 | 322 | 339 | 341 | 356 | 360 |
| 50 | 0.2302741 | 0.1924462 | | | 0.1506559 | 0.1104295 | 0.5049122 | 1.5832178 |
| 51 | 1 | 1 | | | 0.6493776 | 5.697201 | 1 | 1 |
| 52 | 0.7652737 | 0.6398111 | | | 1 | 0.3525465 | 0.2846461 | 0.5421029 |
| 53 | 1000 | 1 | | | 1 | 1000 | 1 | 1 |
| 54 | 1000 | 1000 | | | 1 | 1 | 1 | 1 |
| 55 | 1 | 1 | | | 1 | 1 | 1 | 1 |
| 56 | 4.153261 | 3.4440367 | | | 1 | 3.1242863 | 3.5506568 | 2.2214293 |
| 57 | 0.5878276 | 0.6191371 | | | 0.6220113 | 0.4494125 | 1 | 0.5945598 |
| 58 | 1 | 0.4683949 | | | 0.7959084 | 0.6271375 | 0.3730103 | 0.5217741 |
| 59 | 4.1319258 | 2.995273 | | | 1.2846596 | 2.9025351 | 1 | 1.4264635 |
| 60 | 1 | 1000 | | | 1 | 1 | 1 | 1 |
| 61 | 5.6214162 | 6.9042965 | | | 2.2569201 | 2.2468979 | 1 | 1 |
| 62 | 5.3108966 | 7.0359924 | | | 1 | 2.6156985 | 1 | 1.8739862 |
| 63 | 4.6261345 | 5.0718903 | | | 1.191131 | 2.4554083 | 1 | 1.8423226 |
| 64 | 5.1380913 | 4.8590317 | | | 1.2885633 | 4.5177994 | 6.2283836 | 1.8193594 |
| 65 | 4.6898408 | 5.6663494 | | | 0.8962081 | 3.0579655 | 3.9702992 | 1.3341321 |
| 66 | 0.6637872 | 0.564549 | | | 0.8019552 | 0.3852401 | 0.3090142 | 0.5453761 |
| 67 | 5.4421071 | 5.5385557 | | | 1.4348627 | 4.8264363 | 4.0886572 | 2.0019328 |
| 68 | 12.822814 | 1000 | | | 1 | 1 | 1 | 1 |
| 69 | 5.3769593 | 4.5710673 | | | 1.2118369 | 3.6877732 | 3.1482078 | 2.0489044 |
| 70 | 1 | 1000 | | | 1 | 1 | 1000 | 1 |
| 71 | 0.3364955 | 1000 | | | 1 | 1 | 1 | 1.6577941 |
| 72 | 0.3334017 | 0.7028577 | | | 0.4969611 | 0.3718552 | 1 | 0.3535417 |
| 73 | 1000 | 1000 | | | 1 | 1 | 1 | 1 |
| 74 | 6.3069157 | 4.3965228 | | | 1 | 3.8354952 | 1 | 1 |
| 75 | 1000 | 1000 | | | 1 | 1 | 1 | 1 |
| 76 | 3.5535293 | 3.0590426 | | | 1.6650017 | 2.0426637 | 3.2980479 | 1 |
| 77 | 0.8304992 | 0.6544282 | | | 0.8805329 | 0.3897704 | 0.3420576 | 0.5302694 |
| 78 | 0.6548828 | 0.5535253 | | | 0.8770014 | 0.289843 | 0.2527432 | 0.487694 |
| 79 | 0.6316901 | 0.5412481 | | | 0.8600383 | 0.2993017 | 0.2633721 | 0.4811371 |
| 80 | 6.4977517 | 10.313482 | | | 1.4275985 | 5.2351585 | 6.1210307 | 2.6317786 |
| 81 | 4.8689392 | 14.159931 | | | 2.2721325 | 9.0718824 | 6.0770753 | 1.9669224 |
| 82 | 5.3442911 | 3.3394168 | | | 2.1708569 | 1.1251203 | 5.5226962 | 1.7475581 |
| 83 | 3.0672381 | 2.7869016 | | | 1.3678352 | 2.884002 | 1 | 2.1467394 |
| 84 | 1 | 1 | | | 1 | 1 | 1 | 1 |
| 85 | 0.4453562 | 1.108791 | | | 0.1130673 | 0.3665836 | 0.3493032 | 0.2965622 |
| 86 | 4.7920148 | 7.0346153 | | | 1 | 2.9932852 | 4.8217308 | 1.8670924 |
| 87 | 5.318426 | 1 | | | 1 | 4.5841889 | 1 | 2.6246629 |
| 88 | 1 | 1 | | | 1 | 1.7192828 | 2.2578598 | 1.5221199 |
| 89 | 4.4921961 | 4.4159215 | | | 1.6992097 | 4.5108873 | 3.9017518 | 2.8922083 |
| 90 | 5.0785877 | 5.6717231 | | | 1.3078304 | 2.9208073 | 5.2445224 | 2.6862936 |
| 91 | 1 | 1 | | | 1 | 1.6580276 | 1 | 1.7110142 |
| 92 | 8.8238181 | 7.9705368 | | | 1.263179 | 3.7076516 | 5.6674918 | 1.9260404 |
| 93 | 0.6868911 | 0.4333981 | | | 0.8280941 | 0.335551 | 0.3170669 | 0.5093947 |
| 94 | 3.9142599 | 1000 | | | 1 | 2.8458652 | 1 | 1 |
| 95 | 1000 | 1000 | | | 3.2201054 | 1 | 1 | 1 |
| 96 | 3.1997627 | 3.4174584 | | | 1 | 2.5563722 | 5.1681988 | 1.8914991 |
| 97 | 1 | 1 | | | 0.001 | 1000 | 1 | 1 |
| 98 | 6.1130689 | 6.3583141 | | | 1 | 1.7731865 | 1 | 2.0988819 |

Table 4

| SEQ ID NO | Patient ID | | | | | | | |
|--------------|------------|-----------|-----|-----|-----------|-----------|-----------|-----------|
| | 295 | 296 | 300 | 322 | 339 | 341 | 356 | 360 |
| 99 | 0.7617141 | 0.5614788 | | | 0.8546958 | 0.3351186 | 0.3287172 | 0.5816688 |
| 100 | 0.6624843 | 0.6183922 | | | 1 | 0.3372258 | 0.2865471 | 0.441354 |
| 101 | 1 | 1000 | | | 1 | 3.8733301 | 1 | 1 |
| 102 | 4.5555864 | 1 | | | 1 | 2.1807555 | 1 | 1.2617871 |
| 103 | 0.7254476 | 0.5055827 | | | 0.3602299 | 0.267267 | 0.4672147 | 1 |
| 104 | 0.723446 | 0.4016459 | | | 1 | 0.2919915 | 0.3023225 | 0.5056618 |
| 105 | 5.0184743 | 5.6479462 | | | 1.5493587 | 1 | 3.8488928 | 2.1919181 |
| 106 | 6.7672087 | 6.0391607 | | | 1.1958899 | 5.749471 | 4.6579761 | 1.8590041 |
| 107 | 2.3893013 | 0.7730148 | | | 2.1844998 | 0.6200675 | 1.2994367 | 1 |
| 108 | 3.5731347 | 3.4695358 | | | 1.9881361 | 3.2519309 | 3.3781602 | 2.2014253 |
| 109 | 1 | 1000 | | | 0.6615919 | 1 | 1 | 1 |
| 110 | 3.4989161 | 10.355633 | | | 1.7283468 | 4.0131379 | 7.0248071 | 2.5629687 |
| 111 | 3.1091323 | 3.04557 | | | 1.1284399 | 3.4504885 | 2.4863698 | 1.458061 |
| 112 | 1 | 1000 | | | 0.5039838 | 1 | 1 | 0.6203062 |
| 113 | 0.7017116 | 0.6338995 | | | 1 | 0.3453461 | 0.2922143 | 0.6919004 |
| 114 | 0.6025039 | 0.3848015 | | | 1 | 0.2564149 | 0.292107 | 0.5076 |
| 115 | 2.2875265 | 2.4755673 | | | 1.3212218 | 2.3029088 | 1 | 1.5772488 |
| 116 | 0.6494159 | 0.5702135 | | | 0.8885013 | 0.362925 | 0.2904644 | 0.5800659 |
| 117 | 0.4772648 | 0.3757871 | | | 0.8770114 | 0.3912943 | 0.2680545 | 0.611187 |
| 118 | 0.5030522 | 0.3781997 | | | 0.4546136 | 0.254191 | 0.2487645 | 0.422162 |
| 119 | 0.6420084 | 0.5183468 | | | 0.7225424 | 0.3228113 | 0.2843816 | 0.4794919 |
| 120 | 0.5725525 | 0.4371369 | | | 0.6458965 | 0.3212668 | 0.2912407 | 0.5064122 |
| 121 | 5.1752283 | 1 | | | 1 | 3.0490971 | 1 | 1.5465582 |
| 122 | 0.4112964 | 0.2764356 | | | 0.1645201 | 0.1548195 | 0.3586807 | 0.498676 |
| 123 | 10.330386 | 9.1215696 | | | 1.8997387 | 3.8249794 | 3.8229967 | 2.5494412 |
| 124 | 15.89227 | 1 | | | 2.2409228 | 7.6222897 | 1 | 1.6211842 |
| 125 | 3.7027041 | 1 | | | 0.552388 | 2.8858004 | 1 | 1 |
| 126 | 2.1944899 | 0.7367572 | | | 2.3566262 | 0.6479357 | 1 | 0.6776635 |
| 127 | 0.7844078 | 0.6766064 | | | 0.8023274 | 0.3528142 | 0.2956615 | 0.5085345 |
| 128 | 0.7558813 | 0.5325025 | | | 0.8502387 | 0.3485447 | 0.2885134 | 0.4726713 |
| 129 | 1000 | 1000 | | | 0.001 | 1 | 1000 | 1 |
| 130 | 1 | 1000 | | | 1 | 1000 | 1 | 1 |
| 131 | 1.7660222 | 1000 | | | 0.6036698 | 1 | 1 | 1 |
| 132 | 1000 | 1000 | | | 1.3414347 | 1 | 1 | 1 |
| 133 | 4.8575397 | 8.0874012 | | | 1.5619352 | 3.8317337 | 1 | 1.7510777 |
| 134 | 0.6856381 | 0.5599637 | | | 0.8542732 | 0.3554294 | 0.3100766 | 0.5097479 |
| 135 | 1 | 0.795193 | | | 1 | 0.4654539 | 0.4292007 | 0.6347465 |
| 136 | 1.6271714 | 1.5832464 | | | 0.5007139 | 0.1945969 | 1 | 0.7597184 |
| 137 | 1 | 1 | | | 1.3475016 | 2.0827294 | 1 | 1 |
| 138 | 1 | 0.318801 | | | 0.293957 | 0.2235016 | 1 | 0.4270356 |
| 139 | 5.4070271 | 9.1051176 | | | 1.3179117 | 2.164165 | 4.5960778 | 2.0897574 |
| 140 | 1 | 1000 | | | 1.2065347 | 1 | 1 | 2.5424399 |
| 141 | 5.1340216 | 5.4626942 | | | 1.4012383 | 4.3930034 | 4.7702636 | 2.154093 |
| 142 | 6.310381 | 9.3612463 | | | 1.5375972 | 5.9892748 | 5.5342226 | 1.8934333 |
| 143 | 5.3285004 | 5.1448633 | | | 1.7437001 | 4.3459295 | 5.3742005 | 2.4541391 |
| 144 | 3.9239628 | 5.0056427 | | | 0.6871271 | 1.8012949 | 2.0943846 | 1 |
| 145 | 5.2027512 | 1 | | | 0.7637731 | 5.0295379 | 1 | 2.1229465 |
| 146 | 4.3911199 | 1 | | | 1.4590598 | 2.4261055 | 1 | 1.5105303 |
| 147 | 3.8573401 | 2.622022 | | | 1 | 1.7973824 | 2.5613019 | 1 |

Table 4

| SEQ ID NO | Patient ID | | | | | | | |
|--------------|------------|-----------|-----|-----|-----------|-----------|-----------|-----------|
| | 295 | 296 | 300 | 322 | 339 | 341 | 356 | 360 |
| 148 | 3.8354005 | 3.9722845 | | | 1.2462259 | 4.0927064 | 4.0083098 | 1.5337475 |
| 149 | 0.6591908 | 0.5411427 | | | 0.9153747 | 0.2900558 | 0.2624926 | 0.5264001 |
| 150 | 2.2450557 | 1 | | | 0.7135679 | 0.2774259 | 1 | 0.4448591 |
| 151 | 4.8557322 | 1000 | | | 1.3824641 | 3.0095668 | 1 | 1 |
| 152 | 3.3405153 | 2.5164393 | | | 1.5119714 | 2.8083186 | 3.0413257 | 1 |
| 153 | 3.151265 | 1000 | | | 1.351013 | 1.3629816 | 1 | 1 |
| 154 | 4.6011843 | 3.7098301 | | | 1.4506889 | 3.329804 | 5.0005604 | 2.3509648 |
| 155 | 5.5757406 | 1 | | | 1 | 1 | 1 | 1 |
| 156 | 4.8100344 | 1000 | | | 1 | 2.1193768 | 1 | 1 |
| 157 | 3.4570551 | 4.1162467 | | | 1 | 2.3900828 | 1 | 1.2901155 |
| 158 | 9.5190259 | 4.6931819 | | | 3.1995102 | 2.5919282 | 1 | 3.5441136 |
| 159 | 1 | 0.5722954 | | | 0.826937 | 0.4494194 | 0.3139808 | 0.5087208 |
| 160 | 0.7106604 | 0.5273903 | | | 0.8522811 | 0.3250695 | 0.2956088 | 0.4827702 |
| 161 | 0.7317129 | 0.612844 | | | 1 | 0.3757059 | 0.2886684 | 0.523989 |
| 162 | 1 | 1.1426251 | | | 0.3942467 | 0.5100773 | 1 | 1 |
| 163 | 2.9000272 | 1.9073994 | | | 2.0408868 | 1 | 2.544751 | 1 |
| 164 | 5.5080977 | 5.9941611 | | | 1 | 2.0128873 | 3.2733485 | 2.6158735 |
| 165 | 1 | 0.4285766 | | | 0.7526253 | 0.1952147 | 1 | 1 |
| 166 | 10.08009 | 1 | | | 1.4584762 | 2.5004848 | 1 | 1 |
| 167 | 0.6085363 | 0.1327895 | | | 1 | 0.3832839 | 1.8222595 | 0.3847456 |
| 168 | 0.79222 | 11.706822 | | | 0.2884535 | 5.7408909 | 1 | 1 |
| 169 | 4.2569764 | 6.1684476 | | | 1.3000431 | 2.28174 | 1 | 1 |
| 170 | 3.0466459 | 2.7563884 | | | 1 | 1.387205 | 2.5298599 | 1 |
| 171 | 5.3944134 | 1 | | | 1.4186541 | 3.6460944 | 1 | 1.7134185 |
| 172 | 6.8595412 | 2.2370061 | | | 1.4976443 | 1 | 2.1901028 | 1.3871221 |
| 173 | 4.9682134 | 4.1760778 | | | 1.8530247 | 2.4305603 | 3.9306708 | 1 |
| 174 | 3.8010357 | 5.2413625 | | | 1.5259363 | 2.4453593 | 5.6441688 | 1.5070696 |
| 175 | 4.7467717 | 3.6942393 | | | 1.6552625 | 2.6415075 | 1 | 1.5889795 |
| 176 | 1 | 1000 | | | 1 | 1 | 1 | 1 |
| 177 | 0.7966888 | 1.2628431 | | | 0.2659769 | 0.2988487 | 0.6179804 | 0.5239561 |
| 178 | 1 | 1000 | | | 1 | 2.8502444 | 1 | 1 |
| 179 | 8.8851291 | 8.6493015 | | | 1.9762941 | 8.9574375 | 3.6303813 | 1 |
| 180 | 2.7745607 | 2.4873467 | | | 1.5692396 | 2.6125136 | 2.3462988 | 1 |
| 181 | 1 | 1000 | | | 1 | 1.5428757 | 1 | 1 |
| 182 | 3.8093857 | 3.4165029 | | | 1 | 1.935886 | 2.6445783 | 1 |
| 183 | 5.363403 | 6.2023544 | | | 1 | 1.9274775 | 1 | 1 |
| 184 | 2.8216668 | 6.1847652 | | | 0.6940693 | 2.6581666 | 2.6359903 | 2.0125709 |
| 185 | 6.2314329 | 3.5289854 | | | 1.4142373 | 1.4657919 | 1 | 1 |
| 186 | 2.6129553 | 5.4063948 | | | 1 | 2.3918811 | 3.8252027 | 1 |
| 187 | 3.1237199 | 2.7266491 | | | 1 | 1.6382728 | 3.2195611 | 1.7275694 |
| 188 | 8.1283496 | 1 | | | 1.6103998 | 6.268101 | 6.0392435 | 2.033652 |
| 189 | 6.2577803 | 1 | | | 1 | 5.7289749 | 4.5425374 | 2.5491812 |
| 190 | 0.7615145 | 1 | | | 0.5606181 | 0.636809 | 1.3979986 | 1 |
| 191 | 1 | 1000 | | | 1 | 1 | 1 | 1 |
| 192 | 0.7711675 | 0.6027214 | | | 0.8479951 | 0.3635977 | 0.3198075 | 0.5598256 |
| 193 | 6.5468094 | 6.1055791 | | | 1 | 7.0088529 | 5.676389 | 2.4501699 |
| 194 | 1 | 1.448295 | | | 0.5348715 | 0.4295204 | 0.679882 | 1 |
| 195 | 0.6969489 | 0.4318612 | | | 0.8665981 | 0.3259756 | 0.2874729 | 0.4991964 |
| 196 | 5.0141385 | 1 | | | 1 | 2.6900435 | 3.002299 | 2.1426451 |

Table 4

| SEQ ID NO | Patient ID | | | | | | | |
|--------------|------------|-----------|-----|-----|-----------|-----------|-----------|-----------|
| | 295 | 296 | 300 | 322 | 339 | 341 | 356 | 360 |
| 197 | 0.6653896 | 0.5743374 | | | 1 | 0.3791448 | 0.2842352 | 0.4734144 |
| 198 | 1 | 1000 | | | 0.7857668 | 2.9149042 | 1 | 1.8146376 |
| 199 | 4.2261101 | 1 | | | 1 | 1 | 2.0297233 | 1 |
| 200 | 8.7466608 | 1000 | | | 1 | 1 | 1 | 1 |
| 201 | 4.0513809 | 4.567572 | | | 1.5187024 | 2.6902631 | 2.7192492 | 1.4043053 |
| 202 | 1 | 1000 | | | 1 | 1 | 1 | 1 |
| 203 | 1 | 1000 | | | 1 | 4.0355079 | 1 | 1.8978179 |
| 204 | 1 | 1000 | | | 0.4960757 | 8.3941703 | 1 | 2.4416736 |
| 205 | 3.2793041 | 1 | | | 1.1639357 | 1.339225 | 1 | 1.5632422 |
| 206 | 3.3782622 | 4.5654029 | | | 2.1324635 | 3.7039038 | 4.5807276 | 1 |
| 207 | 3.6560527 | 4.0579962 | | | 1.453828 | 2.8914015 | 3.75656 | 1 |
| 208 | 1 | 1 | | | 2.2120372 | 1.7328531 | 1 | 1000 |
| 209 | 0.4388303 | 0.3926315 | | | 0.4694539 | 0.4540664 | 1 | 0.6168543 |
| 210 | 0.880444 | 0.6305023 | | | 1 | 0.4473602 | 0.3550847 | 0.4920936 |
| 211 | 1 | 1000 | | | 1.2510654 | 10.683495 | 1 | 2.3958626 |
| 212 | 3.7663549 | 1 | | | 0.4021849 | 2.4803043 | 2.4032905 | 1 |
| 213 | 0.6489058 | 0.5531438 | | | 0.8548769 | 0.2927054 | 0.2476478 | 0.4718327 |
| 214 | 4.8196597 | 4.1486602 | | | 1.5992017 | 3.0704719 | 4.2254815 | 1.8388328 |
| 215 | 1 | 1000 | | | 1 | 3.2882145 | 1 | 2.1107119 |
| 216 | 0.6591853 | 0.4408793 | | | 1 | 0.286562 | 0.250663 | 0.5184733 |
| 217 | 3.8721106 | 2.9602943 | | | 1.1579895 | 1.509475 | 2.8954253 | 1.364352 |
| 218 | 5.5967154 | 1 | | | 1.3668492 | 1 | 2.5886403 | 1.3698662 |
| 219 | 8.6096009 | 1000 | | | 1.3454894 | 1 | 1 | 1.4318359 |
| 220 | 5.32147 | 1 | | | 1 | 1.8919695 | 3.2999633 | 1 |
| 221 | 0.5985119 | 0.4947588 | | | 1 | 0.3133388 | 0.2408675 | 0.5434523 |
| 222 | 0.6443815 | 0.5360342 | | | 0.8790136 | 0.3543517 | 0.2683402 | 0.5576369 |
| 223 | 0.5278195 | 0.4912671 | | | 1 | 0.263835 | 0.2399984 | 0.5364804 |
| 224 | 0.5350828 | 0.4404832 | | | 0.8110605 | 0.3863384 | 0.2700436 | 0.5189765 |
| 225 | 0.472685 | 0.3345917 | | | 0.8516171 | 0.4187918 | 0.3219483 | 0.6708885 |
| 226 | 8.0087936 | 1000 | | | 1 | 2.475019 | 1 | 1 |
| 227 | 4.6524321 | 4.0952711 | | | 1.6047152 | 2.5369125 | 4.2223416 | 1.8906407 |
| 228 | 1 | 1000 | | | 0.5892622 | 2.150629 | 1 | 1 |
| 229 | 1 | 1000 | | | 1 | 1.7414263 | 1 | 1 |
| 230 | 2.8559983 | 1.8423181 | | | 2.0089929 | 2.4593757 | 4.0046776 | 1.9149006 |
| 231 | 0.7628452 | 0.5944954 | | | 1 | 0.3407059 | 0.2700748 | 0.50717 |
| 232 | 1000 | 1000 | | | 3.6254193 | 1 | 1000 | 1 |
| 233 | 1 | 1000 | | | 1 | 1000 | 1 | 2.3009742 |
| 234 | 1000 | 1000 | | | 1 | 1 | 1 | 1 |
| 235 | 0.892276 | 0.5075375 | | | 1 | 0.5254117 | 0.3692873 | 0.4166192 |
| 236 | 9.1215132 | 7.546531 | | | 1.2007294 | 6.7667771 | 5.2006352 | 1.7895322 |
| 237 | 1 | 1 | | | 1 | 1 | 1 | 1.6129202 |
| 238 | 0.1866111 | 0.1527441 | | | 0.1702952 | 0.6811922 | 0.3325596 | 0.6380599 |
| 239 | 0.6254138 | 0.4805959 | | | 1 | 0.2753323 | 0.2404845 | 0.4893145 |
| 240 | 3.812535 | 1.2503552 | | | 0.3925061 | 0.523428 | 1 | 0.7104798 |
| 241 | 3.7460731 | 1.35665 | | | 0.4320163 | 0.6034358 | 1.2086562 | 0.7529617 |
| 242 | 2.6900737 | 3.7570352 | | | 1 | 3.661065 | 1.5588046 | 1 |
| 243 | 5.1710533 | 6.8089163 | | | 1.2620622 | 4.3290713 | 4.9569364 | 2.1909574 |
| 244 | 6.1362283 | 1000 | | | 1.2352693 | 3.2560974 | 1 | 1 |
| 245 | 2.4898674 | 1.5263948 | | | 1.5127663 | 1.5209037 | 4.2142888 | 1 |

Table 4

| SEQ ID | Patient ID | | | | | | | | |
|--------|------------|-----------|-----------|-----|-----|-----------|-----------|-----------|-----------|
| | NO | 295 | 296 | 300 | 322 | 339 | 341 | 356 | 360 |
| 246 | | 3.6633215 | 4.1655809 | | | 1 | 1.5127355 | 3.0260543 | 2.0956265 |
| 247 | | 6.6847288 | 11.218389 | | | 2.0494589 | 7.0085509 | 6.1427734 | 2.4476508 |
| 248 | | 1 | 1 | | | 1 | 2.9107788 | 1 | 1 |
| 249 | | 1.0845979 | 1.5698828 | | | 0.5450635 | 0.3338624 | 1 | 1 |
| 250 | | 9.8232026 | 6.5679753 | | | 1.2153784 | 5.4137965 | 4.983019 | 2.3713159 |
| 251 | | 3.8829002 | 2.9191789 | | | 1 | 1.638513 | 1 | 2.1330006 |
| 252 | | 38.200556 | 1000 | | | 1 | 1 | 1 | 1 |
| 253 | | 1 | 1 | | | 2.1196556 | 2.8309426 | 1 | 1 |
| 254 | | 0.7729639 | 0.5601344 | | | 0.9097807 | 0.300956 | 0.2683529 | 0.4958862 |
| 255 | | 1.8485243 | 1 | | | 0.6655761 | 0.3844233 | 1 | 0.3991144 |
| 256 | | 1000 | 1000 | | | 1 | 1 | 1 | 1 |
| 257 | | 0.6261955 | 0.5797329 | | | 1 | 0.2714747 | 0.2254852 | 0.4835827 |
| 258 | | 3.5965269 | 4.4741938 | | | 1 | 1.9473215 | 1 | 1.8279074 |
| 259 | | 5.0230152 | 1 | | | 1.8946981 | 2.3583775 | 2.2868084 | 2.145818 |
| 260 | | 0.6332759 | 0.1729094 | | | 1 | 0.1337056 | 1 | 1 |
| 261 | | 4.2247185 | 4.6111073 | | | 1.0962542 | 3.6681899 | 3.8101789 | 1.6998731 |
| 262 | | 1000 | 1000 | | | 1 | 1000 | 1 | 1 |
| 263 | | 1000 | 1 | | | 1.8370577 | 1000 | 1 | 1000 |
| 264 | | 4.885495 | 1000 | | | 2.4666953 | 3.861922 | 1 | 1 |
| 265 | | 1 | 0.6467145 | | | 1 | 0.3601794 | 0.2875539 | 1 |
| 266 | | 0.0192671 | 1 | | | 1 | 0.0129869 | 1 | 0.152751 |
| 267 | | 7.5882157 | 6.5261622 | | | 1.2165254 | 5.9370666 | 4.410074 | 1.8961623 |
| 268 | | 4.5006238 | 8.2831138 | | | 1.7132349 | 2.9901346 | 9.8087442 | 2.44072 |
| 269 | | 7.8270948 | 10.743486 | | | 2.5985871 | 5.9014145 | 1 | 1.9003428 |
| 270 | | 3.3947627 | 4.9953347 | | | 1.823465 | 3.1575291 | 3.4810483 | 1.539486 |
| 271 | | 0.6575885 | 0.6054465 | | | 1 | 0.3058981 | 0.2474044 | 0.5358507 |
| 272 | | 0.5381046 | 0.3629212 | | | 1 | 0.440297 | 0.2956945 | 0.6985666 |
| 273 | | 3.3121885 | 4.1457498 | | | 1.9816668 | 3.0549453 | 1 | 2.072088 |
| 274 | | 1.450313 | 0.5415678 | | | 0.3827468 | 0.237168 | 1 | 0.2579579 |
| 275 | | 0.747925 | 0.5742356 | | | 1 | 0.3924406 | 0.2760965 | 0.5803184 |
| 276 | | 3.8245333 | 1000 | | | 1 | 1 | 1 | 1.7895322 |
| 277 | | 1000 | 1000 | | | 1 | 1000 | 1000 | 1 |
| 278 | | 9.4791111 | 1000 | | | 1 | 1.7687934 | 1 | 1.3368256 |
| 279 | | 3.6950526 | 4.9904115 | | | 1.4299025 | 2.5189835 | 3.2773943 | 1.5584908 |
| 280 | | 2.6894749 | 2.4701172 | | | 0.6922483 | 1 | 1 | 0.4528724 |
| 281 | | 1 | 0.5438241 | | | 0.8400266 | 0.3272523 | 0.2987887 | 0.508183 |
| 282 | | 2.416364 | 1.8595767 | | | 1 | 2.2998955 | 4.0677498 | 1.5966678 |
| 283 | | 4.5008012 | 3.5595785 | | | 1.8705412 | 2.5434746 | 1 | 1 |
| 284 | | 2.2152707 | 3.404113 | | | 0.6775086 | 1.5784454 | 2.0111472 | 1.2433043 |
| 285 | | 0.6313741 | 0.8171605 | | | 0.2141418 | 0.5151156 | 0.6268432 | 0.4265583 |
| 286 | | 5.0973836 | 4.0816823 | | | 1 | 1.95225 | 1 | 1 |
| 287 | | 1 | 1 | | | 0.4861353 | 1 | 1 | 2.3896784 |
| 288 | | 5.7244717 | 1 | | | 1 | 4.1969033 | 1 | 2.2668571 |
| 289 | | 5.1817653 | 4.7345118 | | | 1.4300031 | 4.2208315 | 3.2876887 | 2.282537 |
| 290 | | 4.4566448 | 3.8941702 | | | 1.3915796 | 3.7458639 | 3.8101789 | 2.2658811 |
| 291 | | 4.6157996 | 3.0824707 | | | 1.5039024 | 4.7531759 | 2.4317961 | 1.8112846 |
| 292 | | 3.935207 | 4.9669143 | | | 1.2852532 | 1.4885601 | 2.5007518 | 1 |
| 293 | | 0.4873059 | 0.4470706 | | | 1.7912492 | 0.5224396 | 0.3553893 | 0.4146032 |
| 294 | | 6.3473184 | 1000 | | | 0.7861692 | 1 | 1 | 1.8707955 |

Table 4

| SEQ ID | Patient ID | | | | | | | |
|--------|------------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|
| | 295 | 296 | 300 | 322 | 339 | 341 | 356 | 360 |
| 295 | 7.831658 | 4.7919993 | | | | 5.8285591 | 4.5425374 | 1 |
| 296 | 0.7602005 | 0.6397057 | | | | 0.3474053 | 0.269941 | 0.5382623 |
| 297 | 0.6539568 | 0.5489327 | 2.1599741 | 0.3134934 | | 0.3227769 | 0.2472536 | 0.4852561 |
| 298 | 4.5869128 | 5.0965501 | 1.2571986 | | 1.6213061 | 1.7614832 | 3.8252027 | 1.1487555 |
| 299 | 0.6074773 | 0.4963139 | 2.4562901 | 0.3463832 | | 0.372521 | 0.2048498 | 0.4735242 |
| 300 | 3.5888644 | 3.2403706 | 0.5290359 | | | 1.6061283 | 3.2397538 | 1 |
| 301 | 0.4563842 | 0.4018712 | 2.2761074 | | | 0.3316659 | 1.8162682 | 1 |
| 302 | 5.4477126 | 1000 | | 2.034484 | 1.3045203 | 1.973158 | | 1.9619436 |
| 303 | 1.9993014 | 0.6826051 | | | 0.2377151 | 0.6996498 | | 1 |
| 304 | 1.9000272 | 0.3801544 | 0.1773284 | 0.417288 | 1.3890039 | 0.2644665 | | 1 |
| 305 | 2.807179 | 2.5412081 | 0.8746437 | 2.4284006 | | 2.8840913 | | 1 |
| 306 | 0.2543926 | 0.2328132 | 0.0858767 | | 0.3861072 | 0.1919062 | 0.2290601 | 0.4213525 |
| 307 | 4.6222978 | 5.0008284 | 1.1562178 | 1.6905853 | 2.1142528 | 2.7339942 | | 1.6027336 |
| 308 | | 1.9611409 | | | 0.5733756 | 1.2460725 | | 0.4394626 |
| 309 | 0.231261 | 0.4154673 | 0.4870855 | 0.677961 | 0.2093728 | 0.1278231 | 0.264967 | 0.564325 |
| 310 | 14.968751 | 1.6278063 | 0.0767331 | | 1.7067153 | 0.2219091 | | 0.6627989 |
| 311 | | | | 0.6476018 | 1.3993468 | 0.5401077 | | 1 |
| 312 | 5.4832307 | 9.1345699 | 0.5894057 | | 2.2191001 | 8.3971562 | 11.459077 | 2.1384749 |
| 313 | 3.3647503 | 1000 | 1.8061615 | | 2.1822159 | 1.3980503 | | 1 |
| 314 | 2.1333618 | | 0.4086697 | | 0.2994705 | | | 1 |
| 315 | 0.0737529 | 0.0765991 | 0.0195843 | 0.1411293 | 0.1735651 | 0.5815462 | 0.2818665 | 0.6190465 |
| 316 | | 1.7129621 | 0.6809456 | 2.3144454 | 1.4912857 | 2.8478214 | 5.4620239 | 1 |
| 317 | 3.720014 | 5.5693596 | | | 1.7388205 | 2.2496915 | 9.8354247 | 1.4720788 |
| 318 | 1000 | | | 1000 | 12.954814 | 7.5972976 | | 1 |
| 319 | 3.4094722 | 3.7097139 | 0.7227632 | | 1.9273667 | 5.0580582 | 4.9917743 | 1.8458939 |
| 320 | | 0.1922318 | 0.2310111 | 0.039974 | 0.4778851 | 0.0409992 | | 0.1321869 |
| 321 | | 0.7938123 | | 0.3784577 | 0.8479045 | | 0.3845209 | 0.598668 |
| 322 | 3.1616609 | | 0.4770994 | 2.3216937 | | 2.2670851 | 5.3316967 | 1 |
| 323 | | 0.5913017 | 1.9132702 | 0.3946628 | | 0.4188261 | 0.2688626 | 0.4591973 |
| 324 | 1.3738266 | 2.512944 | 0.1856647 | 1.1379293 | 0.3620308 | 0.8401783 | | 1 |
| 325 | 0.6813134 | | | | | 0.5744831 | | 1 |
| 326 | 0.5936604 | 0.6257571 | 2.2109564 | 0.379839 | | 0.4006157 | 0.2398146 | 0.4880701 |
| 327 | | 1000 | 2.5837144 | 2.1718463 | 1.5802264 | 2.0924147 | | 1 |
| 328 | 0.646749 | 0.3110764 | 0.5098051 | 2.0853747 | 0.9741822 | 0.7932828 | | 1.4497946 |
| 329 | 0.6551877 | 0.5699046 | 1.2042703 | 0.4693271 | 0.7452404 | 0.2971258 | 0.3008703 | 0.4593365 |
| 330 | 2.4955395 | 2.2695976 | 1.2949619 | | 1.8550772 | 6.9208759 | | 1.1762015 |
| 331 | | 1000 | | 2.2020177 | | 3.7718857 | | 1 |
| 332 | | 2.4054065 | 1.4832813 | | | 1.6145093 | | 1 |
| 333 | 2.623329 | | | | 2.5364594 | 1.8347917 | 2.2763382 | 1 |
| 334 | 0.6716992 | 0.5597784 | 2.0731041 | 0.3669974 | | 0.3278564 | 0.2320685 | 0.4430908 |
| 335 | 0.7428795 | 0.3119375 | 1.3806091 | 0.8439455 | | 0.4061482 | 0.357045 | 0.4002151 |
| 336 | | | | 0.7752426 | 2.9589779 | 1.460081 | | 1.6688064 |
| 337 | 0.685688 | 0.5692324 | 2.0393018 | 0.3353242 | | 0.3521896 | 0.2457109 | 0.4046776 |
| 338 | 16.089599 | 1.8509365 | 0.1259138 | | 1.5980749 | 0.24222 | | 0.625162 |
| 339 | 3.5600386 | 4.7339268 | 0.5715451 | 1.4442306 | 1.0533132 | 1.6510537 | 3.6480288 | 1.4077852 |
| 340 | | 1000 | | 1000 | | 6.7593364 | | 1 |
| 341 | | 1000 | 2.9283991 | | | 1.6624893 | | 2.5168408 |
| 342 | | | | | | 2.2857829 | | 2.8927104 |
| 343 | 6.8203139 | 7.6126805 | 0.5201913 | 2.2363556 | | 1.8776716 | | 1 |

Table 4

| SEQ ID NO | Patient ID | | | | | | | |
|--------------|------------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|
| | 295 | 296 | 300 | 322 | 339 | 341 | 356 | 360 |
| 344 | 1.3491924 | 0.7033881 | 0.6869861 | 0.2663488 | 1 | 0.3015532 | 0.545229 | 0.4628021 |
| 345 | 1.5783354 | 1 | 1 | 1 | 1 | 0.4431868 | 1 | 1 |
| 346 | 0.7009464 | 0.5937542 | 1.7821578 | 0.2256568 | 1 | 0.2185869 | 0.2369488 | 0.4538859 |
| 347 | 0.6303262 | 0.5317431 | 2.1574396 | 0.2942559 | 1 | 0.310806 | 0.2052166 | 0.4503675 |
| 348 | 5.4557799 | 9.2065873 | 1.8130467 | 1 | 2.6035472 | 4.3619228 | 5.7904291 | 1.6130503 |
| 349 | 4.2169174 | 1 | 1 | 2.9922226 | 1.4098204 | 3.7153188 | 6.6468011 | 1 |
| 350 | 1 | 0.5276192 | 0.3676238 | 0.5906542 | 0.542347 | 0.4841448 | 1 | 0.6026335 |
| 351 | 4.7188385 | 1 | 1 | 1.5761212 | 1 | 2.416482 | 6.2844774 | 1 |
| 352 | 4.7130889 | 1000 | 1 | 1 | 1 | 2.4760829 | 4.6948132 | 1 |
| 353 | 5.454244 | 5.9677391 | 0.3416991 | 1 | 0.4682365 | 2.6545973 | 5.3771066 | 1.8636472 |
| 354 | 4.4647841 | 2.2323008 | 0.2992089 | 0.3527762 | 1 | 0.3140458 | 1 | 1 |
| 355 | 1 | 1 | 0.001 | 1 | 1 | 0.2747695 | 1 | 1 |
| 356 | 1000 | 1000 | 1 | 1000 | 1 | 3.236775 | 1000 | 1 |
| 357 | 1 | 1 | 0.1576659 | 0.2985308 | 0.2738447 | 0.3392645 | 0.3719533 | 0.5917624 |
| 358 | 2.8173088 | 1.7578563 | 1.9257272 | 1.4219835 | 1 | 0.6606068 | 2.3736025 | 1 |
| 359 | 0.7143974 | 0.6100463 | 1.8509612 | 0.3313535 | 1 | 0.3254402 | 0.2544621 | 0.4735467 |
| 360 | 1 | 0.9368081 | 0.2132153 | 0.3197974 | 0.5151517 | 0.3409668 | 1.3471451 | 0.4097641 |
| 361 | 1.7381611 | 1 | 3.1378318 | 1 | 0.5289153 | 0.859638 | 1 | 1 |
| 362 | 1000 | 1 | 1 | 1 | 1 | 2.3196984 | 1 | 1 |
| 363 | 4.1906032 | 3.0187955 | 1 | 1.8067097 | 1.4297214 | 1.909823 | 3.6194793 | 1 |
| 364 | 3.8615927 | 1 | 0.8469443 | 1.7125152 | 1 | 1.8242416 | 3.2964079 | 1.3318929 |
| 365 | 1000 | 1 | 1000 | 1000 | 1 | 2.9125429 | 1 | 1 |
| 366 | 1 | 6.4611681 | 2.0536492 | 1 | 1.7260931 | 3.2606895 | 3.609625 | 1 |
| 367 | 2.3971856 | 1.7753692 | 0.2972753 | 1.502034 | 1 | 0.3713884 | 1 | 1 |
| 368 | 2.748679 | 1 | 1.9067248 | 1.991435 | 1 | 1.6658596 | 3.6597771 | 1.6310485 |
| 369 | 3.9211351 | 1 | 4.0417708 | 0.4710614 | 0.4905219 | 1.7802496 | 0.4082027 | 2.7119405 |
| 370 | 0.4960107 | 0.4753202 | 0.8453225 | 0.3169347 | 1 | 0.3930789 | 0.2957495 | 0.7352924 |
| 371 | 4.3227064 | 4.3699083 | 0.3751351 | 2.6821081 | 1.9146695 | 0.6141575 | 1 | 1 |
| 372 | 1.7181566 | 1 | 5.1037694 | 1 | 1.6399092 | 4.7820669 | 3.2060662 | 1 |
| 373 | 2.2182924 | 3.0544028 | 0.2260245 | 1 | 0.5538066 | 1.8565165 | 2.7548454 | 1 |
| 374 | 4.5390194 | 5.4176365 | 4.5263361 | 1.7792251 | 1.3782888 | 2.3087502 | 1 | 1 |
| 375 | 6.3934708 | 3.2719266 | 0.4520554 | 1 | 1 | 4.1020484 | 3.1801757 | 4.1458943 |
| 376 | 3.8763355 | 7.5083041 | 0.3236794 | 1 | 1.4012483 | 5.6609586 | 1 | 1.4785658 |
| 377 | 0.1052401 | 0.4227305 | 0.7712852 | 0.6976914 | 0.5715042 | 0.6699488 | 0.3956909 | 0.4012188 |
| 378 | 1 | 0.589772 | 0.3011769 | 1 | 1 | 0.5177583 | 1 | 0.6990061 |
| 379 | 0.6685943 | 0.5360124 | 2.0910417 | 0.3838389 | 1 | 0.5311844 | 0.2526068 | 0.4888265 |
| 380 | 1 | 1.1001399 | 0.4932061 | 0.3955732 | 1 | 0.7461608 | 1 | 0.001 |
| 381 | 0.5801762 | 0.5843982 | 1.9644801 | 0.3538694 | 1 | 0.3348165 | 0.213261 | 0.4359675 |
| 382 | 1 | 1 | 1 | 1.5346589 | 1 | 2.262548 | 5.5142739 | 1 |
| 383 | 0.768057 | 1 | 0.5098094 | 0.4390073 | 1 | 0.5243272 | 1 | 1 |
| 384 | 3.5455065 | 1 | 0.539104 | 1 | 1 | 3.0670536 | 3.5550999 | 1.6180622 |
| 385 | 1 | 1 | 1.7678315 | 2.2268475 | 1 | 6.7411603 | 14.510929 | 1 |
| 386 | 0.6346731 | 0.575391 | 1.8585996 | 0.3088776 | 1 | 0.2735546 | 0.2428307 | 0.4265837 |
| 387 | 0.5229792 | 0.4482914 | 2.3043091 | 0.1965932 | 1 | 0.2774671 | 0.17517 | 0.4288727 |
| 388 | 0.4764553 | 0.3962503 | 1 | 0.4760032 | 1 | 0.4443468 | 1 | 1 |
| 389 | 2.5368792 | 3.759455 | 0.8050702 | 1.3824919 | 0.4400551 | 1.5613607 | 1 | 1 |
| 390 | 1 | 0.7901353 | 0.1250399 | 0.4418857 | 0.3326724 | 0.2334477 | 0.8026164 | 0.5023212 |
| 391 | 1.3377763 | 0.7818548 | 0.4142212 | 0.4039869 | 0.6675079 | 0.1668042 | 0.5955241 | 0.6682341 |
| 392 | 5.4987774 | 9.429772 | 0.8552826 | 1 | 2.3077994 | 6.4204907 | 1 | 1.6618997 |

Table 4

| SEQ ID | Patient ID | | | | | | | |
|--------|------------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|
| | 295 | 296 | 300 | 322 | 339 | 341 | 356 | 360 |
| 393 | 1 | 1 | 0.3515633 | 1 | 0.4210295 | 0.4671974 | 1 | 1 |
| 394 | 0.5998204 | 0.5309147 | 2.1145942 | 0.3118742 | 1 | 0.4180848 | 0.2169792 | 0.4689426 |
| 395 | 3.2699339 | 1.9599382 | 1 | 1.7462132 | 1.7799103 | 1.5305958 | 2.5271274 | 1 |
| 396 | 1 | 1000 | 2.3088433 | 0.9538532 | 1 | 1.2721972 | 1 | 1.560534 |
| 397 | 2.6427847 | 1 | 0.6694212 | 1.8651012 | 1.4213405 | 3.6752805 | 4.5860092 | 1 |
| 398 | 2.6224419 | 3.1938487 | 0.4864372 | 1 | 1 | 4.6090575 | 4.5796727 | 1 |
| 399 | 1 | 0.4448179 | 0.4609381 | 0.1694497 | 0.2160232 | 0.4730044 | 0.395451 | 1 |
| 400 | 0.2844771 | 1 | 1 | 0.3534826 | 1 | 0.2304824 | 1 | 1 |
| 401 | 0.4838239 | 1.5633391 | 0.1375142 | 0.3416628 | 0.2224423 | 0.2161433 | 0.6918741 | 0.4857771 |
| 402 | 1 | 1 | 1 | 1 | 1 | 0.001 | 1 | 1 |
| 403 | 1.3286556 | 1 | 1 | 0.1685565 | 0.1549117 | 1 | 0.5184839 | 1 |
| 404 | 0.5017604 | 0.5183141 | 0.7946711 | 0.6311545 | 0.3084451 | 0.2635467 | 1 | 0.3953256 |
| 405 | 0.7417262 | 0.1861204 | 0.0556108 | 0.5072076 | 0.1403834 | 0.1966836 | 0.7501076 | 0.3314324 |
| 406 | 3.5309965 | 2.69994 | 1.9597743 | 1 | 1 | 4.2990752 | 3.0134448 | 1.5678506 |
| 407 | 0.6231849 | 1.38337 | 0.5188339 | 0.1984333 | 0.258431 | 0.353885 | 0.1163598 | 0.2801701 |
| 408 | 3.9215232 | 1 | 1 | 1.6185259 | 1.8742638 | 2.6807563 | 4.0462317 | 1.8966299 |
| 409 | 0.0889116 | 1 | 0.2821558 | 1 | 1 | 0.2409227 | 1 | 0.001 |
| 410 | 5.8600236 | 6.4307094 | 1.5724986 | 3.5134345 | 2.5221625 | 4.5857059 | 7.4428252 | 1.8933975 |
| 411 | 0.5126331 | 0.8255427 | 0.3741781 | 0.5922441 | 0.35203 | 0.149541 | 0.6239914 | 0.7178712 |
| 412 | 0.5382265 | 0.5160977 | 2.7689129 | 0.2315168 | 1 | 0.285601 | 0.1794455 | 0.5291413 |
| 413 | 6.3647281 | 1 | 1 | 1 | 0.7860485 | 1.8037522 | 1 | 1 |
| 414 | 0.7409666 | 1.1390789 | 4.5949046 | 0.8161989 | 0.7785227 | 1 | 1 | 1 |
| 415 | 0.1759047 | 1 | 8.9727434 | 0.9247122 | 1 | 1 | 1 | 1 |
| 416 | 5.7196868 | 1 | 1 | 1.9129319 | 0.8129923 | 4.1400617 | 3.1434804 | 1.9916446 |
| 417 | 3.971967 | 1 | 1 | 1.8001626 | 2.3562439 | 1.5727551 | 6.2021609 | 1 |
| 418 | 1 | 1 | 1 | 1.8472974 | 1 | 2.3448759 | 1 | 1 |
| 419 | 2.8862103 | 3.3211373 | 1 | 2.0622594 | 0.5193069 | 1.5552516 | 4.1358488 | 1 |
| 420 | 0.8496332 | 1.4928876 | 0.5249515 | 4.0760238 | 1 | 0.1755216 | 1 | 0.617521 |
| 421 | 1.3899999 | 1 | 1 | 0.4398929 | 0.1945125 | 1 | 0.4829342 | 1 |
| 422 | 2.6042116 | 1 | 0.2655965 | 1 | 1 | 0.4967953 | 1 | 1 |
| 423 | 2.7067737 | 1 | 0.3355526 | 1 | 1.8949597 | 3.7014876 | 4.4725579 | 1.9279344 |
| 424 | 0.6178622 | 0.5519666 | 0.3606333 | 1 | 0.2406328 | 0.3697136 | 1 | 0.5706473 |
| 425 | 4.0418332 | 1 | 1 | 1.8668353 | 1.4931671 | 2.539006 | 1 | 1.7162418 |
| 426 | 1 | 0.7473485 | 1 | 1 | 1 | 0.5819306 | 1 | 1 |
| 427 | 5.5917531 | 6.3739668 | 1.6250088 | 1 | 2.0992818 | 6.3493581 | 5.1374913 | 3.502278 |
| 428 | 0.6475141 | 0.5675102 | 1.8661061 | 0.2578859 | 1 | 0.3919944 | 0.2327557 | 0.4226777 |
| 429 | 3.3737379 | 3.6205759 | 1 | 1 | 1.7336993 | 4.0515218 | 2.6621014 | 1 |
| 430 | 5.4134088 | 1000 | 1 | 2.9811157 | 1 | 1 | 6.1704092 | 1 |
| 431 | 1 | 1 | 1.1426837 | 1.2408713 | 0.1698224 | 1.9424892 | 1 | 1 |
| 432 | 0.1885462 | 0.0947952 | 0.0738787 | 0.2836634 | 0.0644518 | 0.1008266 | 0.3115875 | 1 |
| 433 | 2.9921712 | 2.0061368 | 2.6517867 | 1 | 1.415676 | 3.8259885 | 2.6215698 | 1.513709 |
| 434 | 0.6976197 | 0.5995822 | 2.0780801 | 0.3111754 | 1 | 0.2843037 | 0.2381405 | 0.4735108 |
| 435 | 1000 | 1000 | 1 | 1 | 1000 | 1 | 1 | 1 |
| 436 | 0.2538271 | 0.3158616 | 1 | 1 | 1 | 0.2005756 | 1 | 1 |
| 437 | 0.734352 | 0.5715796 | 1.135402 | 0.3719147 | 1 | 0.5397439 | 0.3641816 | 0.4415703 |
| 438 | 1 | 1000 | 1 | 1.966726 | 1.1785344 | 4.4666551 | 1 | 1 |
| 439 | 7.8534811 | 6.1257735 | 0.4808827 | 1 | 1 | 6.8003219 | 7.8296177 | 1.3798669 |
| 440 | 3.1011261 | 3.1163521 | 1 | 1.2050002 | 1.6161548 | 2.5604495 | 3.2876887 | 1.4972975 |
| 441 | 4.4080251 | 3.8816641 | 1.822123 | 1 | 1 | 1.4470461 | 4.0298336 | 1.4454352 |

Table 4

| SEQ ID NO | Patient ID | | | | | | | |
|--------------|------------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|
| | 295 | 296 | 300 | 322 | 339 | 341 | 356 | 360 |
| 442 | 1 | 1 | 1 | 0.4502972 | 1 | 1 | 1 | 1 |
| 443 | 0.7409666 | 0.6685476 | 1.5980576 | 0.3254608 | 1 | 0.35232 | 0.2676036 | 0.4655018 |
| 444 | 0.6893252 | 0.5847507 | 2.1082701 | 0.3888945 | 0.8184857 | 0.4414982 | 0.2198832 | 0.492348 |
| 445 | 3.8567468 | 5.5896921 | 0.3409838 | 1 | 1 | 2.1656339 | 2.2780331 | 1.1885613 |
| 446 | 0.3708936 | 0.7293124 | 0.384371 | 0.7596241 | 0.4921518 | 0.4076308 | 1 | 0.6494235 |
| 447 | 1 | 1000 | 1.3795625 | 2.2853571 | 1 | 2.77951 | 2.1886567 | 1 |
| 448 | 4.0781885 | 1 | 0.8324367 | 2.0335396 | 1.4182618 | 2.1498945 | 3.8694871 | 1 |
| 449 | 2.9154741 | 4.9138668 | 0.6284199 | 2.0683673 | 1.3641629 | 5.1464333 | 5.4582761 | 1.2094072 |
| 450 | 0.7720879 | 0.6435644 | 1 | 1.3090314 | 0.2677879 | 0.436206 | 1 | 0.001 |
| 451 | 3.8571571 | 2.9022182 | 2.0954885 | 1 | 1.429973 | 2.0016645 | 2.5212004 | 1 |
| 452 | 1000 | 1000 | 1 | 1 | 1.6353314 | 1 | 1 | 2.3304168 |
| 453 | 0.8004036 | 1.6473612 | 0.5001212 | 0.584096 | 0.4407695 | 0.3753696 | 1 | 0.6941147 |
| 454 | 1000 | 1 | 1 | 3.5093404 | 1 | 2.1746876 | 1 | 2.2692237 |
| 455 | 0.6979413 | 0.653033 | 2.0612443 | 0.3493363 | 1 | 0.3878828 | 0.2398421 | 0.4851337 |
| 456 | 1 | 0.4015696 | 1 | 1 | 1 | 0.58156 | 1 | 0.3365394 |
| 457 | 0.6860151 | 0.6017041 | 0.7467487 | 0.2845882 | 1 | 0.4762442 | 1 | 1 |
| 458 | 1 | 1 | 1 | 2.3922332 | 1 | 7.335563 | 1 | 1.776875 |
| 459 | 3.3996307 | 1 | 1 | 1.4908807 | 1 | 1.5867921 | 2.7790985 | 2.0908936 |
| 460 | 1000 | 1000 | 1000 | 1000 | 1000 | 1 | 1000 | 1000 |
| 461 | 0.7353722 | 0.6643147 | 1.9520097 | 0.3286618 | 0.8135255 | 0.3464786 | 0.2939702 | 0.4794482 |
| 462 | 1 | 1 | 0.7690138 | 2.2183387 | 1 | 6.2387639 | 2.1863708 | 1.5998613 |
| 463 | 6.3576256 | 6.1600727 | 0.6230828 | 1.6927827 | 2.1306625 | 7.3760817 | 3.3497101 | 2.4203368 |
| 464 | 4.6258684 | 5.708246 | 1.3666865 | 1 | 2.1512778 | 5.194077 | 1 | 1.7324785 |
| 465 | 4.6236839 | 1 | 1 | 1 | 1.6808279 | 1.6782492 | 3.9244655 | 1.4252638 |
| 466 | 1.2217577 | 0.4903552 | 1 | 1 | 0.5642703 | 0.3580927 | 2.6109005 | 1.7916807 |
| 467 | 3.4967703 | 4.0637006 | 1.1261253 | 1 | 1.8987024 | 4.5659716 | 3.8072612 | 1.4492692 |
| 468 | 3.8281206 | 2.5255228 | 2.8218344 | 1.2306667 | 1.6742781 | 4.2288007 | 3.1893559 | 1.631288 |
| 469 | 1 | 1 | 1 | 1 | 1 | 2.1670548 | 3.0417909 | 2.0597943 |
| 470 | 0.7157004 | 0.6283368 | 1.8084324 | 0.4747463 | 0.76985 | 0.3940674 | 0.2511934 | 0.4724145 |
| 471 | 0.1897604 | 1 | 0.001 | 0.3367984 | 0.2671541 | 0.1883026 | 0.5195404 | 0.2145376 |
| 472 | 0.5440704 | 0.4919502 | 2.4258211 | 0.265877 | 0.816081 | 0.2911129 | 0.1843621 | 0.4412936 |
| 473 | 5.7982524 | 7.8055845 | 1 | 1.4797099 | 1 | 7.6915621 | 5.9631871 | 2.2047261 |
| 474 | 1.4700569 | 1.6113834 | 0.193551 | 1 | 0.2751124 | 0.7780377 | 1 | 0.7447509 |
| 475 | 1000 | 1000 | 1 | 2.6402254 | 1 | 3.3123898 | 1000 | 1 |
| 476 | 8.8279043 | 9.3358852 | 0.4169286 | 1 | 1.5242058 | 6.1127461 | 8.0045196 | 2.5139299 |
| 477 | 7.1534495 | 6.6712544 | 1 | 1.7636613 | 1 | 3.5671162 | 4.2286262 | 1 |
| 478 | 1 | 1 | 1.268898 | 0.6651311 | 0.2700819 | 1.70725 | 1 | 0.6047548 |
| 479 | 5.9062148 | 1 | 1 | 1.7850913 | 1.7801014 | 2.1116616 | 5.8047953 | 1.4850882 |
| 480 | 1 | 1000 | 28.390834 | 19.129319 | 1 | 1 | 1 | 1 |
| 481 | 1 | 1 | 0.3647033 | 1 | 1 | 0.3368415 | 1 | 1 |
| 482 | 1 | 1000 | 1 | 2.1204292 | 1 | 4.3081084 | 3.9706956 | 2.2875503 |
| 483 | 0.6575219 | 0.6353711 | 2.1454237 | 0.3366878 | 0.8065431 | 0.2822788 | 0.2216675 | 0.4589696 |
| 484 | 1 | 0.741179 | 0.2636826 | 0.8114434 | 0.1772374 | 0.2528044 | 1 | 0.3171156 |
| 485 | 4.5385426 | 4.987701 | 1 | 2.4107841 | 1 | 2.9893658 | 4.4983553 | 1 |
| 486 | 0.0782661 | 0.0964338 | 0.0618295 | 0.1899255 | 0.0532236 | 0.0183958 | 0.1714912 | 0.2235455 |
| 487 | 5.8543849 | 3.8472777 | 0.6280968 | 1.8617863 | 1.5007432 | 2.3536482 | 1.9631044 | 1 |
| 488 | 0.6849118 | 0.5990045 | 2.0141529 | 0.4769927 | 0.8267056 | 0.3699195 | 0.2192119 | 0.4702505 |
| 489 | 1 | 1 | 1 | 2.5551065 | 1.630009 | 4.8487584 | 5.3331265 | 1.9318829 |
| 490 | 4.1000116 | 1 | 1 | 1.9578561 | 2.0582725 | 3.0299188 | 5.3424389 | 1.8029235 |

Table 4

| SEQ ID NO | Patient ID | | | | | | | |
|--------------|------------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|
| | 295 | 296 | 300 | 322 | 339 | 341 | 356 | 360 |
| 491 | 0.7757362 | 0.8363375 | 0.4306492 | 0.6371634 | 1 | 0.3579623 | 1 | 0.6003755 |
| 492 | 5.73703 | 9.0413335 | 0.4487636 | 1.7047 | 1.5193865 | 4.1978368 | 5.0520078 | 1.7502807 |
| 493 | 1 | 1.4661095 | 0.3412565 | 0.5083849 | 1 | 0.4732584 | 1 | 0.6702454 |
| 494 | 6.0178588 | 3.6967608 | 0.2947238 | 1.8677036 | 1 | 3.6579624 | 4.1938483 | 1.5364343 |
| 495 | 1 | 0.219802 | 1 | 0.0943023 | 0.4774424 | 0.1344744 | 1 | 0.1700911 |
| 496 | 1 | 1 | 0.5999536 | 0.8298189 | 0.3964903 | 0.6092772 | 0.6959295 | 1 |
| 497 | 0.5186323 | 1 | 1 | 1 | 0.4309498 | 0.2541154 | 1 | 1 |
| 498 | 1 | 1000 | 1 | 3.0158188 | 1.8377217 | 2.0146994 | 1000 | 2.2998628 |
| 499 | 5.8710738 | 5.2694196 | 1.3910216 | 1.7369603 | 1.8694043 | 2.8187657 | 2.6696059 | 1 |
| 500 | 1 | 1 | 3.3592229 | 0.0952339 | 1 | 2.3577735 | 0.1471308 | 1.7693913 |
| 501 | 3.9443721 | 4.1392679 | 0.6335722 | 1 | 1 | 2.7292786 | 3.9834209 | 1.6085091 |
| 502 | 1 | 1 | 1 | 0.7272045 | 1 | 0.2807962 | 1 | 0.5682248 |
| 503 | 7.8605725 | 1 | 0.5332895 | 1.9844639 | 1.1286512 | 2.3559133 | 7.2199052 | 1.5305545 |
| 504 | 8.2167011 | 1 | 1 | 1.8289275 | 0.7087083 | 3.0239128 | 2.9263138 | 1.5571073 |
| 505 | 1.5136755 | 1 | 0.1123001 | 0.3626145 | 1 | 0.4307491 | 1 | 0.3018498 |
| 506 | 2.9948325 | 4.4565319 | 0.8041881 | 1.594743 | 1 | 4.6035937 | 1 | 2.0729042 |
| 507 | 4.4858199 | 1 | 0.4464931 | 1 | 1 | 1.9517695 | 5.4129638 | 1 |
| 508 | 1 | 1000 | 1 | 1 | 1.5816752 | 3.7332958 | 12.152294 | 1.4770369 |
| 509 | 1 | 1000 | 1 | 1 | 1 | 2.632241 | 1000 | 1 |
| 510 | 0.4313564 | 1 | 1 | 0.6388528 | 1 | 1 | 1 | 1 |
| 511 | 13.113224 | 39.884687 | 2.0704568 | 6.9333458 | 2.6799215 | 1.9443151 | 10.58676 | 5.3223961 |
| 512 | 1 | 0.6203652 | 1 | 1 | 0.001 | 0.5275739 | 0.7599682 | 0.3833046 |
| 513 | 1 | 0.7210064 | 1.3987783 | 0.272377 | 1 | 1 | 0.2862089 | 0.4753499 |
| 514 | 7.2640401 | 7.0616586 | 0.6701985 | 2.392352 | 1 | 5.057715 | 7.508865 | 2.265265 |
| 515 | 1 | 1 | 2.3247334 | 2.2643087 | 0.363218 | 1.9061301 | 5.2681401 | 1.1509374 |
| 516 | 1 | 1 | 1 | 1.5315372 | 1 | 1 | 3.5646583 | 1 |
| 517 | 0.3556906 | 1.2049886 | 0.1062506 | 0.6074216 | 1 | 0.3751637 | 0.3029258 | 0.2033305 |
| 518 | 1000 | 1000 | 1 | 1 | 1 | 1.2704743 | 1 | 1 |
| 519 | 1 | 1 | 0.2239175 | 0.915802 | 1 | 0.623273 | 1 | 0.4433737 |
| 520 | 0.2130473 | 0.1818003 | 0.3055764 | 0.6998802 | 1 | 0.09631 | 1 | 0.7045274 |
| 521 | 5.2571815 | 2.944242 | 4.7022389 | 1 | 2.3126287 | 3.2968701 | 1.5622946 | 1 |
| 522 | 6.3082741 | 4.7820619 | 0.5407876 | 1 | 1.6382994 | 3.5147295 | 3.2068417 | 1.4266263 |
| 523 | 1 | 1000 | 1 | 1 | 2.1432088 | 2.2275068 | 1 | 1 |
| 524 | 1 | 1 | 2.1051098 | 0.3534308 | 1 | 0.3741546 | 0.2513426 | 0.4940998 |
| 525 | 3.5784463 | 3.1216823 | 0.4389147 | 3.8932499 | 1 | 2.1760055 | 1 | 1.5481147 |
| 526 | 4.6967548 | 2.5297702 | 1 | 1 | 1 | 2.9017594 | 4.5749319 | 1.117655 |
| 527 | 4.9116429 | 1 | 0.5000301 | 2.0978125 | 0.7563781 | 1.9081688 | 1 | 1 |
| 528 | 1 | 1000 | 1 | 1.9381688 | 1.1926402 | 2.8418153 | 3.8448002 | 1 |
| 529 | 1 | 1 | 1 | 1 | 0.001 | 1 | 1 | 0.001 |
| 530 | 1.672359 | 0.2318212 | 1 | 1 | 0.001 | 0.3167022 | 1 | 1 |
| 531 | 1 | 1000 | 1 | 1.5314885 | 1 | 2.1564017 | 1000 | 1 |
| 532 | 1 | 1 | 1 | 1 | 1 | 1.6973383 | 1 | 2.2491122 |
| 533 | 0.3694687 | 0.7788682 | 0.0705681 | 0.722776 | 0.1086807 | 0.2023053 | 0.5152399 | 0.1948497 |
| 534 | 4.4858199 | 3.5485003 | 0.6650504 | 1.3841598 | 1.6417504 | 2.8806524 | 4.2639856 | 1.6677486 |
| 535 | 2.0463354 | 1000 | 1 | 2.6495163 | 0.001 | 1.2826306 | 1000 | 1 |
| 536 | 1 | 0.6327005 | 2.0904535 | 0.3678743 | 1 | 0.2721749 | 0.2180916 | 0.4847526 |
| 537 | 1 | 1000 | 1.4682376 | 1.1881828 | 2.095861 | 1.6981071 | 1 | 2.771015 |
| 538 | 8.7301937 | 2.4622582 | 1 | 2.1370744 | 1 | 4.0847784 | 5.4381266 | 2.3376086 |
| 539 | 4.8222767 | 5.5919266 | 0.5576578 | 3.8310346 | 1 | 2.2487168 | 1 | 1 |

Table 4

| SEQ ID NO | Patient ID | | | | | | | |
|--------------|------------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|
| | 295 | 296 | 300 | 322 | 339 | 341 | 356 | 360 |
| 540 | 5.5018269 | 3.9540521 | 1 | 2.0100427 | 1 | 1.6246682 | 1.6391699 | 1 |
| 541 | 6.1712363 | 1000 | 0.7083501 | 2.2340745 | 1 | 2.9306298 | 1 | 1 |
| 542 | 3.0218675 | 3.3220747 | 1.4913681 | 1.6325638 | 1.8119148 | 3.9030173 | 5.1012515 | 1 |
| 543 | 1 | 0.5615333 | 2.11199 | 0.3189043 | 1 | 0.4832525 | 0.1992958 | 0.4629285 |
| 544 | 1 | 0.2675229 | 0.8532449 | 0.5117159 | 1 | 0.1438301 | 0.7228959 | 0.297181 |
| 545 | 1 | 1000 | 1 | 2.3073527 | 0.3723435 | 2.7898816 | 2.9885384 | 1 |
| 546 | 1000 | 1000 | 1 | 1 | 4.2235856 | 2.7159691 | 1 | 1 |
| 547 | 8.0380852 | 1 | 0.6772171 | 1.980956 | 1 | 1.9122049 | 5.5917978 | 1 |
| 548 | 4.4630764 | 3.9784104 | 1 | 2.2223287 | 1 | 1.6589955 | 4.4715523 | 1.4324718 |
| 549 | 7.6021601 | 5.0377328 | 0.5765615 | 1.8148069 | 1 | 1.7893583 | 4.6465488 | 1.3179013 |
| 550 | 1 | 5.4820383 | 1.3908805 | 1 | 1.9656595 | 2.3178794 | 1 | 1 |
| 551 | 0.2027623 | 0.2416096 | 0.1000093 | 0.156031 | 0.1155525 | 0.0851696 | 0.1113123 | 0.1135364 |
| 552 | 1000 | 1000 | 1 | 1000 | 1 | 1.9409654 | 1000 | 1 |
| 553 | 1 | 1 | 0.1663093 | 0.3173584 | 1 | 0.722164 | 0.6078375 | 0.485282 |
| 554 | 1 | 0.5407576 | 2.7478387 | 0.2285032 | 1 | 0.2597303 | 0.1683732 | 0.4829661 |
| 555 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 |
| 556 | 6.0610006 | 1 | 1 | 1 | 1 | 3.9354158 | 2.4996517 | 1.6575742 |
| 557 | 1.60221 | 1 | 1 | 1 | 0.7875375 | 0.5284525 | 1.7833681 | 0.4115028 |
| 558 | 5.468316 | 1000 | 1 | 1 | 1.2812086 | 1.9282394 | 1 | 0.7720849 |
| 559 | 4.9302447 | 1 | 1 | 1 | 0.622303 | 2.222901 | 1 | 1 |
| 560 | 1 | 1000 | 1 | 1 | 1 | 5.3550193 | 1 | 1 |
| 561 | 2.9486413 | 1000 | 1 | 1 | 0.7516997 | 1.3929914 | 1.7632085 | 1 |
| 562 | 1.8739847 | 1.4662367 | 1 | 1 | 1.5135812 | 1.6729639 | 1.9949071 | 0.5738306 |
| 563 | 0.6032025 | 0.5634154 | 1 | 1 | 1 | 0.3248224 | 0.2296354 | 0.4479362 |
| 564 | 3.0919278 | 1000 | 1 | 1 | 1.2593759 | 3.0669163 | 4.6843078 | 1 |
| 565 | 0.7370799 | 0.7456917 | 1 | 1 | 1 | 0.3861531 | 0.2717874 | 0.4784663 |
| 566 | 6.3128372 | 5.9233391 | 1 | 1 | 1 | 4.8007441 | 5.212904 | 2.2443666 |
| 567 | 48.854008 | 1 | 1 | 1 | 0.566534 | 4.4318542 | 1 | 16.271202 |
| 568 | 0.7173914 | 0.6940249 | 1 | 1 | 1 | 0.3655951 | 0.2737591 | 0.4964353 |
| 569 | 1.7412106 | 1 | 1 | 1 | 1.4578223 | 0.7660804 | 0.3607726 | 1 |
| 570 | 0.4264439 | 0.4008284 | 1 | 1 | 0.5344993 | 0.1368837 | 0.129667 | 0.3438634 |
| 571 | 1 | 1 | 1 | 1 | 1 | 0.4526043 | 0.3520455 | 1 |
| 572 | 6.4263829 | 1000 | 1 | 1 | 1 | 6.0343307 | 1 | 1 |
| 573 | 6.0093148 | 1 | 1 | 1 | 1 | 5.2029522 | 7.0911852 | 2.2235536 |
| 574 | 0.7777544 | 1 | 1 | 1 | 1 | 0.472064 | 1 | 0.4981443 |
| 575 | 1 | 1 | 1 | 1 | 1 | 0.481914 | 0.2944228 | 0.5643982 |
| 576 | 0.789797 | 0.7085294 | 1 | 1 | 0.6736753 | 0.3702215 | 0.2993239 | 0.4979905 |
| 577 | 0.7953304 | 1 | 1 | 1 | 0.6595797 | 0.3966894 | 1 | 0.6830521 |
| 578 | 4.4365072 | 1 | 1 | 1 | 1.3022163 | 2.1375872 | 2.3897175 | 1.2062411 |
| 579 | 0.7230856 | 0.776234 | 1 | 1 | 0.7869238 | 0.3605157 | 0.2697067 | 0.4585487 |
| 580 | 1.4933826 | 0.6080443 | 1 | 1 | 0.4327206 | 0.5514747 | 0.4815776 | 1 |
| 581 | 3.5197079 | 1 | 1 | 1 | 2.0570752 | 5.6537719 | 3.9533305 | 2.3241332 |
| 582 | 3.9853792 | 6.5728222 | 1 | 1 | 1.3813071 | 2.4830088 | 3.2757748 | 1.7309789 |
| 583 | 4.5743101 | 4.5237569 | 1 | 1 | 1.3239585 | 3.5208179 | 3.9695068 | 2.0032163 |
| 584 | 4.8777605 | 1 | 1 | 1 | 1 | 1.7485101 | 2.2216644 | 1.3912331 |
| 585 | 5.2880588 | 5.5112108 | 1 | 1 | 1.9327091 | 1.2479944 | 6.6668551 | 1.9409961 |
| 586 | 4.4374276 | 1 | 1 | 1 | 1 | 1.8427471 | 3.2628759 | 1 |
| 587 | 1.2622714 | 1 | 1 | 1 | 0.5353142 | 0.4497557 | 1 | 0.3819297 |
| 588 | 1 | 2.1372731 | 1 | 1 | 0.2366084 | 1.0806891 | 1 | 1 |

Table 4

| SEQ ID NO | Patient ID | | | | | | | |
|--------------|------------|-----------|-----|-----|-----------|-----------|-----------|-----------|
| | 295 | 296 | 300 | 322 | 339 | 341 | 356 | 360 |
| 589 | 1.3956165 | 1.2884622 | | | 0.5603967 | 1 | 1 | 1.6293209 |
| 590 | 1 | 0.5525225 | | | 1 | 0.3944586 | 0.2727267 | 0.456447 |
| 591 | 1 | 0.578523 | | | 0.7705643 | 0.4961226 | 0.3355503 | 0.4206877 |
| 592 | 0.7785583 | 0.6578981 | | | 0.890926 | 0.4222033 | 0.2361665 | 0.4381416 |
| 593 | 1.6879169 | 1 | | | 0.6493173 | 0.7374572 | 0.4575458 | 1 |
| 594 | 1.1971734 | 1 | | | 0.5774705 | 0.3951244 | 1 | 0.3777496 |
| 595 | 3.9682744 | 4.7462222 | | | 1 | 1.6099035 | 2.5639436 | 1.5150163 |
| 596 | 1 | 0.853498 | | | 0.7779392 | 0.4153117 | 0.3662237 | 0.4660204 |
| 597 | 11.89532 | 1 | | | 1 | 3.0093884 | 1 | 1 |
| 598 | 5.0431695 | 1000 | | | 1 | 2.650067 | 1 | 1 |
| 599 | 5.5717985 | 1 | | | 0.566866 | 2.939965 | 1 | 1 |
| 600 | 10.994489 | 1 | | | 0.311061 | 3.6947951 | 1 | 1 |
| 601 | 0.3483774 | 0.239128 | | | 0.5389765 | 0.3789664 | 0.2975037 | 0.6481437 |
| 602 | 4.8287859 | 1 | | | 1 | 1.9291111 | 1 | 1 |
| 603 | 2.0279165 | 1.6499773 | | | 1 | 1.9126236 | 1 | 1.3178144 |
| 604 | 1.3920736 | 1 | | | 1 | 1.38483 | 1 | 1.6649161 |
| 605 | 0.6201798 | 0.6689109 | | | 1 | 0.4760726 | 0.4347315 | 1 |
| 606 | 4.7984464 | 10.594801 | | | 1.4472279 | 3.401925 | 3.9423588 | 2.4027716 |
| 607 | 5.1247401 | 3.9832791 | | | 1.4393902 | 2.994912 | 4.2044881 | 1.7284952 |
| 608 | 2.1875204 | 1 | | | 1.6242339 | 1.5146025 | 2.985398 | 1 |
| 609 | 1 | 1 | | | 0.1937277 | 1.2655596 | 1 | 1 |
| 610 | 1 | 1 | | | 0.8190893 | 0.6729004 | 0.5358995 | 0.3155772 |
| 611 | 1 | 1 | | | 0.3347651 | 1 | 1 | 1 |
| 612 | 0.7719825 | 0.6717558 | | | 1 | 0.3159266 | 0.2757252 | 0.464479 |
| 613 | 0.5625281 | 0.5684549 | | | 1 | 0.2487821 | 0.2266312 | 0.4976039 |
| 614 | 0.6610593 | 0.5986956 | | | 0.8861067 | 0.2378613 | 0.2521392 | 0.4008392 |
| 615 | 0.8141817 | 0.8083023 | | | 0.7823158 | 0.3726102 | 0.3243955 | 0.477559 |
| 616 | 3.3469636 | 2.4973385 | | | 1.3594945 | 2.5359241 | 2.2352736 | 1.9556503 |
| 617 | 0.7863151 | 0.2506095 | | | 0.0427801 | 1.3894427 | 0.1014761 | 0.5973411 |
| 618 | 0.718018 | 1 | | | 0.0615139 | 1.367759 | 0.1002656 | 0.5712308 |
| 619 | 1.4982729 | 0.2802071 | | | 0.7154493 | 0.6161138 | 1 | 1 |
| 620 | 1.4073764 | 2.5791007 | | | 0.3013318 | 1 | 0.8059177 | 0.8432487 |
| 621 | 1.85851 | 1 | | | 0.1732733 | 0.6820708 | 1 | 1 |
| 622 | 3.4895791 | 1 | | | 1.6221613 | 3.0115025 | 4.9409264 | 1.6688621 |
| 623 | 3.5183162 | 1 | | | 1.6812505 | 6.1420489 | 1 | 1.8177056 |
| 624 | 2.2686863 | 1 | | | 3.3948074 | 1.1788456 | 1 | 1 |
| 625 | 1 | 1 | | | 1 | 3.1635558 | 1000 | 1 |
| 626 | 1.3109742 | 0.4481315 | | | 0.2426752 | 0.719336 | 0.5529376 | 0.7558075 |
| 627 | 0.3640517 | 0.2463911 | | | 0.5934577 | 0.2628123 | 0.313202 | 0.6884608 |
| 628 | 0.5888644 | 0.2294777 | | | 1 | 0.628023 | 0.4802866 | 0.631256 |
| 629 | 4.2909087 | 7.4819075 | | | 1.5271235 | 3.0664701 | 3.7959971 | 1.5827666 |
| 630 | 9.9099296 | 1 | | | 3.4409278 | 2.4981235 | 1 | 1 |
| 631 | 1 | 1 | | | 1 | 0.2673151 | 1 | 1 |
| 632 | 1.1953326 | 1 | | | 0.433616 | 0.4930407 | 1 | 1 |
| 633 | 6.0213685 | 5.7869707 | | | 2.3314632 | 2.0741562 | 5.1202958 | 1.751047 |
| 634 | 4.5101714 | 3.6330857 | | | 1.3175998 | 1.2649487 | 4.3722609 | 1 |
| 635 | 0.3451838 | 0.2823508 | | | 0.619335 | 0.3565963 | 0.3090863 | 0.6308418 |
| 636 | 3.8399692 | 1 | | | 1 | 2.8482195 | 2.6610328 | 1.5807398 |
| 637 | 4.7503701 | 6.0536397 | | | 1.2147446 | 3.5088126 | 4.0719142 | 1.7729681 |

Table 4

| SEQ ID NO | Patient ID | | | | | | | |
|--------------|------------|-----------|-----|-----|-----------|-----------|-----------|-----------|
| | 295 | 296 | 300 | 322 | 339 | 341 | 356 | 360 |
| 638 | 0.643755 | 1 | | | 0.6128556 | 0.263938 | 0.3985576 | 1 |
| 639 | 3.4053305 | 2.0392079 | | | 1.7032744 | 1.9921509 | 1 | 1.546056 |
| 640 | 5.264528 | 1000 | | | 1 | 3.061981 | 1 | 1 |
| 641 | 1.4236772 | 1 | | | 0.2731908 | 0.7688055 | 1 | 1 |
| 642 | 0.6934669 | 0.6826923 | | | 1 | 0.4982848 | 0.2471768 | 0.4631772 |
| 643 | 0.6321171 | 0.5903969 | | | 1 | 0.2345734 | 0.2288835 | 0.4492929 |
| 644 | 6.3563116 | 1 | | | 0.5462407 | 1.8963625 | 1 | 1 |
| 645 | 3.8980478 | 4.9680262 | | | 1.6469419 | 2.8707132 | 4.9936544 | 1.7166838 |
| 646 | 0.559961 | 0.5041257 | | | 0.8745766 | 0.2923759 | 0.2548713 | 0.4663051 |
| 647 | 0.7531756 | 0.656194 | | | 1 | 0.461562 | 0.2700271 | 0.4708772 |
| 648 | 4.4418687 | 1 | | | 1 | 1.810232 | 1 | 1.672631 |
| 649 | 5.4130041 | 4.9507494 | | | 1 | 3.5741793 | 3.4529436 | 1.6994108 |
| 650 | 5.1899988 | 5.0908638 | | | 1 | 1.3632974 | 2.6807615 | 1.151839 |
| 651 | 1 | 1 | | | 1.5012664 | 3.7931507 | 1 | 1 |
| 652 | 4.2608908 | 1000 | | | 1.8756624 | 2.8043443 | 1 | 1 |
| 653 | 1.6822837 | 1 | | | 0.3470799 | 1 | 1 | 1 |
| 654 | 0.3232165 | 1 | | | 0.3719209 | 0.2880446 | 1 | 0.4588643 |
| 655 | 0.7746273 | 2.1747734 | | | 1.9472375 | 1.1601066 | 1 | 1 |
| 656 | 1.1807451 | 1 | | | 0.4631757 | 1.2745859 | 0.3430134 | 1 |
| 657 | 1.3578197 | 1 | | | 0.3857249 | 0.42232 | 1 | 1 |
| 658 | 4.004297 | 3.5546444 | | | 1.2631991 | 2.9199767 | 2.7603899 | 1 |
| 659 | 0.433685 | 1 | | | 0.1858599 | 0.3226877 | 0.4088069 | 1 |
| 660 | 1000 | 1 | | | 3.1005083 | 2.3240845 | 1 | 1 |
| 661 | 1.2931764 | 1 | | | 0.6032673 | 0.4442919 | 1 | 1 |
| 662 | 1 | 0.4137306 | | | 1 | 1 | 0.2552181 | 0.4681127 |
| 663 | 1 | 1 | | | 0.001 | 0.4229789 | 0.3167185 | 1 |
| 664 | 5.2109681 | 4.9540703 | | | 1.9696437 | 4.9370305 | 4.0848781 | 2.904812 |
| 665 | 1000 | 1 | | | 1 | 2.4940119 | 1 | 1 |
| 666 | 4.6627005 | 2.3173186 | | | 1.4127281 | 1.8013086 | 1 | 1.3582728 |
| 667 | 29.572225 | 3.7254247 | | | 1 | 2.696832 | 2.0528752 | 9.2366313 |
| 668 | 2.993402 | 2.2237369 | | | 0.7265669 | 1.809875 | 1.5719266 | 1 |
| 669 | 4.2462589 | 1 | | | 0.6034887 | 2.2131952 | 1 | 1 |
| 670 | 3.284599 | 1 | | | 1 | 2.5066281 | 1000 | 1 |
| 671 | 0.5444696 | 1.67996 | | | 0.3621314 | 0.6639634 | 1 | 0.9578447 |
| 672 | 10.374154 | 5.4940758 | | | 1 | 3.8934075 | 1 | 1 |
| 673 | 2.634163 | 2.1283895 | | | 1.1020998 | 2.4564379 | 1 | 1.5917367 |
| 674 | 4.3155041 | 0.6359887 | | | 3.1335592 | 0.7235848 | 0.5372386 | 4.5930697 |
| 675 | 1 | 1 | | | 1.4734674 | 1.925782 | 1 | 1000 |
| 676 | 3.0623534 | 2.2975275 | | | 1 | 1.5077933 | 4.403239 | 1.6514689 |
| 677 | 4.7402015 | 1000 | | | 2.1479375 | 6.3994454 | 5.3018472 | 3.7205676 |
| 678 | 0.6802267 | 0.5673067 | | | 1 | 0.2760119 | 0.2444906 | 0.444511 |
| 679 | 4.3316275 | 3.595887 | | | 0.603046 | 1.8450809 | 3.4123591 | 1 |
| 680 | 1000 | 1000 | | | 0.6730012 | 2.2639414 | 1 | 1 |
| 681 | 1000 | 1 | | | 1.2536813 | 3.2347295 | 1 | 1 |
| 682 | 2.3449509 | 1.6952493 | | | 1.2923262 | 1.5665362 | 1.7727173 | 1 |
| 683 | 7.6992387 | 1 | | | 1 | 3.8946568 | 1 | 1 |
| 684 | 0.569004 | 0.5722482 | | | 0.2964522 | 0.3795018 | 1 | 1 |
| 685 | 0.8592252 | 0.4391244 | | | 0.6059235 | 0.6363766 | 0.6311402 | 0.7020688 |
| 686 | 1 | 1 | | | 0.5962044 | 0.3480574 | 1 | 0.6838416 |

Table 4

| SEQ ID NO | Patient ID | | | | | | | |
|--------------|------------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|
| | 295 | 296 | 300 | 322 | 339 | 341 | 356 | 360 |
| 687 | 1 | 1 | | | 0.001 | 0.2419317 | 0.2060362 | 1 |
| 688 | 0.6763067 | 0.539286 | | | 1 | 0.3160501 | 0.3115143 | 0.5076464 |
| 689 | 0.5586192 | 0.2440403 | | | 0.5004523 | 0.5315688 | 0.38892 | 1 |
| 690 | 2.649743 | 1000 | | | 1 | 1.5033111 | 1 | 1.9796178 |
| 691 | 1000 | 1 | | | 1 | 3.5912503 | 1000 | 1 |
| 692 | 4.1861399 | 1 | | | 0.7017762 | 2.5586854 | 1 | 1 |
| 693 | 0.7523883 | 0.5310637 | | | 1 | 0.3706059 | 0.2881455 | 0.5069283 |
| 694 | 4.7731192 | 1 | | | 1.1651632 | 2.2936972 | 1 | 1 |
| 695 | 3.4539058 | 2.8068671 | | | 1 | 1.124482 | 1 | 1 |
| 696 | 0.0458364 | 0.1742901 | | | 0.0385544 | 0.1180349 | 0.2094396 | 0.2695912 |
| 697 | 6.2668567 | 1.992061 | | | 1 | 1.8217362 | 1 | 1.8823829 |
| 698 | 2.8238901 | 1.523826 | | | 1 | 1.6371814 | 1 | 2.5714056 |
| 699 | 0.6323277 | 0.4874812 | | | 1 | 0.3527593 | 0.2439747 | 0.5043279 |
| 700 | 3.6192316 | 1 | | | 2.3280525 | 2.2695631 | 1000 | 1 |
| 701 | 0.548445 | 0.4253574 | | | 1 | 0.2585291 | 0.2658614 | 0.4461414 |
| 702 | 3.2188136 | 2.448553 | | | 1.1220008 | 1.7214793 | 3.5414885 | 1 |
| 703 | 0.6592629 | 0.528553 | | | 0.8943368 | 0.3270739 | 0.2982935 | 0.461838 |
| 704 | 4.9683964 | 3.8021655 | | | 1.9446517 | 3.8531428 | 5.526533 | 2.0577595 |
| 705 | 0.5686714 | 0.2908929 | | | 0.5516133 | 1 | 0.4350358 | 1 |
| 706 | 0.5981792 | 0.4633082 | | | 1 | 0.2567101 | 0.1997141 | 0.4536038 |
| 707 | 0.6274375 | 0.4919539 | | | 1 | 0.2258423 | 0.2627007 | 0.3955633 |
| 708 | 1 | 1 | | | 0.1049077 | 1 | 0.2851829 | 1 |
| 709 | 6.6080706 | 4.4263821 | | | 1 | 4.1020553 | 5.4463176 | 2.1873626 |
| 710 | 4.0690456 | 7.2348297 | | | 1.83579 | 2.7905543 | 11.325301 | 2.1884159 |
| 711 | 4.1024124 | 1000 | | | 1 | 2.6247111 | 1 | 1.3532541 |
| 712 | 1 | 1000 | | | 1 | 3.2648903 | 1 | 1 |
| 713 | 2.8169207 | 2.469158 | | | 0.5231 | 1.5218029 | 1 | 1 |
| 714 | 1000 | 1000 | | | 1 | 3.1608513 | 1 | 1 |
| 715 | 0.5923852 | 0.4732274 | | | 1 | 0.3561295 | 0.239409 | 0.4616631 |
| 716 | 0.2914742 | 1 | | | 1 | 0.1168543 | 1 | 1 |
| 717 | 0.7285414 | 0.5468617 | 2.0534128 | 0.3905303 | 1 | 0.3049509 | 0.29952 | 0.5204542 |
| 718 | 2.12978 | 1 | 1.4002278 | 1 | 2.3788312 | 2.435372 | 2.5959051 | 1.6250838 |
| 719 | 8.2138568 | 1 | 2.0117219 | 1 | 2.7866805 | 1.568513 | 10.07969 | 3.968192 |
| 720 | 5.3744421 | 1 | 2.6093433 | 1 | 2.8969811 | 1 | 9.0767818 | 2.6071428 |
| 721 | 3.1294696 | 6.398285 | 0.7620316 | 1.882957 | 1.2624144 | 4.2570807 | 1 | 2.0645578 |
| 722 | 6.9951985 | 7.3958034 | 0.558867 | 2.0405147 | 1.5812526 | 5.6922039 | 7.5717605 | 2.9895809 |
| 723 | 4.2963257 | 1 | 0.6344986 | 2.5840172 | 1 | 2.2612713 | 2.7370257 | 1.7867501 |
| 724 | 3.3282176 | 1 | 1 | 1.5745247 | 1 | 2.1657575 | 3.8789212 | 1 |
| 725 | 0.3250905 | 0.2422636 | 0.8190717 | 0.2338028 | 0.4012392 | 0.1824681 | 0.1947247 | 0.4004555 |
| 726 | 1.3475901 | 1 | 1.6431994 | 2.1285782 | 1 | 2.7434049 | 1 | 0.8019903 |
| 727 | 4.5544331 | 1 | 0.5506724 | 1.6834977 | 1.8709738 | 2.6151151 | 5.0353789 | 1.6520965 |
| 728 | 1 | 0.2492179 | 0.5787956 | 0.4491388 | 0.6252308 | 0.1508452 | 0.3725072 | 0.5019026 |
| 729 | 1 | 0.2848869 | 1 | 0.4884073 | 0.6016575 | 0.1995597 | 0.3816504 | 0.3387468 |
| 730 | 0.2512212 | 0.1186302 | 1 | 0.6406791 | 0.5075253 | 0.198736 | 0.3019072 | 0.3264738 |
| 731 | 2.2889182 | 1 | 0.7210538 | 1 | 0.4682868 | 1 | 1 | 1 |
| 732 | 4.2335675 | 1 | 1.119741 | 1.5100358 | 1.4261799 | 2.7834843 | 3.1921716 | 1.6155523 |
| 733 | 1.3400717 | 1.5211118 | 1.3623853 | 1 | 1 | 4.2776799 | 1 | 0.67501 |
| 734 | 2.9192278 | 2.4151694 | 1.1254999 | 1 | 1.7402089 | 3.8173534 | 4.590773 | 1.702536 |
| 735 | 1.2581684 | 1 | 0.3201175 | 1 | 1 | 0.6234927 | 1 | 0.5602146 |

Table 4

| SEQ ID NO | Patient ID | | | | | | | |
|--------------|------------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|
| | 295 | 296 | 300 | 322 | 339 | 341 | 356 | 360 |
| 736 | 1.5922965 | 1 | 1 | 1 | 1.9599347 | 3.0951346 | 2.8473375 | 0.9044381 |
| 737 | 8.341408 | 1 | 9.5405596 | 1.5319754 | 0.7313761 | 1 | 1 | 2.7355348 |
| 738 | 11.475635 | 1 | 1 | 4.5347971 | 1.3002343 | 8.611103 | 8.6259939 | 2.4906348 |
| 739 | 0.4207497 | 1 | 0.2748546 | 1.3167938 | 0.2500601 | 0.2538683 | 1 | 1 |
| 740 | 1.4885977 | 1 | 1 | 1 | 2.2230642 | 1 | 1 | 1 |
| 741 | 3.984858 | 1 | 1 | 1.8567645 | 1 | 1 | 1 | 1 |
| 742 | 3.2969245 | 1 | 1 | 1 | 2.5932044 | 3.2827919 | 4.4331763 | 2.1876977 |
| 743 | 0.1754612 | 0.2233191 | 0.3413179 | 0.2742293 | 1 | 0.0566562 | 0.5129673 | 0.2147934 |
| 744 | 3.3179658 | 3.3115197 | 0.7434337 | 2.9403682 | 1.2567197 | 1.8168146 | 3.7304875 | 1.1813991 |
| 745 | 4.9001713 | 1 | 1 | 1.4097526 | 1.5143459 | 4.4844056 | 4.4406004 | 2.0202565 |
| 746 | 0.4268653 | 1 | 12.555524 | 1 | 1.8187061 | 0.5195086 | 1 | 2.9517191 |
| 747 | 3.3011272 | 4.7104878 | 0.5124372 | 2.0898063 | 1.5080878 | 2.7640315 | 4.2731476 | 1.6116203 |
| 748 | 0.3202058 | 0.3295086 | 1 | 0.5573687 | 1.6180664 | 0.1372955 | 0.3639184 | 0.3022019 |
| 749 | 0.1396825 | 0.0606486 | 0.0537466 | 0.0807872 | 0.0765755 | 1 | 0.4641289 | 0.1527753 |
| 750 | 0.2416569 | 0.258385 | 0.3426418 | 1 | 0.2268088 | 0.1776838 | 0.2764918 | 0.4356484 |
| 751 | 5.1661741 | 1 | 0.8268447 | 3.0503737 | 1.4290473 | 2.6406083 | 6.581906 | 1.8785633 |
| 752 | 1 | 1 | 12.027191 | 14.844964 | 1 | 4.0583104 | 1 | 1.9559181 |
| 753 | 6.1468405 | 1 | 1 | 3.6111176 | 2.5056521 | 4.5945194 | 7.0285311 | 1.8052021 |
| 754 | 0.6818124 | 0.5357217 | 2.4911128 | 0.4622896 | 0.8242809 | 0.2538272 | 0.2703777 | 0.5122313 |
| 755 | 0.3794488 | 1 | 9.6307155 | 1 | 1.985661 | 0.4855794 | 1 | 2.5850341 |
| 756 | 1 | 1 | 1 | 1 | 1 | 1 | 1000 | 1 |
| 757 | 3.3178383 | 1 | 0.7592968 | 2.9230666 | 0.6112257 | 0.7590653 | 4.0462317 | 1.6477404 |
| 758 | 4.5528696 | 1 | 0.6998062 | 3.0992252 | 0.6640871 | 2.428 | 4.0673338 | 1.962791 |
| 759 | 4.0183856 | 1 | 1 | 1 | 0.7523738 | 1 | 2.9892122 | 2.081665 |
| 760 | 4.6792286 | 4.7303951 | 1 | 1 | 1.6807474 | 4.1754324 | 5.202676 | 2.0766498 |
| 761 | 4.5129492 | 5.3250686 | 0.6376222 | 1.6387823 | 1 | 3.8461277 | 4.0487029 | 1.9046868 |
| 762 | 7.9312649 | 1 | 5.94108 | 2.0434567 | 0.7715101 | 1.3591858 | 1.9612652 | 6.7055552 |
| 763 | 1 | 1 | 1 | 1 | 0.3240298 | 1 | 1 | 1 |
| 764 | 1 | 1 | 1 | 3.6162667 | 1.7713885 | 1 | 1 | 0.7455561 |
| 765 | 1 | 1000 | 1 | 1000 | 1.9744127 | 1 | 1000 | 1 |
| 766 | 3.7950033 | 2.2166518 | 1 | 1.5652673 | 1.4283531 | 3.9314415 | 3.2644827 | 2.3093712 |
| 767 | 2.6315571 | 1 | 1.1894205 | 1 | 1 | 4.2729025 | 3.5878096 | 1.5192059 |
| 768 | 4.4445412 | 1 | 1 | 1.3485602 | 2.0107636 | 1 | 4.6432941 | 1.4368152 |
| 769 | 4.8093635 | 1 | 1 | 2.2959193 | 1.4906317 | 1 | 3.5323675 | 1.944242 |
| 770 | 1 | 0.2136216 | 0.5047124 | 0.4085874 | 0.6914735 | 1 | 0.5093152 | 0.8895283 |
| 771 | 2.8321015 | 1 | 1 | 1 | 0.8094306 | 1 | 1 | 3.652743 |
| 772 | 4.0724389 | 1 | 0.6715714 | 1 | 1.928574 | 5.7079021 | 5.8234931 | 1.5378758 |
| 773 | 0.3790828 | 0.2423799 | 0.843037 | 0.2620654 | 1 | 0.3509266 | 0.306587 | 1 |
| 774 | 0.2375762 | 0.1868653 | 2.4754843 | 0.0471758 | 1 | 0.3787261 | 0.3368119 | 0.6180096 |
| 775 | 1 | 1 | 1.1588849 | 2.5370796 | 0.5889805 | 1 | 1 | 1 |
| 776 | 4.9811543 | 8.8275048 | 0.4846566 | 2.0412926 | 1.5264293 | 3.8565611 | 5.4181253 | 1.7353953 |
| 777 | 0.7213169 | 0.6113325 | 1.8222906 | 0.4662212 | 1 | 0.3389831 | 0.3194582 | 0.5254733 |
| 778 | 3.0076126 | 1 | 1.178457 | 2.9800095 | 1.2344242 | 1 | 3.7322377 | 3.9977024 |
| 779 | 2.9798846 | 1 | 0.6363459 | 1 | 1 | 2.3271253 | 2.1962704 | 3.5367173 |
| 780 | 0.2952999 | 0.2500754 | 0.3321988 | 0.2255195 | 0.4403771 | 0.0689772 | 0.4644433 | 0.3400845 |
| 781 | 5.3233274 | 1 | 1.0769611 | 2.1762602 | 2.0838781 | 6.3759565 | 1 | 3.1150394 |
| 782 | 1 | 0.633162 | 3.3210044 | 1 | 1.902425 | 1 | 1 | 1.5512611 |
| 783 | 6.9586769 | 1 | 1.2312057 | 3.5680676 | 1 | 5.5014646 | 1 | 1.8099403 |
| 784 | 3.5281799 | 5.1642402 | 0.2519811 | 1 | 1.6282081 | 3.0462554 | 6.5515496 | 1.5489541 |

Table 4

| SEQ ID NO | Patient ID | | | | | | | |
|--------------|------------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|
| | 295 | 296 | 300 | 322 | 339 | 341 | 356 | 360 |
| 785 | 0.2208429 | 0.1003143 | 0.1345024 | 0.4617845 | 0.1045958 | 0.0940449 | 0.3582833 | 1 |
| 786 | 6.0878304 | 1 | 0.7641932 | 1.5202787 | 1.1638552 | 3.4077526 | 6.2099075 | 1.7096976 |
| 787 | 3.2838117 | 1 | 0.6096644 | 3.4158045 | 0.6093845 | 1.686342 | 1 | 1.6774013 |
| 788 | 1 | 1 | 1.3328293 | 1.6903481 | 2.8631856 | 1 | 1 | 1 |
| 789 | 0.0519908 | 0.0831865 | 0.0477738 | 0.2070491 | 0.087512 | 1 | 0.1482877 | 0.2353654 |
| 790 | 2.8126736 | 1 | 1.3227761 | 1.7934626 | 1.287195 | 3.1145942 | 2.4012592 | 1 |
| 791 | 3.3748136 | 3.1118103 | 0.439889 | 2.018547 | 1.4144083 | 2.1931314 | 3.8676058 | 1.401569 |
| 792 | 0.4007951 | 0.3275429 | 2.279715 | 0.1197222 | 1.3606012 | 0.5196733 | 0.3605992 | 0.4297243 |
| 793 | 0.152141 | 0.1219075 | 0.1830625 | 0.2070376 | 0.2454119 | 0.5585653 | 0.3705948 | 0.8250259 |
| 794 | 3.9350684 | 8.3036388 | 0.9134693 | 1.655504 | 1.9730745 | 2.4240875 | 5.7204743 | 1.6929654 |
| 795 | 0.3904324 | 0.2614842 | 1 | 0.5401013 | 0.4066018 | 0.146919 | 0.2780828 | 0.5205165 |
| 796 | 0.4334244 | 0.239128 | 0.4607332 | 0.2721877 | 1 | 0.4835476 | 0.4024166 | 1 |
| 797 | 3.3832024 | 4.5574857 | 0.6546536 | 1 | 1 | 3.0316349 | 3.9075015 | 1.3920273 |
| 798 | 7.2850925 | 1 | 1 | 1.7304109 | 1.3540514 | 2.803397 | 1 | 2.4100109 |
| 799 | 2.390998 | 2.8936397 | 0.2526536 | 2.8539892 | 0.5310785 | 1.8018852 | 2.5252021 | 1.3535289 |
| 800 | 2.9333163 | 1.381655 | 1 | 1.5536095 | 1.5120318 | 3.8025064 | 4.7691196 | 3.0234815 |
| 801 | 0.2937918 | 0.2194386 | 0.7236166 | 0.2729231 | 0.6072415 | 0.3347479 | 0.3302045 | 0.6491747 |
| 802 | 6.4291607 | 4.693469 | 0.5861283 | 1.5099885 | 2.3181221 | 6.0897994 | 6.9438648 | 3.260714 |
| 803 | 0.48358 | 0.1678554 | 0.4689751 | 0.3841878 | 0.6390146 | 0.4134378 | 0.4439163 | 1 |
| 804 | 1 | 1 | 0.3755609 | 1 | 0.2311049 | 1 | 0.5889895 | 0.6245489 |
| 805 | 2.6323998 | 1 | 0.6755856 | 1.8258783 | 1.7592346 | 1 | 3.0588678 | 1.4963564 |
| 806 | 4.3491037 | 3.3541393 | 1 | 1.4431493 | 2.0811817 | 3.6208483 | 3.5704181 | 1.7624984 |
| 807 | 2.5064067 | 1 | 1 | 1 | 2.258892 | 3.8556551 | 3.505902 | 1.3755766 |
| 808 | 4.0528668 | 1 | 1 | 2.5787624 | 1.2800818 | 3.5111121 | 1 | 1.8626057 |
| 809 | 1.6238724 | 1.6931892 | 0.3862021 | 2.1497548 | 1.4627321 | 1.7472951 | 2.8817894 | 0.7274922 |
| 810 | 4.645252 | 1 | 0.6282694 | 1.6931991 | 1.2179943 | 4.0086419 | 4.4585201 | 1.9251874 |
| 811 | 6.0280108 | 7.3661513 | 0.5480226 | 1.9478052 | 1.285223 | 3.6224682 | 6.1732823 | 1.8197236 |
| 812 | 11.452703 | 1 | 0.5556407 | 1 | 1.644819 | 9.1100193 | 7.7172017 | 2.5408893 |
| 813 | 4.4618289 | 1 | 1 | 1 | 1 | 6.9139981 | 1 | 1.5850248 |
| 814 | 5.6340687 | 7.6287874 | 1 | 1 | 1.1880322 | 2.5452112 | 6.0419957 | 1.7505565 |
| 815 | 4.9490239 | 1 | 0.916078 | 1 | 2.0351519 | 5.5373844 | 4.7042528 | 1.6145349 |
| 816 | 0.6155556 | 0.5113598 | 2.4150143 | 0.4368739 | 1 | 0.3165993 | 0.2675856 | 0.4766439 |
| 817 | 0.6877117 | 0.5650286 | 2.2408184 | 0.4376436 | 0.892566 | 0.3347616 | 0.2722301 | 0.4909821 |
| 818 | 0.6807534 | 0.5471233 | 2.171863 | 0.6110805 | 1 | 0.3127622 | 0.2919783 | 0.4910231 |
| 819 | 0.5639696 | 0.440218 | 1 | 0.3189233 | 0.7682905 | 0.386661 | 0.38779 | 0.5737976 |
| 820 | 0.7068957 | 0.5837079 | 2.2483891 | 0.3751022 | 1 | 0.2644253 | 0.2928447 | 0.6185295 |
| 821 | 3.3252014 | 1 | 0.4935801 | 1 | 1.547437 | 3.7964729 | 5.5074021 | 1.8977818 |
| 822 | 2.9678142 | 1 | 1 | 1 | 2.9223452 | 4.0067748 | 5.0629401 | 1.556671 |
| 823 | 3.3756563 | 5.3623036 | 0.6837939 | 2.0227837 | 1.5682435 | 6.363203 | 4.4665309 | 1.4480519 |
| 824 | 0.7928021 | 0.435273 | 0.3971506 | 0.4371712 | 1.2523834 | 0.1425465 | 1 | 0.3656015 |
| 825 | 1 | 0.5831483 | 0.2389499 | 0.4353858 | 0.346597 | 0.2393577 | 0.317596 | 0.6563854 |
| 826 | 4.2772027 | 5.0837787 | 1.3514118 | 1.7984158 | 1.8191387 | 2.7427734 | 3.3092984 | 1.2014724 |
| 827 | 0.7094628 | 0.6182215 | 2.2584394 | 0.3796504 | 1 | 0.3065365 | 0.3045844 | 0.4903248 |
| 828 | 0.7673141 | 1 | 0.1739365 | 0.5506617 | 0.5196792 | 0.2918199 | 0.1877066 | 1 |
| 829 | 4.8283368 | 5.4337905 | 0.2671076 | 2.5452543 | 1.2671532 | 4.2318483 | 4.9464566 | 1.841237 |
| 830 | 0.1114222 | 0.09663 | 1 | 0.4486495 | 0.1188626 | 0.0800216 | 0.217424 | 0.2349794 |
| 831 | 0.3542934 | 0.2150822 | 0.0876522 | 0.2127807 | 0.2213758 | 1 | 0.0661143 | 0.2060843 |
| 832 | 6.499404 | 1 | 2.3062161 | 1 | 1.5463202 | 3.7591803 | 3.7182815 | 1.216618 |
| 833 | 0.0788095 | 0.0608956 | 1 | 0.4392714 | 0.0734767 | 0.0704599 | 0.2002581 | 0.2131223 |

Table 4

| SEQ ID NO | Patient ID | | | | | | | |
|--------------|------------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|
| | 295 | 296 | 300 | 322 | 339 | 341 | 356 | 360 |
| 834 | 0.6495656 | 0.6038405 | 1.9050343 | 0.5034294 | 0.8911273 | 0.2891978 | 0.2953673 | 0.4930983 |
| 835 | 0.4488271 | 0.3007903 | 0.4703888 | 0.5957219 | 0.6486633 | 0.1227162 | 0.7487661 | 0.351138 |
| 836 | 0.622514 | 0.5434971 | 2.1031736 | 0.6120896 | 0.891077 | 0.3349401 | 0.2791229 | 0.496349 |
| 837 | 0.7101226 | 0.5852848 | 2.0498491 | 0.6390223 | 0.8553699 | 0.3404863 | 0.3031082 | 0.4872021 |
| 838 | 4.7186611 | 3.1621146 | 1.2117816 | 2.0150018 | 1 | 3.5208522 | 1 | 1.4900457 |
| 839 | 3.0295688 | 1 | 0.8110966 | 2.8360163 | 2.0074636 | 2.9155906 | 3.9225303 | 1.5789425 |
| 840 | 3.4513165 | 1 | 0.4262228 | 2.175376 | 1 | 1.947452 | 1 | 2.1570672 |
| 841 | 2.467318 | 1 | 1.6191962 | 1.3976087 | 1.6950142 | 2.4821371 | 2.3416024 | 1.1411904 |
| 842 | 4.1612395 | 1 | 0.8048195 | 3.0283279 | 0.758008 | 4.1417709 | 1 | 1.5317973 |
| 843 | 1.4473522 | 1.3083077 | 0.1403831 | 0.3448068 | 1 | 0.360145 | 1 | 0.2507455 |
| 844 | 3.4100211 | 4.7202071 | 1 | 1 | 1.8030308 | 6.3768831 | 4.9470719 | 2.5188063 |
| 845 | 3.8979812 | 1 | 0.8006645 | 1.5273623 | 2.067408 | 2.6235304 | 3.4892936 | 2.3997152 |
| 846 | 0.609246 | 1 | 0.1291015 | 0.4681371 | 0.1960619 | 0.2825602 | 0.5661039 | 0.3326298 |
| 847 | 1 | 1 | 0.7416067 | 1 | 1.6456139 | 1.7583532 | 2.3738859 | 1.2887686 |
| 848 | 1.3735882 | 1.1780725 | 1.9178169 | 0.7061882 | 2.2005775 | 0.1860443 | 1 | 0.5407542 |
| 849 | 0.6896911 | 0.5990117 | 2.2931985 | 0.4773187 | 1 | 0.3185006 | 0.30113 | 0.4829427 |
| 850 | 3.642197 | 3.8220329 | 1 | 1.2623917 | 2.0002195 | 2.8528459 | 3.6079878 | 1.6299318 |
| 851 | 0.3367672 | 0.4880407 | 0.3687091 | 0.2324045 | 0.3290403 | 0.1404942 | 0.3554179 | 0.2597363 |
| 852 | 1.7932679 | 2.828166 | 0.2165537 | 1 | 1 | 1.601344 | 2.4484123 | 1.5651754 |
| 853 | 3.2033833 | 1 | 1 | 1.9897904 | 1.6982941 | 1 | 4.2786637 | 1.611984 |
| 854 | 3.722204 | 4.7821891 | 0.5813501 | 2.1809882 | 1.153623 | 3.401877 | 5.2060808 | 1.8673365 |
| 855 | 0.7104386 | 0.5214388 | 0.5654924 | 0.6806423 | 0.5720375 | 0.3745665 | 1 | 0.5190951 |
| 856 | 2.6803708 | 1 | 1.9047902 | 1.2381293 | 1.3528843 | 2.3594964 | 2.4151107 | 1.537663 |
| 857 | 0.1668007 | 0.1116105 | 1 | 0.2609033 | 0.629869 | 0.0558668 | 0.2357941 | 0.3046902 |
| 858 | 0.8235186 | 1 | 3.3682314 | 1.6659782 | 0.1559581 | 0.4794704 | 1 | 0.6422774 |
| 859 | 1.4168298 | 0.8086983 | 0.2008729 | 0.6015149 | 0.5202728 | 0.2615561 | 0.797355 | 0.6159272 |
| 860 | 0.3584185 | 0.2148024 | 0.3987703 | 0.4765257 | 0.5161779 | 0.0859453 | 1 | 0.2200311 |
| 861 | 3.1617385 | 1 | 1 | 1 | 1.5688573 | 2.7450935 | 1 | 1.7938666 |
| 862 | 3.1617385 | 1 | 1 | 1 | 1.5688573 | 2.7450935 | 1 | 1.7938666 |
| 863 | 0.6602055 | 0.5387556 | 2.2869646 | 0.4228206 | 1 | 0.3026652 | 0.2760179 | 0.5031832 |
| 864 | 1.2442906 | 0.6972186 | 0.3236482 | 2.1199628 | 0.63496 | 0.1717189 | 1.3881429 | 0.3647426 |
| 865 | 1 | 1 | 0.4450491 | 1 | 0.215993 | 1 | 1 | 0.7885871 |
| 866 | 4.5666421 | 3.9902589 | 0.7289996 | 1 | 1.7711168 | 4.2688389 | 5.0436796 | 2.7109111 |
| 867 | 1 | 1 | 1 | 1 | 1.8584376 | 1 | 5.2716312 | 1.6897895 |
| 868 | 0.638094 | 0.5289163 | 2.4422641 | 0.4126497 | 1 | 0.2652147 | 0.2683058 | 0.4191411 |
| 869 | 7.824001 | 1 | 0.740855 | 2.5951504 | 1 | 3.6531644 | 5.7139 | 2.0636204 |
| 870 | 5.4874944 | 7.2660659 | 1 | 1.8335205 | 1 | 4.2275514 | 5.849185 | 2.1829214 |
| 871 | 4.985734 | 3.2312726 | 0.848855 | 1.2708483 | 2.2343831 | 4.9716736 | 3.4722355 | 2.9080224 |
| 872 | 4.6526871 | 1 | 1 | 1 | 1.4832971 | 3.576218 | 4.5014099 | 2.3489765 |
| 873 | 4.8608608 | 4.1862476 | 1 | 1 | 1.8226702 | 5.2854037 | 4.7594182 | 1.7807358 |
| 874 | 3.3623274 | 2.8982251 | 0.7882648 | 1 | 1.5735961 | 3.0049336 | 3.4988087 | 2.0049435 |
| 875 | 3.6636542 | 1 | 1 | 1 | 0.8173488 | 1.7689925 | 1.5414067 | 1 |
| 876 | 3.3071873 | 1 | 0.6737226 | 1.397163 | 1.494294 | 1 | 1 | 2.2730411 |
| 877 | 0.2331627 | 0.2889345 | 0.1197894 | 0.1785773 | 0.1282899 | 0.0707344 | 0.1610811 | 0.1432041 |
| 878 | 0.2282281 | 0.1721537 | 2.3788409 | 0.047893 | 1.4224875 | 0.4126485 | 0.3252257 | 0.3668329 |
| 879 | 2.8181128 | 1 | 0.5673579 | 2.0192237 | 1.4457489 | 3.9850088 | 1 | 1.61417 |
| 880 | 0.6038678 | 0.6362104 | 1.7260519 | 0.4320326 | 1 | 0.3903196 | 0.2856252 | 0.5614225 |
| 881 | 0.4464097 | 0.2473903 | 0.093368 | 0.4803879 | 0.122887 | 0.0948754 | 0.1679608 | 0.3476837 |
| 882 | 0.4137027 | 0.3445835 | 0.4676397 | 0.5389475 | 0.4138257 | 0.1642851 | 0.3719325 | 0.6088313 |

Table 4

| SEQ ID NO | Patient ID | | | | | | | |
|--------------|------------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|
| | 295 | 296 | 300 | 322 | 339 | 341 | 356 | 360 |
| 883 | 0.1757606 | 0.1132637 | 0.0411246 | 0.2986844 | 0.0663232 | 0.027779 | 0.0704288 | 0.2276612 |
| 884 | 8.3107746 | 1 | 1.2964492 | 1.5491144 | 2.6057305 | 8.7988221 | 10.248508 | 2.0702003 |
| 885 | 5.4381761 | 5.039822 | 0.6138992 | 1 | 1 | 4.7246625 | 4.5425374 | 2.2449713 |
| 886 | 5.3815557 | 10.333476 | 0.5817084 | 1 | 1.8297432 | 6.2968753 | 12.398522 | 2.1311366 |
| 887 | 6.5568172 | 6.4375402 | 0.2818886 | 2.4287678 | 1.3432357 | 5.242208 | 5.0201259 | 1.805952 |
| 888 | 3.7323616 | 1 | 0.7673661 | 1.1949302 | 1.782003 | 4.0939007 | 4.589184 | 2.5085058 |
| 889 | 1 | 1 | 0.5381426 | 0.4201405 | 1 | 0.4192517 | 0.731054 | 0.4897172 |
| 890 | 5.6779423 | 1 | 0.51064 | 1 | 1.6074217 | 4.9216893 | 5.5051153 | 2.3890503 |
| 891 | 0.6523212 | 0.5752312 | 2.5400368 | 0.397715 | 1 | 0.2670337 | 0.2863429 | 0.4847503 |
| 892 | 0.5828265 | 0.5604578 | 2.2298362 | 0.4494739 | 0.8924151 | 0.274797 | 0.275559 | 0.4581054 |
| 893 | 1.832473 | 1 | 0.7217717 | 1 | 1.5942416 | 1 | 1.7466388 | 1 |
| 894 | 3.6020991 | 1 | 0.6000849 | 1 | 2.1611076 | 1 | 1 | 1.737627 |
| 895 | 4.1756996 | 1 | 1 | 1 | 0.5526999 | 1 | 2.5599831 | 3.8694479 |
| 896 | 5.499842 | 7.1207012 | 2.0376942 | 1 | 1.8419876 | 2.6734941 | 4.3775542 | 1.5037152 |
| 897 | 3.0659906 | 1 | 0.2730502 | 1 | 1.5755379 | 3.0327057 | 4.330371 | 1.4188122 |
| 898 | 3.5130989 | 1 | 0.8635316 | 1.2793849 | 1.5752461 | 2.5297807 | 2.9545727 | 1.6760797 |
| 899 | 3.4300423 | 2.9796603 | 0.7383065 | 1 | 1.5442074 | 2.4564997 | 3.7776102 | 2.0602612 |
| 900 | 3.3655044 | 1 | 0.2870789 | 1 | 1.6615004 | 2.6367644 | 5.2286654 | 1.3628456 |
| 901 | 1 | 1 | 0.8659928 | 1 | 1.2611165 | 1 | 4.4297202 | 1.8975657 |
| 902 | 4.0558275 | 5.4411918 | 0.2866871 | 1 | 1.4336352 | 3.1891039 | 7.1588297 | 1.3980416 |
| 903 | 0.6586918 | 0.5486093 | 2.3111171 | 0.3711727 | 1 | 0.2481574 | 0.2720626 | 0.4639273 |
| 904 | 4.4851324 | 3.0532328 | 0.7752345 | 1.4252219 | 1.5407866 | 4.028939 | 4.0188398 | 2.7981567 |
| 905 | 0.249519 | 0.2253284 | 1 | 0.2096124 | 0.6535228 | 0.3313982 | 0.3146589 | 0.6173799 |
| 906 | 4.3991484 | 7.6272686 | 1 | 1 | 1.8902108 | 4.3494096 | 6.041078 | 1.6520146 |
| 907 | 0.3536835 | 0.0942066 | 0.6544663 | 0.4804023 | 1 | 0.0485772 | 0.5703167 | 0.256285 |
| 908 | 0.7366253 | 0.6305605 | 0.4960677 | 0.5255399 | 0.4912363 | 0.4445253 | 0.6054135 | 0.5441148 |
| 909 | 0.4126658 | 0.4254519 | 0.7748 | 0.3935701 | 0.6008929 | 0.2281692 | 0.3533246 | 0.4155734 |
| 910 | 0.2894616 | 0.3431883 | 0.3038667 | 1 | 0.2915826 | 0.0911208 | 0.3321818 | 0.3512502 |
| 911 | 0.3126986 | 0.4333073 | 0.199072 | 1 | 0.2767122 | 0.1643606 | 0.4127608 | 0.3777253 |
| 912 | 0.4115015 | 0.3943791 | 0.7619145 | 0.2433097 | 0.7074406 | 0.342168 | 0.3225148 | 0.6519217 |
| 913 | 0.4618178 | 0.420674 | 2.0840292 | 0.4210031 | 1 | 0.3243008 | 0.3293678 | 0.4864247 |
| 914 | 0.7003975 | 0.632606 | 1.9854747 | 0.4959781 | 0.8795267 | 0.3296136 | 0.3168068 | 0.4809426 |
| 915 | 0.7026819 | 0.7996221 | 5.0541606 | 0.7342967 | 1.3014014 | 0.8208284 | 1 | 1.5810147 |
| 916 | 0.465893 | 0.1941321 | 0.560136 | 0.3659855 | 1 | 0.4074729 | 0.385057 | 1 |
| 917 | 5.1974617 | 5.0337869 | 0.267923 | 2.1496589 | 1.3121165 | 5.2245947 | 4.3167417 | 1.924113 |
| 918 | 0.6304925 | 0.5458988 | 2.1055075 | 0.3851397 | 0.8781383 | 0.2780574 | 0.2730037 | 0.4662964 |
| 919 | 6.3123049 | 1 | 0.6838752 | 1 | 1 | 5.4396809 | 5.3067989 | 2.3949444 |
| 920 | 7.9615822 | 1 | 1.0879785 | 3.3495588 | 1.6673762 | 7.7191146 | 7.0584663 | 2.407052 |
| 921 | 1.4638027 | 1 | 0.2626041 | 0.5268673 | 0.4398439 | 0.2579113 | 1 | 0.6248299 |
| 922 | 4.1716964 | 1 | 0.7167622 | 1 | 1.127474 | 3.2663043 | 3.9615994 | 1.6926214 |
| 923 | 4.2013041 | 1 | 1 | 1.4764003 | 1.4860639 | 1 | 1 | 1.3168772 |
| 924 | 0.6572225 | 1 | 5.6092345 | 0.7253327 | 1.8174183 | 1 | 1 | 1.7331993 |
| 925 | 3.3969638 | 1 | 0.7123364 | 1.5332915 | 2.2892969 | 2.4626019 | 7.100046 | 1.5688346 |
| 926 | 0.7127008 | 0.6142465 | 1.9905715 | 0.4780764 | 1 | 0.300805 | 0.3008135 | 0.4843487 |
| 927 | 2.2671782 | 2.8148279 | 1 | 2.0747795 | 0.6318813 | 1.3519785 | 3.5662564 | 1.3639983 |
| 928 | 0.4391131 | 0.4556526 | 1.6710035 | 0.467987 | 1 | 0.161814 | 0.614657 | 0.5688131 |
| 929 | 1 | 1 | 0.5480192 | 1 | 0.2537123 | 1 | 1 | 0.7905511 |
| 930 | 1 | 1 | 0.3974294 | 0.3761886 | 0.4084732 | 1 | 0.470075 | 0.4642741 |
| 931 | 5.471055 | 5.9921337 | 1 | 1 | 1.1658272 | 6.2625686 | 5.9928368 | 2.1732423 |

Table 4

| SEQ ID NO | Patient ID | | | | | | | |
|--------------|------------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|
| | 295 | 296 | 300 | 322 | 339 | 341 | 356 | 360 |
| 932 | 3.8646422 | 3.5027414 | 4.3407131 | 1.4319135 | 2.0844516 | 8.1436036 | 4.49023 | 2.9593197 |
| 933 | 5.4916916 | 4.9519339 | 2.1619116 | 1 | 1.6351201 | 5.0287005 | 3.6821383 | 1.859834 |
| 934 | 3.1404144 | 1 | 0.7318204 | 2.0815012 | 1 | 2.3124225 | 4.2165226 | 1.3513337 |
| 935 | 2.1752061 | 3.3324407 | 0.7639051 | 1 | 1.5439559 | 1.5547505 | 2.7327006 | 1 |
| 936 | 0.4523977 | 0.842914 | 1 | 1 | 0.7976389 | 0.2548156 | 1 | 1 |
| 937 | 1 | 0.6531093 | 0.2412483 | 0.5273285 | 0.6656365 | 0.4347028 | 1.6438443 | 0.5420118 |
| 938 | 5.1153644 | 7.5214643 | 1 | 1 | 1 | 3.7067592 | 5.9391455 | 1.6797966 |
| 939 | 3.8746112 | 6.7903788 | 1 | 1 | 1 | 1.7812792 | 4.1714166 | 2.2080369 |
| 940 | 0.6665595 | 0.5761468 | 2.3622678 | 0.3532442 | 1 | 0.2601764 | 0.2828406 | 0.4908832 |
| 941 | 2.1150206 | 1 | 0.4667206 | 2.0876334 | 1 | 6.0279265 | 0.4537355 | 1.4139567 |
| 942 | 0.1171774 | 0.0954346 | 0.1273944 | 0.1555897 | 0.1994122 | 0.031616 | 0.3542624 | 0.1618445 |
| 943 | 0.533802 | 0.2664802 | 0.3858078 | 0.2176398 | 0.8334869 | 0.0755599 | 0.4188725 | 0.2646953 |
| 944 | 4.1312272 | 4.2381433 | 2.4109661 | 1 | 1.7337597 | 3.4013484 | 3.3536642 | 1.7622188 |
| 945 | 5.8434622 | 7.6173022 | 1.2822352 | 1.2550595 | 2.3683474 | 6.9863936 | 5.598882 | 2.1419566 |
| 946 | 1 | 1 | 1 | 1 | 1.7306911 | 1.329176 | 1 | 1.6177218 |
| 947 | 4.8812868 | 7.9327605 | 1 | 1 | 1.2445558 | 4.2707128 | 6.0613316 | 1.8014293 |
| 948 | 4.1704767 | 1 | 1 | 1 | 1.8110797 | 1 | 1 | 1 |
| 949 | 3.3860024 | 4.787403 | 0.4118956 | 2.3235969 | 1.305788 | 3.3917113 | 3.6503724 | 1.7017536 |
| 950 | 3.7297889 | 1 | 1 | 1 | 1.1598509 | 7.1798923 | 1 | 1.7247086 |
| 951 | 0.6112587 | 0.5225652 | 2.9351462 | 0.273888 | 1 | 1 | 0.2734899 | 0.4979186 |
| 952 | 2.1798912 | 2.6317994 | 2.209888 | 1 | 1.2477552 | 1.2970314 | 1.3652247 | 1.6162052 |
| 953 | 2.2364118 | 2.5104769 | 1 | 1.4598065 | 1.4079893 | 3.1932224 | 3.1380243 | 1.4315899 |
| 954 | 1.234072 | 1.2547152 | 0.4523019 | 1 | 0.7356924 | 0.1995253 | 2.673374 | 0.6831828 |
| 955 | 1 | 1 | 0.1093966 | 0.4720859 | 0.3492431 | 0.3147048 | 1 | 1 |
| 956 | 1 | 1 | 1 | 1.2040066 | 1.2908573 | 1 | 1 | 1.7987395 |
| 957 | 3.910096 | 1 | 0.5876095 | 1 | 1.3601887 | 6.2919263 | 5.3153091 | 2.1372864 |
| 958 | 2.5742935 | 1 | 1.7502917 | 1.2622264 | 1.8588501 | 3.5866583 | 1.4644498 | 2.1141484 |
| 959 | 2.4945304 | 3.0619711 | 1 | 1 | 1.8284151 | 3.3522496 | 2.3220537 | 1.8553475 |
| 960 | 2.3827477 | 2.1082787 | 0.7570246 | 1 | 1.2820739 | 3.1425036 | 2.8262956 | 1.5402448 |
| 961 | 4.6430286 | 1 | 1 | 0.8109245 | 2.2876871 | 4.1809992 | 5.0049651 | 2.3692369 |
| 962 | 3.9156238 | 1.8825506 | 0.6498141 | 1.7754229 | 1.2615994 | 2.9271291 | 3.4749657 | 1.5811898 |
| 963 | 3.9049618 | 1 | 0.6088049 | 1 | 1.5983968 | 3.0284431 | 3.1682697 | 2.2591232 |
| 964 | 2.49137 | 1 | 1.347929 | 1 | 1 | 1.88457 | 1 | 1 |
| 965 | 3.0566814 | 1 | 0.8404231 | 1 | 1 | 3.7229928 | 3.1479587 | 1 |
| 966 | 6.0285874 | 5.7217695 | 0.6096436 | 1 | 2.075638 | 2.5030931 | 4.7025843 | 1.6906467 |
| 967 | 1.4208662 | 1 | 0.3230017 | 1 | 1 | 1 | 1 | 0.578435 |
| 968 | 3.0940347 | 1 | 1.4106605 | 1 | 2.7760861 | 3.5392205 | 3.5916975 | 1.8843696 |
| 969 | 0.6040564 | 0.599059 | 2.2024107 | 0.4166674 | 1 | 0.2786477 | 0.2627666 | 0.4242776 |
| 970 | 3.7235846 | 5.3919157 | 0.4589643 | 2.3373474 | 1.369616 | 7.4971711 | 5.3309821 | 1.4373316 |
| 971 | 2.9197379 | 1 | 1.0736611 | 1 | 1.1553535 | 1 | 1.6957773 | 2.2055529 |
| 972 | 0.3568161 | 0.3683713 | 0.3246285 | 0.5123253 | 0.4312214 | 0.1191949 | 0.5671533 | 0.3780409 |
| 973 | 0.3080246 | 0.2490181 | 1 | 0.2513549 | 1 | 0.3163727 | 0.3601813 | 1 |
| 974 | 0.6307088 | 0.5800273 | 1.9043021 | 0.4426895 | 0.8234358 | 0.323024 | 0.3288504 | 0.4897915 |
| 975 | 0.3402048 | 0.3790281 | 1 | 0.2963315 | 1 | 0.3271905 | 0.3647661 | 1 |
| 976 | 0.4463209 | 0.4327841 | 1.3252924 | 0.2471686 | 0.8062412 | 0.3763786 | 0.3291361 | 0.4972154 |
| 977 | 8.7934897 | 6.4848324 | 1.3632496 | 1 | 3.1024199 | 6.1520499 | 10.761487 | 2.0100624 |
| 978 | 4.8491675 | 1 | 1.3122648 | 1.2650762 | 2.175646 | 4.8866344 | 4.4645255 | 1.8584858 |
| 979 | 2.2207597 | 1 | 1.3685217 | 1 | 1.2992986 | 1 | 1 | 1 |
| 980 | 2.4954785 | 1 | 0.7672868 | 1 | 1.7385086 | 3.7482252 | 6.732305 | 2.3694614 |

Table 4

| SEQ ID | Patient ID | | | | | | | |
|--------|------------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|
| | 295 | 296 | 300 | 322 | 339 | 341 | 356 | 360 |
| 981 | 0.756835 | 0.6315814 | 1.1004444 | 0.7258462 | 0.5575293 | 0.5832073 | 1 | 0.7556248 |
| 982 | 2.7656618 | 2.2337033 | 0.6990328 | 1 | 1.2240511 | 2.0414145 | 2.9230879 | 1.4262804 |
| 983 | 4.2210425 | 4.2397239 | 0.6967552 | 1 | 1 | 4.1661933 | 3.5819937 | 2.0633649 |
| 984 | 6.5725082 | 8.820089 | 0.7670723 | 1.8098991 | 1 | 3.9280437 | 5.6554042 | 1.9228919 |
| 985 | 0.7494608 | 1 | 5.6895786 | 1 | 1.6162654 | 1 | 1 | 1.8288101 |
| 986 | 1.9444441 | 2.4855845 | 1.173788 | 1 | 1.6241031 | 5.5604134 | 3.575875 | 1.3378452 |
| 987 | 0.6405225 | 0.2974875 | 0.2918862 | 0.4622275 | 0.364687 | 0.2575475 | 0.3271383 | 0.37141 |
| 988 | 0.6738006 | 0.6310255 | 2.0623884 | 0.4057661 | 0.8379339 | 0.2724151 | 0.2900789 | 0.4763736 |
| 989 | 0.5263724 | 0.1209556 | 0.403009 | 0.2437195 | 0.727402 | 0.4047067 | 0.4738383 | 0.8679688 |
| 990 | 1.7021052 | 2.1227904 | 1 | 1.7856205 | 1.4023752 | 2.4100847 | 2.3177238 | 1 |
| 991 | 2.4673235 | 1.2980071 | 0.2367156 | 1 | 1.3510331 | 0.3436987 | 1 | 0.4794184 |
| 992 | 0.606313 | 0.5864656 | 2.4310123 | 0.3922374 | 0.7313761 | 0.3927083 | 0.2682805 | 0.4910423 |
| 993 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 0.001 |
| 994 | 1 | 1 | 0.8183914 | 1 | 1 | 1 | 1 | 1.4712989 |
| 995 | 0.4613632 | 0.4348006 | 2.1508571 | 0.3459778 | 1 | 0.2860952 | 0.2777488 | 0.5228929 |
| 996 | 4.4170737 | 1 | 1 | 1 | 2.223517 | 4.8853851 | 4.3569348 | 1.542288 |
| 997 | 0.6633492 | 1 | 0.473423 | 5.3731884 | 1 | 0.195908 | 2.22502 | 0.6886694 |
| 998 | 1.6755804 | 2.467839 | 0.8921576 | 1 | 0.7818328 | 2.1293503 | 1 | 2.0834434 |
| 999 | 0.8881342 | 1 | 0.3686938 | 1 | 1 | 0.2516856 | 0.5156473 | 1 |
| 1000 | 0.4366735 | 0.4453992 | 0.4577592 | 0.249693 | 1 | 0.5232358 | 0.3982304 | 1 |
| 1001 | 0.1298854 | 0.2726787 | 0.0745368 | 1 | 0.1522757 | 0.0954383 | 0.2642768 | 0.2892024 |
| 1002 | 0.4384533 | 0.4722209 | 0.5057486 | 1 | 0.5460696 | 0.2464757 | 0.4233307 | 0.4898011 |
| 1003 | 2.2173221 | 2.5233173 | 0.5580905 | 1 | 1.3580256 | 3.4932517 | 3.4631657 | 1.5761051 |
| 1004 | 3.4077756 | 1 | 0.5227742 | 1.3961914 | 1.6812907 | 2.5678558 | 4.1148829 | 1.5846229 |
| 1005 | 0.6964499 | 0.6200999 | 2.0514052 | 0.4964994 | 0.8784099 | 0.2896028 | 0.3128645 | 0.476737 |
| 1006 | 1 | 0.5826724 | 0.4337019 | 1 | 1 | 1 | 0.4803853 | 1 |
| 1007 | 0.25793 | 0.3222164 | 0.2555574 | 0.363172 | 0.2809781 | 1 | 0.4360756 | 0.4272125 |
| 1008 | 0.6409993 | 0.6098392 | 2.0812568 | 0.5142444 | 0.8148133 | 0.2916414 | 0.2761099 | 0.4932175 |
| 1009 | 0.5548656 | 0.5769461 | 2.3040412 | 0.3934672 | 0.8618996 | 0.2990409 | 0.2839714 | 0.5352827 |
| 1010 | 2.7456905 | 2.2703497 | 0.935044 | 1.5728287 | 1.1501519 | 4.2545067 | 2.4326885 | 1.5501308 |
| 1011 | 0.6458175 | 0.6057262 | 1.9461309 | 0.4948118 | 0.9067623 | 0.3573994 | 0.3006634 | 0.5049748 |
| 1012 | 4.5973142 | 1 | 1 | 1.7186231 | 1.8305079 | 3.1137911 | 3.2300193 | 1.7199617 |
| 1013 | 4.543771 | 1 | 1 | 2.0665932 | 1.7138587 | 4.2626063 | 3.7801233 | 1.8699557 |
| 1014 | 0.6001142 | 0.6226687 | 1.5014498 | 0.4546392 | 1 | 0.3841968 | 0.2968886 | 0.5660854 |
| 1015 | 4.8840535 | 4.2237369 | 0.4809787 | 1.6204854 | 1.367956 | 5.2897967 | 5.9685561 | 2.1806363 |
| 1016 | 0.7056759 | 0.7206104 | 1.6864885 | 0.4946087 | 0.8491621 | 0.3196538 | 0.3290762 | 0.4994532 |
| 1017 | 1.8819965 | 1.7182814 | 0.6897466 | 1 | 1.4993447 | 4.2133633 | 2.658365 | 1.6096226 |
| 1018 | 0.1442567 | 0.1802634 | 2.3705569 | 0.0571246 | 1.3713767 | 0.3770787 | 0.3132587 | 0.3692333 |
| 1019 | 3.1342046 | 1 | 0.2962674 | 2.366504 | 0.8089477 | 1 | 2.5871249 | 1.241606 |
| 1020 | 1.5232564 | 1 | 0.8224067 | 2.6831535 | 1.832832 | 3.0158063 | 2.7366491 | 5.1319886 |
| 1021 | 3.9978598 | 1 | 0.7371195 | 2.0695221 | 1.3093296 | 5.4031983 | 4.147493 | 2.1052013 |
| 1022 | 1.1853082 | 0.5095722 | 4.1599893 | 0.6377621 | 1 | 1.7114097 | 0.611435 | 2.1123618 |
| 1023 | 0.5914925 | 0.5885112 | 2.0598873 | 0.4626802 | 1 | 0.3266277 | 0.2916871 | 0.5101562 |
| 1024 | 0.8059315 | 0.6467581 | 0.6178014 | 0.5417529 | 0.7287501 | 0.3453186 | 0.4994344 | 1 |
| 1025 | 3.6516614 | 3.1043365 | 1 | 1 | 1 | 1.6872412 | 1.7234047 | 2.2880214 |
| 1026 | 3.5629661 | 5.9299955 | 0.6563352 | 1 | 1.5710506 | 4.487618 | 4.5193112 | 1.6434882 |
| 1027 | 4.3561397 | 5.511229 | 1.6077962 | 1.2000188 | 1.7837536 | 3.0916613 | 4.1666099 | 1.6251103 |
| 1028 | 4.8984747 | 1 | 1 | 1.8780401 | 1.5204832 | 5.9320146 | 4.9942815 | 1.4861698 |
| 1029 | 2.9941672 | 2.8453266 | 0.8197343 | 1 | 1.2646479 | 1 | 2.4543044 | 1.5194367 |

Table 4

| SEQ ID NO | Patient ID | | | | | | | |
|--------------|------------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|
| | 295 | 296 | 300 | 322 | 339 | 341 | 356 | 360 |
| 1030 | 1 | 0.7518539 | 1 | 1 | 0.4167937 | 0.583983 | 0.4395648 | 0.6738772 |
| 1031 | 6.3717197 | 6.0814897 | 0.7481772 | 1.5314398 | 2.1217886 | 3.2189078 | 5.5373044 | 2.9278634 |
| 1032 | 0.58215 | 0.2906095 | 1 | 0.5201225 | 1 | 0.131461 | 1 | 0.2874283 |
| 1033 | 3.7169368 | 3.3166028 | 1 | 1 | 1.9566145 | 4.5116835 | 4.8199779 | 2.533678 |
| 1034 | 7.4952622 | 4.0136143 | 0.7204102 | 1 | 1.8178509 | 7.5936459 | 5.4381266 | 3.106619 |
| 1035 | 3.2653929 | 1.9116904 | 1.8948941 | 1 | 1.300023 | 2.7618967 | 1 | 1.441954 |
| 1036 | 0.8127124 | 1.0915142 | 0.0850275 | 1 | 0.2874575 | 0.3803323 | 1.811718 | 1 |
| 1037 | 0.4275029 | 0.281388 | 0.6072358 | 0.3858088 | 0.6582516 | 0.4610197 | 0.3688011 | 0.6427316 |
| 1038 | 3.8993119 | 1 | 1 | 1.5498618 | 1 | 3.2343726 | 1 | 1.8011048 |
| 1039 | 1 | 1 | 1.6777155 | 2.3726798 | 1.6742781 | 1 | 1 | 2.5482716 |
| 1040 | 1 | 1 | 1 | 2.3416636 | 1 | 1 | 1 | 2.1086198 |
| 1041 | 1000 | 1000 | 1 | 1 | 1 | 1 | 1000 | 1 |
| 1042 | 4.8530154 | 1 | 0.4585501 | 1 | 1.6773568 | 4.6967806 | 5.1507974 | 1.9671933 |
| 1043 | 6.3179104 | 1 | 0.5254805 | 1 | 1.67458 | 8.1511815 | 6.7380074 | 1.8148353 |
| 1044 | 1 | 1 | 0.5539219 | 1.4094227 | 1.2341224 | 1 | 3.3690037 | 2.0236093 |
| 1045 | 7.0491852 | 1 | 0.8569881 | 2.9970614 | 2.5080869 | 1 | 3.3816067 | 2.2140508 |
| 1046 | 0.4458996 | 0.566442 | 0.1872572 | 0.3709927 | 0.4452568 | 0.1840949 | 0.431412 | 0.5374002 |
| 1047 | 1 | 1 | 4.9058237 | 0.7358104 | 1.3437186 | 1 | 1 | 1.5352783 |
| 1048 | 1.2147772 | 1.6012099 | 1.8154829 | 1 | 1 | 1.7493887 | 1.3554083 | 1.6463296 |
| 1049 | 2.5789121 | 1 | 0.7636271 | 1.4645984 | 1 | 1.6497633 | 1 | 2.0544193 |
| 1050 | 3.7224314 | 1 | 1 | 1 | 2.8012189 | 3.9100598 | 5.1897779 | 1.8327321 |
| 1051 | 0.5194307 | 0.5526933 | 0.1953851 | 0.4782662 | 0.4805815 | 0.0481996 | 1 | 0.3913796 |
| 1052 | 0.6213995 | 0.557126 | 1.7685678 | 0.3790144 | 0.8267358 | 0.2740694 | 0.2963444 | 0.4946351 |
| 1053 | 0.421598 | 0.3582414 | 1 | 0.3271623 | 0.7816618 | 0.4557069 | 0.4343755 | 0.632666 |
| 1054 | 0.3813006 | 0.3274448 | 1.3838656 | 0.1956306 | 0.8468078 | 0.248734 | 0.355758 | 0.4907748 |
| 1055 | 0.4869067 | 0.2908602 | 1 | 0.3152902 | 0.8600986 | 0.4316963 | 0.4156291 | 0.6163486 |
| 1056 | 0.4492429 | 0.4102498 | 1 | 0.225217 | 0.6864027 | 0.314389 | 0.3639317 | 1 |
| 1057 | 0.4091839 | 0.3114543 | 1 | 0.2537333 | 0.7689847 | 0.3467395 | 0.3606156 | 0.655658 |
| 1058 | 0.4752854 | 0.397166 | 1 | 0.2315435 | 1 | 0.3464649 | 0.3994181 | 1 |
| 1059 | 4.436047 | 3.5251957 | 0.5790004 | 1.9177281 | 2.262836 | 5.0680797 | 2.9070646 | 2.4104176 |
| 1060 | 0.5902672 | 0.4875248 | 0.8141549 | 0.2857323 | 0.5766354 | 0.284997 | 0.5167125 | 0.4335553 |
| 1061 | 2.3027074 | 1 | 1 | 1.8962204 | 0.6219509 | 1.5296143 | 3.4786127 | 1.3718397 |
| 1062 | 2.7492058 | 1 | 1.3764642 | 1 | 1.4957629 | 5.3068814 | 1.7026737 | 1.4595296 |
| 1063 | 3.2983771 | 1 | 1 | 1.9319523 | 1.4696944 | 4.139293 | 2.9349511 | 1.2040768 |
| 1064 | 6.2384356 | 1 | 0.3227773 | 2.0370642 | 1.6615809 | 4.2668003 | 7.7699663 | 1.9345368 |
| 1065 | 3.3873608 | 1 | 1 | 1 | 2.1200681 | 5.7765361 | 5.9587203 | 1.8529407 |
| 1066 | 0.6525763 | 0.6479535 | 2.0213664 | 0.4368858 | 1 | 0.3413786 | 0.3015158 | 0.5449303 |
| 1067 | 6.9087653 | 1 | 1 | 4.3278924 | 4.3347917 | 1 | 5.598882 | 2.9394836 |
| 1068 | 6.0152474 | 1 | 1 | 1 | 2.0998251 | 1 | 8.3036446 | 2.6850672 |
| 1069 | 0.6488448 | 0.5460986 | 1.3820426 | 0.652442 | 0.7943288 | 0.2355481 | 0.330817 | 0.456016 |
| 1070 | 5.0146763 | 2.0673013 | 1.3131537 | 1 | 1 | 3.3393245 | 1 | 1.8207509 |
| 1071 | 0.299608 | 0.3022654 | 0.7602775 | 0.3126858 | 0.5525289 | 0.3762345 | 0.3324706 | 0.6922741 |
| 1072 | 5.040181 | 1 | 1.2616988 | 1 | 1.6233586 | 4.1538517 | 1.8256051 | 1.8027285 |
| 1073 | 6.0495179 | 1 | 0.913619 | 1.6055829 | 1.2263853 | 10.789236 | 9.1794271 | 2.7593149 |
| 1074 | 1.3576644 | 1 | 0.1705209 | 1.0931411 | 0.2598094 | 0.4796626 | 1 | 0.361611 |
| 1075 | 0.1004497 | 0.0947516 | 0.0199541 | 0.2454913 | 1 | 1 | 0.0303201 | 0.1613287 |
| 1076 | 1 | 1 | 1 | 2.2734963 | 1 | 1 | 1 | 1 |
| 1077 | 8.6698196 | 7.9554038 | 1 | 1 | 1.7653216 | 7.4139372 | 5.1355013 | 3.16784 |
| 1078 | 3.6796667 | 1 | 0.729423 | 2.0905316 | 1.1535425 | 1 | 1 | 1.845928 |

Table 4

| SEQ ID | Patient ID | | | | | | | | |
|--------|------------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|
| | NO | 295 | 296 | 300 | 322 | 339 | 341 | 356 | 360 |
| 1079 | | 3.038379 | 1 | 1 | 1 | 2.5248589 | 4.4843919 | 4.6276274 | 1.9308384 |
| 1080 | | 4.1233706 | 1 | 1 | 1 | 2.7643246 | 1 | 4.9736723 | 2.1350046 |
| 1081 | | 0.409317 | 0.7204033 | 0.2237681 | 0.4764503 | 0.3246033 | 0.2105765 | 0.4060731 | 0.2243576 |
| 1082 | | 3.4134753 | 1 | 0.862884 | 1 | 1.5101001 | 2.4646405 | 3.464674 | 1.9599438 |
| 1083 | | 4.2160746 | 4.5113816 | 0.593057 | 0.8767285 | 1 | 3.4359366 | 4.1418783 | 1.5248591 |
| 1084 | | 1 | 1 | 0.6097165 | 2.9275063 | 1 | 4.947258 | 1 | 2.1671189 |
| 1085 | | 0.2467745 | 0.4890907 | 0.0939327 | 0.1784919 | 0.1762615 | 0.0980329 | 0.201601 | 0.1667109 |
| 1086 | | 4.5028083 | 1 | 0.4365554 | 2.0418981 | 1.1742383 | 1.4933032 | 1 | 1.7244112 |
| 1087 | | 0.6613587 | 0.4561359 | 0.0437257 | 0.8777666 | 0.0860129 | 1.5796191 | 0.1161888 | 0.6934841 |
| 1088 | | 0.2411967 | 0.1860877 | 1 | 0.319346 | 0.6374652 | 0.0949853 | 0.2531438 | 0.4287275 |
| 1089 | | 0.3400108 | 0.41114 | 0.3271035 | 1 | 0.3731786 | 0.2597371 | 0.3657321 | 0.4414904 |
| 1090 | | 3.2782839 | 1 | 1 | 1.8893802 | 1.3087158 | 3.2169172 | 2.7607731 | 1.9015354 |
| 1091 | | 1.3876158 | 1 | 0.189422 | 1 | 0.3360127 | 1 | 1.5986518 | 0.7151754 |
| 1092 | | 5.4229121 | 1 | 1.4262507 | 2.5621712 | 1.5119312 | 1 | 2.2243978 | 1.4304225 |
| 1093 | | 2.2197617 | 3.0657099 | 0.3769452 | 2.5636706 | 0.6494581 | 1.7634189 | 2.1327931 | 1.2520854 |
| 1094 | | 7.1933643 | 4.3663366 | 1 | 1 | 1.5526588 | 6.9320163 | 5.2814311 | 3.6206016 |
| 1095 | | 0.6167477 | 0.587156 | 2.525041 | 0.4930802 | 0.8318771 | 0.3070307 | 0.2931814 | 0.4948971 |
| 1096 | | 5.4479954 | 1 | 1 | 2.4721298 | 1.9679836 | 1 | 2.470003 | 1.602785 |
| 1097 | | 0.5581424 | 0.5738759 | 2.8746852 | 0.3473119 | 1 | 0.2720788 | 0.269019 | 0.492462 |
| 1098 | | 3.2295311 | 1 | 1 | 2.2977804 | 1.6662091 | 3.7841999 | 4.8959204 | 1.761691 |
| 1099 | | 7.0246176 | 7.3942265 | 2.11179 | 1.7099629 | 1.9096087 | 8.5262697 | 3.1988465 | 2.8871141 |
| 1100 | | 3.290454 | 1 | 1.5169145 | 1 | 2.1036081 | 4.6411128 | 3.2476899 | 1.9886737 |
| 1101 | | 5.9160896 | 1 | 1 | 1.8648124 | 1 | 1 | 1 | 1.4949693 |
| 1102 | | 1 | 1 | 1 | 1.9868368 | 1.3674026 | 1 | 1 | 1 |
| 1103 | | 1.3752183 | 1.3782106 | 0.4488393 | 1 | 1.4963263 | 1.5515313 | 1.89123 | 0.6940762 |
| 1104 | | 4.4529355 | 1 | 0.8034128 | 1.3919968 | 1.3067338 | 2.6131519 | 2.7512249 | 1 |
| 1105 | | 1 | 0.9206031 | 0.3223298 | 1 | 0.4527725 | 0.7485701 | 1 | 0.7305753 |
| 1106 | | 3.8348183 | 3.6975602 | 1 | 1 | 1 | 4.2991645 | 3.2323818 | 1.2968086 |
| 1107 | | 1 | 1 | 1 | 2.5009993 | 1.8205372 | 1 | 1 | 1 |
| 1108 | | 1 | 1 | 1 | 2.0157604 | 1 | 1 | 1 | 1.5262789 |
| 1109 | | 1 | 1.9964901 | 0.2966893 | 0.6413186 | 0.4789315 | 0.4556932 | 1 | 0.5308268 |
| 1110 | | 6.4065724 | 1 | 0.5747444 | 1.8527666 | 1.6630599 | 6.458703 | 7.7172017 | 2.5249762 |
| 1111 | | 1 | 1 | 1 | 1 | 1.7921547 | 1 | 2.8742924 | 2.2002142 |
| 1112 | | 1 | 1 | 0.7353295 | 1 | 1 | 1 | 4.2883512 | 2.0064322 |
| 1113 | | 9.2012985 | 9.800981 | 1 | 1 | 1 | 9.7992288 | 6.512929 | 2.0053456 |
| 1114 | | 1.1174713 | 1 | 0.2997066 | 1 | 0.5229692 | 0.7072826 | 1 | 0.7101972 |
| 1115 | | 1 | 0.4893959 | 0.5464627 | 1 | 1 | 1 | 0.4481276 | 1 |
| 1116 | | 5.1426544 | 5.4298519 | 1 | 1 | 2.3018431 | 4.0906883 | 3.287417 | 2.4931189 |
| 1117 | | 0.5919139 | 0.5830902 | 2.6878744 | 0.4740458 | 0.8535388 | 0.2874406 | 0.2874313 | 0.5343502 |
| 1118 | | 1.6957513 | 1 | 0.2196771 | 0.5142828 | 0.3062417 | 0.3677985 | 1 | 0.6261094 |
| 1119 | | 0.5771489 | 0.4359633 | 0.34728 | 0.8137455 | 0.301362 | 0.2076044 | 0.6325656 | 0.3097409 |
| 1120 | | 4.8781929 | 7.2133963 | 1 | 1.8165173 | 1 | 4.1149392 | 4.2480463 | 2.6087073 |
| 1121 | | 4.4506956 | 1 | 1 | 1.7322149 | 1 | 1 | 1 | 1.5257898 |
| 1122 | | 6.7146081 | 4.2480952 | 1 | 1 | 1 | 4.4708834 | 2.7663415 | 1.9659556 |
| 1123 | | 17.632294 | 1 | 18.073695 | 0.4552362 | 1.1616417 | 1 | 1 | 5.0764893 |
| 1124 | | 6.1555065 | 9.7339559 | 1 | 1 | 1 | 6.7956406 | 7.2488532 | 2.6330955 |
| 1125 | | 4.3157647 | 3.3431701 | 1 | 1 | 1.2521117 | 1.8529609 | 2.2554271 | 1.3793149 |
| 1126 | | 5.7211284 | 5.8278608 | 2.6217325 | 1 | 1.9242075 | 6.3985324 | 4.0351484 | 3.2891389 |
| 1127 | | 3.6825664 | 3.7052266 | 2.2682915 | 1 | 1.7937343 | 3.3280468 | 3.4529436 | 2.7759386 |

Table 4

| SEQ ID NO | Patient ID | | | | | | | |
|--------------|------------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|
| | 295 | 296 | 300 | 322 | 339 | 341 | 356 | 360 |
| 1128 | 4.046596 | 5.1129876 | 1 | 2.7340002 | 1.2133762 | 4.8675522 | 3.1891002 | 1.7861755 |
| 1129 | 7.01726 | 1 | 0.5841529 | 1.7541592 | 1 | 1 | 5.5651963 | 1.6165972 |
| 1130 | 4.524138 | 1 | 5.6614043 | 1 | 1.8726641 | 1 | 5.3381369 | 3.2964043 |
| 1131 | 4.1030279 | 1 | 1 | 1.4608244 | 1.3723426 | 3.283039 | 2.850194 | 1.7886039 |
| 1132 | 0.6514008 | 0.6184504 | 2.0791702 | 0.4365058 | 1 | 0.2654412 | 0.2964836 | 0.5535495 |
| 1133 | 3.4174397 | 1 | 1 | 1 | 1 | 3.8303403 | 2.0041549 | 1.5673099 |
| 1134 | 4.2568433 | 1 | 1 | 1 | 2.4207359 | 3.5245863 | 4.1017281 | 1.8972777 |
| 1135 | 4.1921335 | 3.0315197 | 1.2618952 | 1.741543 | 1.39659 | 4.1960727 | 2.5642742 | 2.3410019 |
| 1136 | 4.1977556 | 4.2713889 | 0.7256392 | 1.2827908 | 1.503017 | 3.9410992 | 4.358367 | 2.3343886 |
| 1137 | 4.323721 | 1 | 1.5377094 | 1.6813243 | 1.8684183 | 4.4430152 | 2.1404831 | 2.4098367 |
| 1138 | 3.4332858 | 1 | 0.8405775 | 1 | 1.4778238 | 1 | 3.2966811 | 1.5836691 |
| 1139 | 2.3725403 | 2.7709801 | 1 | 1.2706472 | 1.6266083 | 2.958498 | 3.0109355 | 1.5925226 |
| 1140 | 1.9262526 | 2.0275447 | 1 | 2.5065935 | 1.5537655 | 2.8957053 | 2.0026412 | 3.8394338 |
| 1141 | 4.1812995 | 3.1889908 | 0.7072826 | 1 | 1.8052845 | 1 | 3.7144619 | 2.2409963 |
| 1142 | 3.6944871 | 1 | 0.7386581 | 1 | 1.6818139 | 1 | 3.6290564 | 1.4057663 |
| 1143 | 0.3311506 | 0.2549877 | 0.7772819 | 0.2765063 | 0.6100486 | 0.5021768 | 0.4070747 | 0.7564594 |
| 1144 | 0.3545207 | 0.2970479 | 0.7305255 | 0.3746036 | 0.6594287 | 0.4549381 | 0.4097081 | 0.7458732 |
| 1145 | 4.5384317 | 1 | 0.404222 | 1 | 1.69926 | 4.1554098 | 4.3526437 | 2.705483 |
| 1146 | 1 | 1 | 0.8960572 | 1.8941334 | 1.304299 | 3.6510709 | 2.6662058 | 1.9689753 |
| 1147 | 4.2413409 | 2.4877718 | 1 | 1.605155 | 1.3674831 | 5.2993378 | 3.4377232 | 2.1778814 |
| 1148 | 6.8676528 | 3.8707094 | 0.6105577 | 1 | 1.3428332 | 6.6943541 | 5.6958983 | 2.5625746 |
| 1149 | 2.7013124 | 1.2490144 | 1.7415071 | 2.9101796 | 0.5737579 | 1 | 2.3000322 | 1.3218388 |
| 1150 | 0.3388963 | 1 | 0.0766846 | 1 | 0.1961122 | 0.2217925 | 0.5643608 | 0.2435832 |
| 1151 | 3.1229659 | 6.7761722 | 0.4909456 | 2.3768931 | 1.4919397 | 7.9396852 | 5.3503441 | 1.4473602 |
| 1152 | 6.6347174 | 1 | 1 | 1 | 2.1272317 | 1 | 6.2352183 | 2.8441625 |
| 1153 | 3.0805505 | 1 | 0.6681423 | 1.341278 | 1 | 1.6979972 | 1 | 1.8532498 |
| 1154 | 3.3525524 | 2.5490889 | 0.6630379 | 1.8845035 | 1 | 1.820885 | 3.3214578 | 1.5108727 |
| 1155 | 2.5855433 | 1 | 0.5578217 | 1 | 1.7437806 | 4.6609912 | 5.1058354 | 2.4754657 |
| 1156 | 0.6777427 | 0.6489672 | 1.8930437 | 0.4561628 | 0.8106983 | 0.3671121 | 0.3065965 | 0.4923505 |
| 1157 | 2.5669526 | 1 | 1.4029815 | 1.8927198 | 1.311875 | 1 | 1.6751372 | 1 |
| 1158 | 0.5386313 | 0.4616877 | 1.3561387 | 0.2361494 | 0.8321387 | 0.3670091 | 0.3462924 | 0.5308014 |
| 1159 | 0.3962375 | 0.3557889 | 1.1994836 | 0.2005734 | 0.7873564 | 0.3662884 | 0.3469177 | 0.5594403 |
| 1160 | 2.6772382 | 0.8209429 | 0.3432405 | 0.317254 | 0.6531204 | 0.8929494 | 0.8175802 | 0.6963869 |
| 1161 | 0.3472352 | 0.2658734 | 0.5969356 | 0.412071 | 0.6567726 | 0.4258138 | 0.3262474 | 1 |
| 1162 | 0.3348322 | 0.385114 | 2.1521029 | 0.0856672 | 1 | 0.5388379 | 0.3292424 | 0.4299738 |
| 1163 | 0.361163 | 0.3932819 | 1.3992062 | 0.2231943 | 0.7486612 | 0.4613835 | 0.3455043 | 0.7700868 |
| 1164 | 5.7042288 | 4.5023999 | 0.7422703 | 1 | 1.3866194 | 5.1863617 | 1 | 3.3842117 |
| 1165 | 1 | 2.4595367 | 1 | 1 | 1.45416 | 4.1820425 | 2.7336397 | 1.6882773 |
| 1166 | 3.5762951 | 2.2082296 | 1 | 2.0278913 | 1 | 6.1968312 | 3.0546393 | 2.2071595 |
| 1167 | 6.3932268 | 13.737121 | 0.857157 | 1 | 2.1112545 | 1 | 8.6409858 | 4.0105304 |
| 1168 | 4.062054 | 5.7705041 | 1 | 1 | 1 | 3.9523426 | 3.3980741 | 2.1930719 |
| 1169 | 0.0377026 | 0.1131293 | 0.0302099 | 1 | 0.0522778 | 0.1800039 | 0.1788975 | 0.3704673 |
| 1170 | 0.2938861 | 0.179366 | 1.1802429 | 0.3048058 | 0.702742 | 1 | 0.2953717 | 0.4320977 |
| 1171 | 0.4848607 | 0.5634045 | 2.1843918 | 0.4101768 | 0.8583681 | 0.291964 | 0.2514888 | 0.5000227 |
| 1172 | 1 | 0.1159815 | 0.5402863 | 0.3610739 | 1 | 1 | 1 | 0.2237201 |
| 1173 | 9.1602748 | 1 | 0.5594665 | 1 | 1 | 1 | 2.8388022 | 4.2101366 |
| 1174 | 7.8921373 | 1 | 0.6418559 | 2.7086427 | 1 | 5.602957 | 5.8466056 | 2.4677675 |
| 1175 | 1 | 3.1864438 | 10.285538 | 1 | 1.5691792 | 1 | 1 | 2.8414145 |
| 1176 | 0.2465472 | 0.21227 | 0.6916484 | 0.2176408 | 0.6333502 | 0.3225161 | 0.2933522 | 0.7001368 |

Table 4

| SEQ ID NO | Patient ID | | | | | | | |
|--------------|------------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|
| | 295 | 296 | 300 | 322 | 339 | 341 | 356 | 360 |
| 1177 | 0.2674388 | 0.2571169 | 0.6783427 | 0.2395277 | 0.5791105 | 0.3576534 | 0.3033069 | 0.667993 |
| 1178 | 1 | 0.5267072 | 0.4502864 | 1 | 0.3913491 | 0.4632643 | 0.3765094 | 1 |
| 1179 | 5.7016284 | 7.3538378 | 1.3497447 | 1 | 1.9228391 | 5.7789317 | 3.5985215 | 1.8080094 |
| 1180 | 4.4421127 | 1 | 0.8545531 | 1.1833973 | 1.2501196 | 4.7563128 | 5.4004695 | 2.1014404 |
| 1181 | 4.6762346 | 1 | 0.7933244 | 1.6256242 | 1.3210206 | 8.0202902 | 5.0966758 | 2.3489765 |
| 1182 | 7.9323738 | 1 | 0.6258509 | 1 | 1.8481853 | 5.9145592 | 6.1848014 | 2.3124155 |
| 1183 | 3.394369 | 4.1647525 | 1 | 1 | 2.1470823 | 4.0562512 | 2.979137 | 1.839814 |
| 1184 | 1 | 6.4565392 | 1 | 1 | 2.6650813 | 6.4535824 | 4.3374545 | 1.8889263 |
| 1185 | 2.7193597 | 5.1564611 | 0.765584 | 1.6681698 | 1.2925576 | 2.3512869 | 2.2586291 | 1.9592525 |
| 1186 | 3.1432033 | 4.8671705 | 0.5874894 | 1 | 1.9775115 | 8.782362 | 7.0547105 | 2.0707148 |
| 1187 | 4.6999484 | 4.9371932 | 0.7611146 | 1 | 1.9224266 | 4.8815138 | 4.5019194 | 3.5773357 |
| 1188 | 2.5663427 | 3.03225 | 0.5846163 | 1.5299325 | 0.733489 | 2.6337373 | 3.142487 | 1.6607955 |
| 1189 | 0.5178893 | 0.6361813 | 1.7140915 | 0.4821617 | 1 | 0.4827926 | 0.28638 | 0.5053858 |
| 1190 | 3.5845286 | 1.3886493 | 0.1873097 | 1 | 1.1504537 | 0.3925435 | 2.4744592 | 0.500343 |
| 1191 | 2.2730998 | 1.9453792 | 1 | 1.9148322 | 0.632656 | 1.4436621 | 3.1888445 | 1.3244302 |
| 1192 | 0.3016262 | 0.2302443 | 0.055552 | 0.5641816 | 0.0994747 | 0.0690596 | 0.1326629 | 0.3842665 |
| 1193 | 0.6106765 | 0.6422999 | 2.0569889 | 0.4176497 | 0.7680692 | 0.304642 | 0.2687155 | 0.5087881 |
| 1194 | 0.4531462 | 0.5417349 | 0.3303449 | 1 | 0.4713152 | 0.1997999 | 0.474262 | 0.6948576 |
| 1195 | 7.5630936 | 6.7621946 | 0.5119239 | 1 | 1.6225436 | 6.6046061 | 5.8960062 | 2.5261883 |
| 1196 | 0.5234449 | 0.4351531 | 1 | 0.287113 | 0.6593986 | 0.3223788 | 0.3539346 | 0.5982203 |
| 1197 | 1 | 1 | 0.1148913 | 2.2647344 | 0.395615 | 0.3674553 | 1 | 0.8134939 |
| 1198 | 0.4464097 | 0.4836225 | 0.9464566 | 0.2742824 | 0.6179566 | 0.3261953 | 0.364305 | 0.6013902 |
| 1199 | 1 | 1 | 1.9341223 | 0.7470699 | 1 | 1 | 1 | 1.3728191 |
| 1200 | 1 | 0.5229576 | 1.1760016 | 0.3531821 | 0.7449889 | 0.4147901 | 0.3314013 | 0.6089462 |
| 1201 | 7.1879418 | 4.6634899 | 0.6987069 | 1 | 1 | 6.5502151 | 5.3474667 | 2.4019635 |
| 1202 | 1 | 3.0237878 | 1.1761412 | 2.5345442 | 1 | 2.2321057 | 2.1237963 | 1.7764646 |
| 1203 | 0.3322374 | 0.5703261 | 0.2429681 | 0.3184385 | 0.4100326 | 0.1328819 | 0.3701051 | 0.2649324 |
| 1204 | 4.4984836 | 5.9161813 | 1.2255205 | 1.8066419 | 1.5319026 | 2.9362103 | 3.2490163 | 1.4810845 |
| 1205 | 4.2683149 | 2.4888182 | 1 | 1.5067307 | 1.2067258 | 1.9623402 | 2.3225961 | 1.5142363 |
| 1206 | 3.4239933 | 2.9538777 | 0.7122653 | 1.7605683 | 1.5606775 | 4.4705676 | 2.9299785 | 1.3902466 |
| 1207 | 9.7811753 | 8.4286602 | 0.4376255 | 1.2855629 | 1.4228295 | 7.6541666 | 4.8641871 | 2.4732001 |
| 1208 | 3.6546222 | 1 | 1 | 1 | 0.6566317 | 4.5447753 | 1.8417511 | 0.7632676 |
| 1209 | 1 | 1 | 0.6360577 | 1 | 1.3271781 | 1 | 1 | 1.5207309 |
| 1210 | 2.4334633 | 2.3499573 | 0.4266194 | 1.5714951 | 0.624758 | 1.6828207 | 1.7131609 | 1.2594349 |
| 1211 | 3.91309 | 6.6653756 | 0.7725682 | 1 | 1.7655127 | 6.2007643 | 4.3139325 | 2.242806 |
| 1212 | 1 | 0.6440803 | 1.7986388 | 0.7390266 | 1 | 0.3391409 | 0.2490932 | 0.5520001 |
| 1213 | 4.2731885 | 5.7305732 | 0.2229934 | 1 | 1.4839712 | 3.3568417 | 6.2186457 | 1.9817758 |
| 1214 | 1 | 4.3654428 | 0.6163261 | 1 | 2.3630452 | 7.0450473 | 2.630064 | 2.1679177 |
| 1215 | 1 | 0.6372786 | 2.2251625 | 0.385849 | 0.7668518 | 0.3540635 | 0.2849684 | 0.5633108 |
| 1216 | 3.6306977 | 4.9404996 | 0.27247 | 1 | 1.4375289 | 4.0006727 | 5.6305857 | 1.6676652 |
| 1217 | 1 | 1 | 1.5833597 | 1 | 1.4445214 | 1 | 3.3021551 | 2.1892784 |
| 1218 | 2.8840867 | 2.3473413 | 0.6712226 | 2.1534054 | 0.7916928 | 1 | 1 | 1 |
| 1219 | 0.2290765 | 0.1550477 | 0.045858 | 0.3132916 | 0.1126649 | 0.0731094 | 0.4931798 | 0.1744241 |
| 1220 | 1 | 1 | 0.8241167 | 1 | 1 | 1 | 1 | 1.2196901 |
| 1221 | 9.0262033 | 2.5894377 | 1 | 1 | 1 | 6.7612378 | 1.7827286 | 1.77514 |
| 1222 | 1 | 1 | 6.4895106 | 1 | 1.5454248 | 1 | 1 | 1.5731789 |
| 1223 | 5.6977085 | 6.18228 | 1 | 3.2853858 | 2.7669003 | 1.5574001 | 3.0804258 | 1.7629645 |
| 1224 | 6.5145903 | 9.8810064 | 0.8942914 | 1 | 1 | 4.7548576 | 5.1581452 | 1.9134714 |
| 1225 | 7.2469685 | 7.1334363 | 0.4723097 | 1 | 2.3223981 | 5.4988151 | 4.5591996 | 1.8321612 |

Table 4

| SEQ ID NO | Patient ID | | | | | | | |
|--------------|------------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|
| | 295 | 296 | 300 | 322 | 339 | 341 | 356 | 360 |
| 1226 | 0.0617657 | 0.0326751 | 0.0795688 | 0.2083887 | 0.0959231 | 1 | 0.3054545 | 0.1258791 |
| 1227 | 0.3131421 | 0.2843274 | 0.4316895 | 0.3155442 | 0.395786 | 0.2097734 | 0.2788724 | 0.3729714 |
| 1228 | 2.7484683 | 1.9361795 | 1 | 1.6739649 | 1.6310554 | 5.9211556 | 2.8392075 | 1.648012 |
| 1229 | 3.4897732 | 4.0605759 | 0.7930704 | 1 | 1.3208496 | 4.7385211 | 3.7137682 | 2.2181767 |
| 1230 | 1 | 5.4731874 | 1 | 3.2201787 | 2.0108341 | 4.5022866 | 1 | 1 |
| 1231 | 1 | 3.9355473 | 0.7967977 | 1.6545944 | 1.2567902 | 3.3103238 | 2.1904647 | 1 |
| 1232 | 1 | 0.7045799 | 0.3784063 | 0.5957219 | 0.3430152 | 0.2421925 | 0.438373 | 0.681381 |
| 1233 | 6.8043291 | 5.9563666 | 0.5656198 | 1 | 1.8966902 | 2.0771146 | 5.0296482 | 1.7829586 |
| 1234 | 1 | 1 | 6.826841 | 1 | 0.8429846 | 4.9963569 | 1 | 5.716783 |
| 1235 | 1.5868351 | 1.3860405 | 0.4023907 | 2.0100427 | 1.3116537 | 1.7259684 | 1.7199765 | 0.6717674 |
| 1236 | 1 | 0.5145644 | 0.2352388 | 0.5217727 | 0.2818534 | 0.3747518 | 0.5765668 | 0.6234779 |
| 1237 | 1 | 1 | 0.5986668 | 1.6985109 | 1 | 1 | 2.5712365 | 1.4869655 |
| 1238 | 1 | 0.4954528 | 1 | 1 | 0.8059193 | 0.1653834 | 0.3325763 | 0.4975346 |
| 1239 | 9.428379 | 1 | 0.4574082 | 1 | 1.2464573 | 6.8357681 | 5.7303642 | 2.1536754 |
| 1240 | 5.2687307 | 3.5884058 | 1 | 1 | 1.8580553 | 3.9784536 | 2.6305858 | 1.4921359 |
| 1241 | 1 | 7.2548606 | 0.5012048 | 1 | 1.7366774 | 6.2806486 | 5.6666844 | 2.3438006 |
| 1242 | 1 | 5.052012 | 1 | 1 | 1.6338725 | 1 | 3.7403101 | 1.9099989 |
| 1243 | 2.8570684 | 3.232686 | 1 | 1 | 1.3943464 | 3.9828054 | 2.9642613 | 2.0159795 |
| 1244 | 5.4076813 | 6.6378672 | 1 | 1 | 1.5532826 | 5.6626746 | 4.2685617 | 1.9915653 |
| 1245 | 1 | 1 | 0.4107412 | 1 | 1.467813 | 5.7102359 | 5.466528 | 1.608121 |
| 1246 | 1 | 1 | 1 | 1 | 2.3899588 | 7.0137608 | 6.322438 | 1.9992109 |
| 1247 | 1 | 2.9772077 | 0.5291756 | 1 | 2.2274308 | 2.3226156 | 2.7162779 | 1.7130075 |
| 1248 | 1 | 4.3517885 | 1.5139529 | 1 | 1.7890961 | 1 | 1 | 2.1350502 |
| 1249 | 1 | 8.349078 | 1 | 1 | 1 | 1 | 6.9209079 | 2.4902626 |
| 1250 | 1 | 0.6060205 | 2.1647193 | 0.4550471 | 1 | 0.3166885 | 0.2803012 | 0.5606858 |
| 1251 | 1 | 0.2673376 | 0.6130994 | 0.2572141 | 0.4518066 | 0.4072601 | 0.3367834 | 0.7737399 |
| 1252 | 1 | 1 | 0.5056969 | 0.6472364 | 0.5849661 | 0.2971396 | 0.4260834 | 0.4536409 |
| 1253 | 1 | 1 | 1 | 1 | 1.9906816 | 3.6309179 | 1 | 1 |
| 1254 | 1 | 6.8087892 | 1 | 1 | 2.590186 | 3.5757375 | 4.0184338 | 2.3805751 |
| 1255 | 1 | 2.1920538 | 1.1094737 | 1.3160386 | 1.8334055 | 5.4977992 | 1 | 2.851056 |
| 1256 | 1 | 2.6537015 | 0.6163815 | 1.5827997 | 1.4894445 | 3.1818829 | 1 | 2.0750121 |
| 1257 | 1 | 0.6214552 | 0.2975977 | 0.4810978 | 0.5071128 | 0.3870385 | 1 | 0.4469691 |
| 1258 | 1 | 2.8336307 | 1.7131201 | 1 | 1.5214893 | 1 | 1 | 1 |
| 1259 | 0.4584634 | 0.3384467 | 1 | 0.319859 | 0.6881131 | 0.260554 | 0.3856094 | 0.5171004 |
| 1260 | 1 | 0.5936634 | 1.6749896 | 0.4362766 | 1 | 0.55989 | 0.2975727 | 0.557581 |
| 1261 | 1 | 0.6321264 | 1.8744414 | 0.3948375 | 0.7280962 | 0.339388 | 0.2722283 | 0.50591 |
| 1262 | 4.2546809 | 2.8346807 | 1 | 1 | 1.4962257 | 2.9577635 | 1 | 1.7923873 |
| 1263 | 1.5807528 | 1.908028 | 0.843691 | 1.3766857 | 1 | 1.3981052 | 1 | 2.0771675 |
| 1264 | 0.3245083 | 0.3234408 | 1.9287677 | 0.0864543 | 1 | 0.5145184 | 0.3222013 | 0.4934853 |
| 1265 | 1 | 0.3753947 | 1.2696658 | 0.3546795 | 1 | 0.4805618 | 0.3661495 | 0.5777832 |
| 1266 | 1 | 0.3315033 | 1.7510134 | 0.1214454 | 0.8648475 | 0.5302852 | 0.323659 | 0.4830757 |
| 1267 | 1 | 7.358979 | 0.3522354 | 1 | 1 | 2.1822313 | 3.1906351 | 1 |
| 1268 | 2.9952151 | 1.9449287 | 1 | 1.6189066 | 1 | 1.7543583 | 1 | 1.8643422 |
| 1269 | 1 | 1 | 1.1834695 | 2.0737973 | 4.7305576 | 6.5626528 | 10.671977 | 3.4080896 |
| 1270 | 3.7601561 | 3.3514397 | 0.4543552 | 1.4170074 | 1.4180706 | 5.364883 | 5.5119814 | 2.7822727 |
| 1271 | 1 | 20.0572 | 4.4088503 | 1.8477933 | 2.4844231 | 1 | 8.4178746 | 3.4143742 |
| 1272 | 0.445772 | 0.4127932 | 0.721255 | 0.2611281 | 0.663423 | 0.3805108 | 0.3136218 | 0.6462919 |
| 1273 | 1 | 3.9179508 | 1 | 1.5358817 | 1.2402999 | 2.6194463 | 2.1593082 | 1.8855778 |
| 1274 | 1 | 0.0476483 | 0.0264725 | 1 | 0.0304451 | 1 | 0.0795878 | 0.641688 |

Table 4

| SEQ ID NO | Patient ID | | | | | | | |
|--------------|------------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|
| | 295 | 296 | 300 | 322 | 339 | 341 | 356 | 360 |
| 1275 | 1 | 0.4723771 | 0.8658835 | 0.7682592 | 0.7332072 | 1 | 1 | 1.5654695 |
| 1276 | 0.4353096 | 0.3440058 | 0.6105117 | 0.274866 | 0.5492389 | 0.2102951 | 0.3252683 | 0.594673 |
| 1277 | 1 | 3.2413807 | 1.1570204 | 1.278231 | 1.475389 | 5.7288788 | 4.5059995 | 3.3992838 |
| 1278 | 4.9564203 | 5.2154128 | 1 | 1 | 1 | 4.4506412 | 3.3270144 | 2.1202005 |
| 1279 | 1 | 7.9078863 | 1 | 1 | 2.8811548 | 7.5891842 | 7.2967268 | 2.2641365 |
| 1280 | 1.8901136 | 0.1257153 | 1.43747 | 0.5654461 | 0.5929748 | 1 | 1.8215918 | 1 |
| 1281 | 9.0210802 | 1 | 0.7119553 | 1 | 1.289338 | 1.9330236 | 3.2216473 | 2.0705861 |
| 1282 | 7.118813 | 7.1569952 | 1.6335072 | 1.1639312 | 1.8536183 | 1 | 4.473564 | 3.104497 |
| 1283 | 1 | 0.6447961 | 1.8519991 | 0.3996811 | 0.7784221 | 0.3517571 | 0.287203 | 0.4868036 |
| 1284 | 1 | 1 | 0.5199062 | 1.1596456 | 1.7572324 | 6.7841364 | 3.8645995 | 2.2040943 |
| 1285 | 5.3433596 | 3.4200745 | 1 | 1.2161923 | 2.1510766 | 3.5034174 | 2.932787 | 1.6319802 |
| 1286 | 5.6799273 | 6.8443637 | 0.6674297 | 1.8687177 | 1 | 3.4530694 | 3.6224461 | 1.4578272 |
| 1287 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 |
| 1288 | 1 | 4.7151494 | 0.6286791 | 1.8726393 | 0.8037561 | 2.3485207 | 1 | 1.5755091 |
| 1289 | 1 | 1 | 1 | 3.1186819 | 1.3393923 | 1 | 1 | 1.8793401 |
| 1290 | 1 | 10.366348 | 1 | 1 | 1.5049789 | 7.2118584 | 4.3298996 | 1.9174344 |
| 1291 | 1 | 7.9026724 | 0.5025493 | 1 | 2.5834752 | 7.2972614 | 3.4155825 | 2.1445753 |
| 1292 | 1 | 1 | 4.0051025 | 1 | 1.4140964 | 1 | 1 | 2.5157642 |
| 1293 | 0.6357542 | 0.5491289 | 2.3789361 | 0.4333341 | 1 | 0.2955128 | 0.3070035 | 0.5029276 |
| 1294 | 3.8257753 | 1 | 0.5186347 | 1.3620927 | 1.502846 | 5.2190211 | 6.9390191 | 1.4976788 |
| 1295 | 0.7346792 | 0.6060387 | 2.409826 | 0.4394076 | 1 | 0.2881201 | 0.3124049 | 0.5289006 |
| 1296 | 1 | 1 | 0.5224603 | 1 | 0.5305955 | 0.2009874 | 1 | 1 |
| 1297 | 1 | 0.7556944 | 0.0916218 | 1 | 0.1949552 | 0.5162207 | 0.6215342 | 0.4029392 |
| 1298 | 1 | 1000 | 0.684463 | 2.5200959 | 1 | 2.5460555 | 1 | 1 |
| 1299 | 1 | 1000 | 1 | 1 | 0.2484504 | 2.4761996 | 1 | 1 |
| 1300 | 1 | 0.5162285 | 2.0674088 | 0.3281336 | 1 | 0.6572709 | 0.232768 | 0.4265328 |
| 1301 | 5.0898597 | 4.1041148 | 0.7036523 | 2.8136607 | 0.449251 | 2.3208035 | 1 | 1.6614579 |
| 1302 | 1 | 2.094817 | 1 | 1 | 1 | 1 | 1 | 1 |
| 1303 | 1.850731 | 0.3197384 | 1 | 0.6180087 | 1 | 0.3992223 | 1 | 0.2493293 |

Table 4

| SEQ ID NO | Patient ID | | | | | | | |
|--------------|------------|-----------|-----------|-----|-----------|-----------|-----------|-----------|
| | 392 | 393 | 413 | 452 | 505 | 517 | 534 | 546 |
| 1 | 1 | 1 | 1 | | 1 | 2.2147482 | 1 | 1 |
| 2 | 0.233066 | 0.6108286 | 0.6187457 | | 1 | 0.3952607 | 0.7199305 | 0.6178858 |
| 3 | 1 | 1 | 1 | | 1 | 1 | 1.5616922 | 1.901404 |
| 4 | 0.2204252 | 0.4557918 | 0.5383118 | | 0.3892502 | 0.1579805 | 0.1572748 | 0.7043966 |
| 5 | 1 | 0.7815453 | 0.4367181 | | 0.3423804 | 1 | 0.8630688 | 0.7006584 |
| 6 | 1 | 1 | 0.4978563 | | 0.3924856 | 1 | 0.8050279 | 1 |
| 7 | 2.1320593 | 1 | 2.119035 | | 1.6690287 | 1.3278055 | 0.4167547 | 1.5451173 |
| 8 | 1.7202424 | 1.8666352 | 1.250723 | | 1.5158514 | 1.3745919 | 2.6167681 | 2.1037934 |
| 9 | 1.1572998 | 0.7798339 | 1.4656255 | | 1 | 0.3694004 | 1 | 1 |
| 10 | 0.2817816 | 0.3403946 | 0.3486104 | | 0.7039875 | 0.6274812 | 0.1727446 | 0.4267268 |
| 11 | 0.4401716 | 1.1379164 | 0.3380667 | | 0.515699 | 0.3050825 | 0.1260463 | 0.6807676 |
| 12 | 1 | 2.0646752 | 2.5298109 | | 2.4944212 | 1 | 1.8535765 | 2.6350653 |
| 13 | 0.6256539 | 0.3450144 | 1 | | 1.5722832 | 0.7128749 | 0.5439145 | 0.4401606 |
| 14 | 1 | 1 | 1.9631365 | | 1 | 1 | 1.7630994 | 2.2152891 |
| 15 | 0.4145033 | 0.6532976 | 1 | | 0.3736269 | 0.7174049 | 0.5942966 | 0.7000905 |
| 16 | 1.145849 | 1.9675398 | 1.523462 | | 2.3174347 | 1.1292997 | 2.0905642 | 3.08271 |
| 17 | 1 | 1.4936544 | 1 | | 1 | 1.8877282 | 1 | 2.7797054 |
| 18 | 1 | 1.4713565 | 1 | | 0.6696347 | 1 | 1.1973226 | 1.588021 |
| 19 | 0.5890999 | 0.7924568 | 0.4955351 | | 1 | 0.1916661 | 0.3332054 | 1 |
| 20 | 1 | 1 | 0.5953324 | | 1 | 1 | 2.4556085 | 2.2752251 |
| 21 | 1 | 1 | 0.2956084 | | 1 | 1.7999217 | 1 | 1 |
| 22 | 1 | 1 | 2.9181458 | | 1 | 1.4698458 | 0.8420409 | 1.5802552 |
| 23 | 1 | 1.6709397 | 1.5818213 | | 1 | 1.1783937 | 1.9584995 | 2.2501314 |
| 24 | 1.2167316 | 1.468824 | 1.2240759 | | 2.1679438 | 1 | 1.624564 | 2.1101821 |
| 25 | 1 | 1 | 0.6346198 | | 0.4592422 | 0.8256968 | 0.689067 | 0.7168759 |
| 26 | 1 | 1 | 1 | | 1 | 1 | 2.2895122 | 2.1778595 |
| 27 | 1 | 0.8433938 | 0.4982717 | | 0.3687768 | 1 | 1 | 1 |
| 28 | 1 | 0.2727094 | 0.6659347 | | 1 | 1.545813 | 1 | 0.3557229 |
| 29 | 1.8682837 | 1.6703066 | 2.7292638 | | 1.6865404 | 2.4063556 | 1.5690438 | 2.110423 |
| 30 | 1.5782166 | 1.2878685 | 3.9761538 | | 3.9047312 | 1.6928398 | 1.4706429 | 4.2684115 |
| 31 | 1 | 0.6123422 | 2.6452181 | | 6.7752199 | 4.8941368 | 11.020045 | 4.9096709 |
| 32 | 0.7657875 | 1.5200479 | 2.3156125 | | 3.6096792 | 1 | 2.2090515 | 3.3782814 |
| 33 | 1 | 1.1967378 | 1.6431981 | | 2.669089 | 1.2275508 | 1.2749883 | 1.7336919 |
| 34 | 1 | 0.6341455 | 2.0907738 | | 3.1309867 | 1.1423421 | 2.2816479 | 2.5561358 |
| 35 | 1 | 0.4970241 | 3.2167931 | | 4.0935032 | 1.3308715 | 2.542052 | 3.3899294 |
| 36 | 1.382993 | 0.5481986 | 2.2382148 | | 2.7443354 | 1.1379838 | 1.6999921 | 2.4454817 |
| 37 | 1.2418987 | 0.5760759 | 2.6546568 | | 3.0680523 | 1.2620492 | 2.1352217 | 2.6382246 |
| 38 | 1.2505935 | 1.4351792 | 1.6419687 | | 3.5257502 | 2.6896202 | 2.1960507 | 1 |
| 39 | 0.4980327 | 0.2472161 | 0.694944 | | 1.1927108 | 0.4665835 | 0.268565 | 0.5028601 |
| 40 | 1.516913 | 1.1496787 | 1 | | 2.3675704 | 1.3273916 | 2.680884 | 3.4025346 |
| 41 | 1.5063345 | 0.7613941 | 3.601916 | | 2.2412441 | 1 | 0.3143828 | 1.6559099 |
| 42 | 1.7306698 | 1.7041096 | 2.3870112 | | 2.4692009 | 1.5497506 | 2.1235544 | 3.4176335 |
| 43 | 1 | 1 | 0.5121699 | | 0.3653294 | 1 | 0.9200511 | 0.6857939 |
| 44 | 1 | 1 | 0.5362959 | | 0.6098951 | 0.5469045 | 1 | 0.7562797 |
| 45 | 0.6557017 | 1 | 1.933732 | | 3.2741478 | 1.8825822 | 1.4877901 | 2.7268867 |
| 46 | 1 | 0.7066484 | 1 | | 1.6854377 | 3.7222912 | 8.5823664 | 1.8826189 |
| 47 | 1 | 1 | 3.1329895 | | 2.3238568 | 2.4071869 | 2.8721937 | 3.4452803 |
| 48 | 1 | 0.7742742 | 1 | | 1 | 0.2975394 | 1 | 1 |
| 49 | 1 | 1 | 1 | | 1 | 1 | 3.2859476 | 3.9127708 |

Table 4

| SEQ ID NO | Patient ID | | | | | | | |
|--------------|------------|-----------|-----------|-----|-----------|-----------|-----------|-----------|
| | 392 | 393 | 413 | 452 | 505 | 517 | 534 | 546 |
| 50 | | 1 | 0.120987 | | 1 | 0.3997625 | 0.1545205 | 0.1273752 |
| 51 | | 1 | 4.872863 | | 1 | 2.4922578 | 1.7283514 | 2.2333296 |
| 52 | | 1 | 0.4928755 | | 0.3743 | 1 | 0.8216094 | 0.7568061 |
| 53 | | 1 | 1 | | 1 | 1 | 1 | 1 |
| 54 | | 1 | 1 | | 1 | 1.5470921 | 1 | 2.9944157 |
| 55 | | 1 | 1 | | 1 | 0.3577917 | 0.6133273 | 1 |
| 56 | 1.3416498 | 1 | 2.1482809 | | 2.4929024 | 1.5886445 | 1.6457742 | 2.2737697 |
| 57 | 0.4460033 | 0.3153762 | 0.3201029 | | 1.3677724 | 0.3852762 | 0.1683643 | 0.3534563 |
| 58 | 1 | 1 | 0.5855249 | | 0.599778 | 1 | 1 | 0.7297651 |
| 59 | 1 | 2.6694793 | 1.5804544 | | 1.4858535 | 1.1497438 | 1.7601835 | 2.1430642 |
| 60 | 1 | 1 | 1 | | 1 | 0.4344076 | 2.7654235 | 2.9763822 |
| 61 | 1 | 1.8687621 | 5.2641062 | | 3.5895737 | 2.4776775 | 1 | 3.7974954 |
| 62 | 0.7101646 | 1 | 2.4421927 | | 1.9400667 | 0.8839991 | 1 | 2.4353003 |
| 63 | 1 | 1 | 1.9684627 | | 2.9434929 | 1.2826596 | 2.0057686 | 1.9842335 |
| 64 | 1 | 1 | 2.2678765 | | 2.8717182 | 1.3784975 | 1.5435982 | 2.1863088 |
| 65 | 1.4183681 | 1.2908462 | 1.8789756 | | 2.6181852 | 1.5074207 | 1 | 1.854364 |
| 66 | 0.8273486 | 0.8292177 | 0.4364271 | | 0.4099169 | 1 | 1 | 0.8107769 |
| 67 | 1.3650211 | 1 | 2.6756118 | | 2.8059599 | 1.5493434 | 2.3814327 | 3.0854888 |
| 68 | 3.0534572 | 1.4133759 | 1.6128288 | | 2.7362438 | 4.1507941 | 3.7333824 | 3.0487446 |
| 69 | 1.2884166 | 0.8333924 | 2.4525632 | | 2.6235143 | 1.2950107 | 1.6257766 | 2.6840428 |
| 70 | 1 | 1 | 1 | | 1 | 2.9337849 | 1 | 2.0062006 |
| 71 | 1 | 1 | 0.5746853 | | 1 | 2.8011717 | 1 | 0.619335 |
| 72 | 0.4771879 | 0.4108596 | 0.3129806 | | 1 | 0.3166069 | 0.24045 | 0.5444905 |
| 73 | 1 | 1 | 1 | | 1 | 1 | 1 | 2.3642785 |
| 74 | 1 | 0.6820158 | 1.6342964 | | 1 | 0.625801 | 1 | 2.3238533 |
| 75 | 1 | 1 | 1 | | 1 | 1 | 1.8379718 | 2.875444 |
| 76 | 1.5756454 | 1.2244074 | 1.8331106 | | 1.7369627 | 1 | 1.773818 | 2.5434733 |
| 77 | 1 | 0.8894835 | 0.4923503 | | 0.4288653 | 1.1358087 | 0.9167192 | 0.7652787 |
| 78 | 1 | 0.8339563 | 0.4776022 | | 0.3531923 | 1.1069104 | 1 | 0.74861 |
| 79 | 1 | 1 | 0.5201878 | | 0.361026 | 1.1376967 | 0.8470595 | 0.7871866 |
| 80 | 1.4815955 | 1.3990613 | 4.2916259 | | 3.017377 | 1.7977267 | 2.0009264 | 4.3625039 |
| 81 | 3.7082365 | 1.677548 | 3.5760927 | | 4.0139466 | 2.0942782 | 4.5198033 | 4.4876976 |
| 82 | 1.6462475 | 2.2578975 | 1.140153 | | 3.2440846 | 1.3685549 | 2.105036 | 1.839563 |
| 83 | 1 | 1 | 3.1834318 | | 2.1480059 | 1.7157247 | 2.0228804 | 3.3044782 |
| 84 | 1.3768558 | 1.2118438 | 1.5788059 | | 1 | 1.3826747 | 1 | 3.1332942 |
| 85 | 0.2098702 | 0.2919208 | 0.4137384 | | 0.3212521 | 0.5331539 | 0.5291131 | 0.3959371 |
| 86 | 1.2310893 | 1.212101 | 2.7228304 | | 2.830954 | 1.2585061 | 1.8925289 | 2.875444 |
| 87 | 2.5690018 | 1 | 2.3076994 | | 2.5269327 | 2.1314296 | 1 | 3.1321261 |
| 88 | 1 | 1.3291899 | 1.5586517 | | 1.9831842 | 1 | 1.5016733 | 2.2700836 |
| 89 | 0.7739249 | 0.8542757 | 2.2871379 | | 2.3802823 | 1 | 2.645147 | 3.1270393 |
| 90 | 1.3293557 | 1 | 1.8522555 | | 2.8655702 | 1.3682373 | 1 | 3.0903379 |
| 91 | 1.4748176 | 1.4821592 | 2.2132179 | | 1.7752853 | 1.226981 | 1 | 2.5348925 |
| 92 | 2.3700426 | 1.5280807 | 1.7692718 | | 4.1038817 | 1.6507357 | 1.1957329 | 2.7969508 |
| 93 | 0.9108634 | 0.8202649 | 0.4138301 | | 0.4303023 | 1 | 0.8720368 | 1 |
| 94 | 1 | 1 | 1 | | 1 | 1 | 2.2472674 | 1.6437172 |
| 95 | 1 | 6.611355 | 2.4868842 | | 1 | 2.6343471 | 6.618101 | 4.7256555 |
| 96 | 1 | 0.7624031 | 1.9729307 | | 2.8643909 | 1.2904327 | 1.4593232 | 2.4212005 |
| 97 | 1 | 1 | 1 | | 1 | 1 | 1 | 2.2205585 |
| 98 | 2.8805798 | 1.8635883 | 2.5485383 | | 1 | 1.9881955 | 1 | 1.7772325 |

Table 4

| SEQ ID NO | Patient ID | | | | | | | |
|--------------|------------|-----------|-----------|-----|-----------|-----------|-----------|-----------|
| | 392 | 393 | 413 | 452 | 505 | 517 | 534 | 546 |
| 99 | 1 | 1 | 0.6108583 | | 0.4005331 | 0.8453558 | 0.7991209 | 0.7293505 |
| 100 | 1 | 0.9076166 | 0.5086976 | | 0.3481571 | 1 | 0.8063656 | 0.7494052 |
| 101 | 2.1309589 | 1.5587378 | 2.2039943 | | 1 | 1.2775293 | 1.7544135 | 2.4229144 |
| 102 | 1.3240598 | 1.3650011 | 1.5810521 | | 1.5643674 | 1.610946 | 1.3945706 | 1.8643518 |
| 103 | 0.4855008 | 0.4754385 | 0.3911822 | | 0.5078276 | 0.5459968 | 1 | 0.5130377 |
| 104 | 1 | 0.7770837 | 0.3635507 | | 0.4122696 | 1 | 0.6533296 | 1 |
| 105 | 1.6474096 | 1 | 2.4023616 | | 2.0908358 | 1.1576439 | 1.5917094 | 4.7764559 |
| 106 | 0.7016473 | 0.7500868 | 2.0691406 | | 3.681468 | 1.4365441 | 2.0646187 | 2.2714785 |
| 107 | 0.3066873 | 1 | 1.6717351 | | 1 | 7.8285198 | 3.8208039 | 1 |
| 108 | 1.880293 | 1.1787828 | 2.0242921 | | 2.3843594 | 1 | 1.7701972 | 3.8911896 |
| 109 | 1 | 1 | 1 | | 1 | 1.2153481 | 1 | 2.2936899 |
| 110 | 2.583655 | 3.3232616 | 4.422422 | | 1.7548303 | 0.8283378 | 1 | 3.2209823 |
| 111 | 1 | 0.8727155 | 1.6563119 | | 2.468763 | 1.1671798 | 2.1517038 | 3.0631946 |
| 112 | 1 | 2.3527181 | 0.6245785 | | 2.5978588 | 1 | 5.1894595 | 1.4653503 |
| 113 | 1 | 1 | 0.4536667 | | 0.391105 | 1 | 0.9469246 | 0.7705875 |
| 114 | 1 | 0.8285945 | 0.3989036 | | 0.3934219 | 1 | 0.8244227 | 1 |
| 115 | 1 | 2.3951376 | 2.3411782 | | 1 | 1.6970372 | 1 | 1.4741621 |
| 116 | 1 | 0.8858628 | 0.5291584 | | 0.4028164 | 0.9500993 | 1 | 0.7473387 |
| 117 | 0.7803097 | 1 | 0.6003727 | | 1 | 1 | 1 | 0.8127591 |
| 118 | 0.4567979 | 0.2946314 | 0.4106842 | | 1 | 0.4070824 | 0.4944038 | 0.4422881 |
| 119 | 0.6772575 | 0.5772235 | 0.513521 | | 0.3706247 | 0.7600248 | 0.7712652 | 0.6324654 |
| 120 | 0.5070563 | 0.4718376 | 0.5589587 | | 0.3736871 | 0.6429381 | 0.7310912 | 0.583896 |
| 121 | 1 | 1.5845872 | 1 | | 1 | 1 | 1.9022924 | 1.8492806 |
| 122 | 0.5185806 | 1 | 0.3139724 | | 0.2610291 | 0.1766857 | 0.3596515 | 0.3853452 |
| 123 | 2.2790729 | 4.4444002 | 3.0895478 | | 1.6461729 | 2.7198718 | 0.3247202 | 4.4336601 |
| 124 | 2.6013727 | 4.1135618 | 1 | | 4.3766481 | 3.9313229 | 9.1179288 | 3.2983457 |
| 125 | 1 | 1.1908319 | 2.2419874 | | 1 | 1.6980145 | 1 | 1.6206865 |
| 126 | 0.3208306 | 0.7423112 | 1.7449018 | | 1 | 8.7169508 | 3.4861671 | 1 |
| 127 | 1 | 0.741223 | 0.5213958 | | 0.3792891 | 1 | 0.8061088 | 0.6846813 |
| 128 | 1 | 0.751541 | 0.5254559 | | 0.3875747 | 1 | 0.8342109 | 0.7259418 |
| 129 | 1 | 1 | 1 | | 1 | 1 | 1 | 1.5029784 |
| 130 | 1 | 1 | 0.7981734 | | 1 | 1 | 1 | 2.0539068 |
| 131 | 1 | 1 | 1 | | 1 | 1 | 1 | 2.3737516 |
| 132 | 1 | 1 | 1.9625221 | | 1 | 2.5404098 | 1 | 2.4015707 |
| 133 | 1.3328381 | 1 | 1.9048647 | | 2.5902212 | 1 | 2.4836745 | 2.7806254 |
| 134 | 1 | 0.8558486 | 0.484225 | | 0.4364983 | 1 | 1 | 0.7797481 |
| 135 | 0.8722746 | 0.8125685 | 0.5001196 | | 0.4643249 | 1 | 0.8393544 | 0.7041014 |
| 136 | 0.2412611 | 0.2349889 | 0.4358226 | | 0.2993434 | 2.1940828 | 0.1461078 | 0.1388276 |
| 137 | 1 | 1 | 1 | | 1 | 1 | 1 | 1.8587274 |
| 138 | 0.7158996 | 1 | 0.6080911 | | 1 | 0.6443432 | 0.2876728 | 1.6498794 |
| 139 | 1.6883189 | 2.1151868 | 2.2062652 | | 1.9721703 | 2.7994327 | 1 | 3.4354191 |
| 140 | 1.5860744 | 5.2002148 | 1 | | 1 | 1 | 1.8719518 | 1.8080375 |
| 141 | 1.368414 | 0.6973592 | 3.2548383 | | 3.1725163 | 1.1723564 | 1.4385231 | 2.7257608 |
| 142 | 1.4106892 | 0.5916766 | 3.9424061 | | 4.311847 | 1.2711738 | 2.2963606 | 3.3521815 |
| 143 | 1.4320094 | 1.3961727 | 2.5345584 | | 1.9774934 | 0.7845827 | 1 | 3.2123617 |
| 144 | 1 | 1.4003573 | 1.8460236 | | 1.9948935 | 1 | 1 | 2.1920648 |
| 145 | 1.6455158 | 1 | 1.9183091 | | 1 | 1.5220567 | 2.2828158 | 2.7601961 |
| 146 | 1.7332125 | 1.7765828 | 1.6189857 | | 2.1704451 | 1.3920654 | 1 | 2.4392854 |
| 147 | 1.3945085 | 1 | 1.1688746 | | 1.5196575 | 1 | 1 | 1 |

Table 4

| SEQ ID | Patient ID | | | | | | | |
|--------|------------|-----------|-----------|-----|-----------|-----------|-----------|-----------|
| NO | 392 | 393 | 413 | 452 | 505 | 517 | 534 | 546 |
| 148 | 0.7695863 | 1 | 1.8237426 | | 2.3783302 | 1.2172587 | 3.1849344 | 1.8906296 |
| 149 | 1 | 0.8780476 | 0.4408232 | | 0.3531905 | 1 | 1 | 0.7325764 |
| 150 | 0.6969419 | 1.6065983 | 0.7377889 | | 1 | 0.7445378 | 0.2842004 | 0.6593303 |
| 151 | 1 | 1.9200948 | 1 | | 1.8967662 | 3.525264 | 1 | 2.6605535 |
| 152 | 1 | 0.8106691 | 1.9780875 | | 2.4403715 | 1 | 1 | 2.2783662 |
| 153 | 1 | 2.1831095 | 1 | | 1 | 1 | 0.5775631 | 1.9388194 |
| 154 | 0.9218053 | 0.7877282 | 2.3375626 | | 1.99833 | 2.126876 | 2.6772822 | 2.2074053 |
| 155 | 1 | 1 | 2.1672139 | | 1 | 1 | 1 | 2.9746579 |
| 156 | 1 | 1 | 2.2952703 | | 1 | 1 | 1 | 2.3457954 |
| 157 | 1 | 1 | 1.9013991 | | 1.5905719 | 0.7478865 | 1 | 2.1835711 |
| 158 | 2.7045258 | 3.1430777 | 1.5147089 | | 1.6737245 | 1.7606078 | 1 | 3.4154864 |
| 159 | 1 | 1 | 0.5473366 | | 0.457215 | 1 | 0.8951483 | 0.7494963 |
| 160 | 1 | 0.8395555 | 0.5591439 | | 0.3798232 | 1.1065269 | 1 | 1 |
| 161 | 1 | 1 | 0.5521109 | | 0.4079683 | 1 | 0.7892155 | 0.7492351 |
| 162 | 0.5713207 | 0.3291961 | 1 | | 1 | 1 | 0.398281 | 0.4855197 |
| 163 | 1.7566672 | 2.2255586 | 1.7384748 | | 2.7395826 | 1.5067096 | 1 | 1.389581 |
| 164 | 2.8659685 | 1.7478646 | 2.1652895 | | 1.7391328 | 1.8114054 | 1 | 1.6888012 |
| 165 | 1 | 0.8212542 | 0.4332609 | | 1 | 1 | 1 | 0.7400202 |
| 166 | 2.6724782 | 2.551965 | 2.9040522 | | 1 | 2.1664886 | 2.134735 | 3.0154212 |
| 167 | 0.3072007 | 0.3206193 | 0.4265664 | | 1 | 1.2852186 | 0.3538014 | 0.5449914 |
| 168 | 1.3676295 | 1.329912 | 3.3853733 | | 2.93431 | 0.4077124 | 0.1526662 | 2.2416174 |
| 169 | 1.3522629 | 1.2281468 | 1.6488768 | | 2.0837001 | 1.0892627 | 1.3158471 | 1.945431 |
| 170 | 1.5302541 | 2.1051261 | 1.4684447 | | 1.5649654 | 1.5734814 | 1 | 1.9703161 |
| 171 | 0.7910854 | 1 | 1.6736155 | | 2.3953551 | 2.1791138 | 1.4683603 | 2.337903 |
| 172 | 1 | 1.4158194 | 2.1851773 | | 2.4678876 | 1 | 1 | 2.2543576 |
| 173 | 1.6750682 | 1.4331908 | 2.0680196 | | 1.9602285 | 1.7634024 | 1.6987587 | 2.237818 |
| 174 | 0.8280825 | 1.1771703 | 2.3548054 | | 2.965187 | 1 | 2.2965859 | 2.9330259 |
| 175 | 1 | 0.6444437 | 1 | | 3.0832743 | 0.6579819 | 1.8255051 | 1.9808313 |
| 176 | 1 | 1 | 2.3947598 | | 1 | 3.3289992 | 1 | 2.4165789 |
| 177 | 0.4870404 | 1 | 0.6790386 | | 1 | 0.478161 | 1 | 0.4125306 |
| 178 | 1 | 1.4306781 | 1.5226957 | | 1 | 1.6939246 | 1 | 1.6914593 |
| 179 | 2.1392393 | 1 | 5.2386621 | | 3.7368106 | 1.8178057 | 2.1985766 | 4.9499033 |
| 180 | 1.3060825 | 1.2103896 | 1.5914274 | | 1.7895263 | 1.3646082 | 2.283261 | 2.3907609 |
| 181 | 1 | 1 | 1.6305022 | | 1 | 1 | 1.8523301 | 1.5750843 |
| 182 | 0.6817304 | 1 | 1.6579385 | | 2.0772946 | 1 | 1.3403077 | 1.658644 |
| 183 | 3.5421997 | 1.9438865 | 2.4170452 | | 1.6141802 | 2.0267262 | 1 | 1.6624032 |
| 184 | 1.5469911 | 1.0624359 | 0.6645283 | | 1.6059491 | 0.4922105 | 0.4605957 | 2.246576 |
| 185 | 1 | 2.2515366 | 2.3209999 | | 2.9872032 | 1.6026607 | 1 | 2.9040864 |
| 186 | 1.2291582 | 1.8122556 | 3.9998861 | | 1.2970897 | 0.6312428 | 1 | 1 |
| 187 | 1.2511765 | 0.6296345 | 2.6422724 | | 2.4068689 | 1 | 1.2765697 | 1.8869624 |
| 188 | 1.4061805 | 0.7460111 | 3.4715873 | | 3.6838062 | 1.212714 | 2.161237 | 3.5789662 |
| 189 | 1 | 1 | 1.5613406 | | 2.7841847 | 1.4194139 | 2.3425383 | 2.0902328 |
| 190 | 1 | 1 | 0.4388729 | | 1.5461233 | 0.2069888 | 0.2338146 | 1.5228903 |
| 191 | 1 | 1.2188478 | 1 | | 1.6223069 | 1.6125387 | 2.5167101 | 1.9877757 |
| 192 | 0.9144168 | 0.8768209 | 0.574896 | | 0.408198 | 1.0655518 | 0.8111775 | 0.7015466 |
| 193 | 1.3460572 | 1.1142236 | 3.3323021 | | 3.220518 | 1.1450552 | 1.5841175 | 4.0686615 |
| 194 | 0.21863 | 0.285728 | 0.3594086 | | 0.4033626 | 0.3414925 | 0.6707298 | 0.4823144 |
| 195 | 0.8715876 | 0.869174 | 0.4517687 | | 0.3907449 | 1 | 1 | 1 |
| 196 | 1 | 1 | 2.6097535 | | 3.3054013 | 1.6643912 | 1 | 1.8805121 |

Table 4

| SEQ ID NO | Patient ID | | | | | | | |
|--------------|------------|-----------|-----------|-----|-----------|-----------|-----------|-----------|
| | 392 | 393 | 413 | 452 | 505 | 517 | 534 | 546 |
| 197 | 1 | 1 | 0.5780645 | | 0.4060334 | 1 | 1 | 0.7596676 |
| 198 | 1 | 1 | 1.7269839 | | 3.4349225 | 1 | 1 | 2.1675418 |
| 199 | 1.5885857 | 1 | 2.9555769 | | 1 | 1 | 0.5145299 | 1 |
| 200 | 1 | 1 | 1 | | 1 | 1 | 1 | 1.7969987 |
| 201 | 1.7249413 | 1.3048442 | 4.7996009 | | 2.5923436 | 3.2019074 | 1.4843006 | 2.7382787 |
| 202 | 1 | 1 | 1 | | 1 | 2.4572659 | 1 | 1.5459961 |
| 203 | 1 | 1 | 1 | | 1 | 2.5121044 | 2.8876908 | 2.0567865 |
| 204 | 2.3059488 | 1 | 2.8749509 | | 2.5792786 | 1 | 1 | 3.0645151 |
| 205 | 1 | 0.7373353 | 0.8915536 | | 1 | 1.3917116 | 1 | 1 |
| 206 | 2.3316417 | 1 | 2.1365694 | | 2.5318044 | 1.3176263 | 1 | 3.8431323 |
| 207 | 1.5824506 | 1 | 2.2791811 | | 2.1044911 | 1.2135395 | 1.6117598 | 2.6279471 |
| 208 | 1 | 1 | 1 | | 1 | 1 | 1 | 2.5531699 |
| 209 | 0.3078023 | 0.2637071 | 0.2398266 | | 1.2276105 | 0.3690021 | 0.2216223 | 0.3001378 |
| 210 | 1 | 1 | 0.5126903 | | 0.4421606 | 1 | 1 | 0.7188778 |
| 211 | 1.3953241 | 1 | 2.8569871 | | 4.1772797 | 1 | 1.920548 | 2.1557614 |
| 212 | 0.4679953 | 0.7057482 | 1 | | 1.5317642 | 0.5618481 | 1 | 1 |
| 213 | 0.8985808 | 0.8311666 | 0.4776308 | | 0.3442057 | 1 | 1 | 0.683987 |
| 214 | 1.3923381 | 1.9129227 | 1.9845265 | | 2.4062864 | 0.8465882 | 2.0266887 | 2.0447729 |
| 215 | 1 | 0.7704062 | 3.8210881 | | 1 | 2.1571608 | 2.0637089 | 2.3520639 |
| 216 | 0.8934134 | 1 | 0.4075366 | | 0.3590629 | 1 | 1 | 0.7596114 |
| 217 | 1.3433958 | 1.8505993 | 2.0698236 | | 1.5625061 | 2.0883446 | 1 | 1.6784956 |
| 218 | 1 | 1 | 1 | | 1.4736785 | 1 | 1 | 3.2826471 |
| 219 | 1 | 1.4319147 | 1.3314754 | | 1.4907864 | 0.7066191 | 1 | 3.4120817 |
| 220 | 1 | 1 | 1.4476683 | | 1.7370928 | 1.6011543 | 1 | 1.741795 |
| 221 | 0.8919585 | 0.8932921 | 0.4664717 | | 0.3682871 | 1 | 1 | 0.7687415 |
| 222 | 1 | 0.9024329 | 0.5218204 | | 0.3962146 | 1 | 1 | 0.7293735 |
| 223 | 0.8393546 | 1 | 0.5492886 | | 0.3427547 | 1 | 1 | 0.6964398 |
| 224 | 0.8572708 | 0.8321361 | 0.5739451 | | 0.4612753 | 1 | 1 | 0.7032281 |
| 225 | 0.7871988 | 1 | 0.6390686 | | 0.5746187 | 1 | 1 | 0.8407518 |
| 226 | 1 | 3.6608665 | 1.9467679 | | 1 | 1 | 1 | 2.8702645 |
| 227 | 1 | 1.3574728 | 1.8856348 | | 1.859371 | 1 | 1 | 2.3769262 |
| 228 | 1 | 1 | 2.3133547 | | 1.6677489 | 1 | 1.654233 | 1.6278229 |
| 229 | 1 | 1.5664244 | 2.019217 | | 2.5587028 | 1 | 1 | 1 |
| 230 | 1.3057489 | 1.4891731 | 3.5003788 | | 3.2753804 | 1.1903055 | 1 | 3.269293 |
| 231 | 1 | 1 | 0.5092257 | | 0.3840398 | 1 | 0.7891091 | 0.7105432 |
| 232 | 1 | 6.2897663 | 1 | | 1000 | 1 | 1 | 1 |
| 233 | 1 | 1 | 0.725911 | | 1 | 1 | 1 | 1 |
| 234 | 1 | 1 | 1 | | 1 | 1 | 1 | 1 |
| 235 | 0.2353685 | 0.4657734 | 1 | | 1 | 1 | 0.2209307 | 0.654915 |
| 236 | 0.5862785 | 0.801558 | 1.9605498 | | 3.8835975 | 1.510748 | 1 | 1.8301645 |
| 237 | 1 | 1 | 1.4995217 | | 2.9592617 | 1.282016 | 1.5392096 | 1 |
| 238 | 0.066853 | 0.1294051 | 0.2762022 | | 0.3929066 | 0.1880075 | 0.1855721 | 0.6101152 |
| 239 | 1 | 0.9011963 | 0.4633254 | | 0.3568538 | 1 | 1 | 0.7334136 |
| 240 | 0.1331924 | 0.8686101 | 0.2754872 | | 1 | 0.3869175 | 0.0905589 | 0.6276121 |
| 241 | 0.1723283 | 1 | 0.3665961 | | 1 | 0.4537628 | 0.1417672 | 0.7015093 |
| 242 | 2.3717181 | 4.6480196 | 2.1369855 | | 3.7519182 | 1.7408167 | 1 | 3.2984634 |
| 243 | 1.3935129 | 0.5997687 | 3.3218367 | | 3.0109809 | 0.8566257 | 1.8197945 | 2.9894758 |
| 244 | 0.6693943 | 0.7517785 | 1.6140446 | | 3.1676073 | 1 | 1 | 2.3752768 |
| 245 | 1.6023381 | 2.0474126 | 1.6550005 | | 1.9435339 | 2.9869415 | 1 | 1.4215127 |

Table 4

| SEQ ID NO | Patient ID | | | | | | | |
|--------------|------------|-----------|-----------|-----|-----------|-----------|-----------|-----------|
| | 392 | 393 | 413 | 452 | 505 | 517 | 534 | 546 |
| 246 | 1.4605315 | 1 | 1.9673599 | | 1.6849481 | 1 | 1 | 1 |
| 247 | 1 | 0.4590959 | 4.6906123 | | 6.446405 | 1.4517796 | 1 | 4.231475 |
| 248 | 1 | 1 | 2.0300497 | | 2.6404338 | 1 | 1 | 2.2700836 |
| 249 | 0.2864378 | 0.7405009 | 0.5432115 | | 0.3018751 | 0.4883972 | 1 | 0.4314683 |
| 250 | 0.6574163 | 0.7348522 | 1.9664785 | | 3.8596925 | 1.4584362 | 2.3628085 | 2.2018308 |
| 251 | 1.3159124 | 0.6833315 | 0.7836879 | | 1.5506357 | 1.1877788 | 1 | 1 |
| 252 | 1 | 2.9834507 | 3.5558143 | | 3.5092182 | 1.8646769 | 1 | 2.563083 |
| 253 | 1 | 1 | 1 | | 1.615529 | 0.7660018 | 1 | 1.8851534 |
| 254 | 0.9497447 | 1 | 0.4322349 | | 0.3576515 | 1 | 1 | 0.7061133 |
| 255 | 0.3635292 | 1 | 0.4268526 | | 1 | 1 | 1 | 1 |
| 256 | 1 | 1 | 1 | | 1 | 2.753875 | 1 | 1 |
| 257 | 1 | 0.8925997 | 0.3758016 | | 0.3248096 | 1 | 1 | 0.7079795 |
| 258 | 1 | 1.2249021 | 1.9569661 | | 1.864002 | 1.6794879 | 1 | 1.9232856 |
| 259 | 2.4612754 | 1 | 1.9529609 | | 2.1865366 | 2.636703 | 1 | 1.810446 |
| 260 | 0.1381461 | 0.1766819 | 0.228833 | | 1 | 0.3443473 | 0.0820705 | 0.1847562 |
| 261 | 0.6825366 | 0.8276943 | 1 | | 2.8505482 | 1.3351366 | 1 | 1.7591679 |
| 262 | 1 | 1 | 1 | | 1000 | 1 | 1 | 1 |
| 263 | 1 | 1 | 1 | | 6.4013459 | 1.3393355 | 0.5410927 | 5.1278725 |
| 264 | 1.8208462 | 2.6620499 | 2.28684 | | 2.1862619 | 1 | 1 | 2.9295859 |
| 265 | 1 | 1 | 0.4615399 | | 0.3407211 | 1 | 0.4793825 | 0.6988517 |
| 266 | 1 | 0.001 | 0.0579426 | | 1 | 0.0616907 | 0.0235556 | 1 |
| 267 | 0.6303081 | 0.7185492 | 2.3603769 | | 4.1409944 | 1.4176289 | 1 | 1.9350442 |
| 268 | 1.8650055 | 1.8733919 | 2.5027653 | | 6.7910854 | 2.4381179 | 1 | 2.8191332 |
| 269 | 1.718095 | 1.4831485 | 3.6097656 | | 6.2647916 | 1.8263375 | 1 | 5.6042475 |
| 270 | 1.5327448 | 1 | 1.7503639 | | 2.2217842 | 1.2868584 | 1 | 3.1627817 |
| 271 | 1 | 0.9202198 | 0.3794203 | | 0.3238018 | 1 | 1 | 0.7226552 |
| 272 | 0.8056181 | 1 | 0.5704395 | | 0.5155844 | 1 | 1 | 0.8578662 |
| 273 | 1.4377437 | 1.203534 | 2.5802228 | | 2.2606072 | 1.3872286 | 2.0259873 | 2.3338884 |
| 274 | 0.2089471 | 0.3910942 | 0.5470364 | | 0.467987 | 0.4465102 | 0.2620759 | 0.5336593 |
| 275 | 1 | 0.8261708 | 0.4850409 | | 0.3693032 | 1 | 1 | 0.7173489 |
| 276 | 1 | 1 | 0.4665237 | | 0.2593503 | 2.1190564 | 0.5554167 | 1 |
| 277 | 1 | 1 | 1 | | 1 | 1 | 1 | 1 |
| 278 | 0.6416976 | 2.12319 | 1.6331715 | | 2.8526511 | 1 | 1 | 2.149844 |
| 279 | 1.338772 | 1.2371293 | 2.2723378 | | 2.7915547 | 2.2765083 | 1 | 2.6669258 |
| 280 | 1 | 0.2386195 | 0.4458696 | | 4.0930217 | 2.2483316 | 1 | 0.4015243 |
| 281 | 1 | 0.7926151 | 0.3940318 | | 0.4365722 | 1 | 1 | 0.7902019 |
| 282 | 0.5180076 | 0.7923282 | 1 | | 2.1281711 | 1.8142349 | 1 | 1.6094534 |
| 283 | 1 | 1.9955358 | 2.2323526 | | 1.9355349 | 1.6040021 | 1 | 3.0178829 |
| 284 | 1 | 1.5111346 | 1.5780396 | | 3.0563314 | 2.3660257 | 1 | 0.8597016 |
| 285 | 0.4591875 | 0.1982478 | 0.5983757 | | 1 | 0.4608112 | 0.1999444 | 0.4465321 |
| 286 | 0.6052856 | 0.884834 | 1 | | 2.1249873 | 1 | 1 | 1.3045699 |
| 287 | 1.8858752 | 1 | 4.134773 | | 2.905403 | 1 | 0.389085 | 2.32216 |
| 288 | 1.5058908 | 1.3344132 | 1.4836325 | | 3.3173745 | 1.8784304 | 1 | 1.5112361 |
| 289 | 1 | 1 | 1.8618404 | | 2.9516066 | 1.3523784 | 1 | 2.6170082 |
| 290 | 1 | 0.8058712 | 2.1193419 | | 2.8303784 | 1.2768909 | 1 | 2.535588 |
| 291 | 1 | 0.717738 | 2.5443282 | | 2.5830117 | 1.3984651 | 1 | 1 |
| 292 | 2.0010708 | 1.4780933 | 1.9394137 | | 2.3939545 | 2.6824672 | 1 | 1.672209 |
| 293 | 1 | 0.7812485 | 0.7792152 | | 0.6132969 | 0.5051656 | 1 | 1.216288 |
| 294 | 1 | 1 | 3.3295217 | | 1 | 1 | 0.5231344 | 1 |

Table 4

| SEQ ID | Patient ID | | | | | | | |
|--------|------------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|
| | 392 | 393 | 413 | 452 | 505 | 517 | 534 | 546 |
| 295 | 1.3592141 | 1 | 2.5819682 | | 3.5395563 | 1 | 1 | 3.3514522 |
| 296 | 1 | 1 | 0.4481365 | | 0.4098083 | 1 | 1 | 0.7769425 |
| 297 | 1 | 0.8403766 | 0.6225323 | 0.5296473 | 0.4917022 | 1 | 1 | 0.671713 |
| 298 | 3.1556909 | 1.6538552 | 3.2289797 | 2.1282697 | 2.0756868 | 1 | 1.3559868 | 2.4419279 |
| 299 | 1 | 1 | 0.5707733 | 0.4676927 | 0.4126136 | 1.1822942 | 1 | 0.6742367 |
| 300 | 1 | 1 | 1.6587216 | 1.2948167 | 2.8024831 | 1.8506117 | 2.3305886 | 1.2633228 |
| 301 | 1 | 0.2381644 | 0.1955894 | 0.6370286 | 0.7438 | 1.2661568 | 0.5519049 | 0.4347707 |
| 302 | 1 | 1.262306 | 1 | 3.6325305 | 3.7988681 | 1 | 1.8201128 | 1.9322123 |
| 303 | 1 | 0.2579496 | 1 | 0.3518887 | 1 | 1 | 0.5772997 | 0.3696239 |
| 304 | 0.1645485 | 0.4513599 | 0.4473441 | 0.4457738 | 0.5398805 | 1.1219652 | 0.7401503 | 0.2330616 |
| 305 | 1 | 3.1824602 | 2.0339063 | 1 | 1.3608551 | 1.5490973 | 1 | 1.5362819 |
| 306 | 0.2607679 | 0.3588641 | 0.2203745 | 0.3264461 | 0.0914081 | 0.2770686 | 0.2286745 | 0.1477724 |
| 307 | 1 | 1.2163549 | 2.6643247 | 2.6867035 | 2.596754 | 3.4560901 | 2.3805247 | 1 |
| 308 | 1 | 1.5969925 | 1 | 0.8446055 | 1.4250419 | 0.5403772 | 1 | 1 |
| 309 | 0.3870741 | 0.1601612 | 0.2492667 | 0.3681598 | 0.3178577 | 0.3823798 | 0.1458221 | 0.2143119 |
| 310 | 1.7818887 | 0.6770102 | 1.3877349 | 0.5923891 | 5.1181639 | 2.1062854 | 0.0500589 | 0.7390438 |
| 311 | 1 | 1 | 0.4946222 | 3.690297 | 0.4772598 | 0.2874326 | 0.7125094 | 1 |
| 312 | 1.9643815 | 1.1783772 | 3.6073923 | 2.507089 | 3.7334006 | 1.6751442 | 1.4628561 | 2.9142511 |
| 313 | 1 | 2.5146501 | 1.4954603 | 1.5533989 | 1 | 1.5337506 | 1 | 1.7019566 |
| 314 | 1 | 0.3222021 | 1.321514 | 1 | 0.5386416 | 0.6971559 | 1 | 0.6776329 |
| 315 | 0.0294433 | 0.1359639 | 0.2261153 | 0.0802827 | 0.2787762 | 0.1272351 | 0.0945797 | 0.5400836 |
| 316 | 1 | 1 | 1.6082492 | 2.8237341 | 2.8682707 | 2.8692971 | 1.3192017 | 1 |
| 317 | 1 | 1.4329237 | 2.2842219 | 1 | 5.5766382 | 2.6238189 | 1.3142776 | 1 |
| 318 | 1 | 11.449688 | 1 | 1.4021563 | 1 | 2.3723153 | 0.0552562 | 1 |
| 319 | 1.4687843 | 1.1568805 | 2.3760285 | 1.955068 | 2.7266171 | 1.425672 | 1.6695967 | 2.1078239 |
| 320 | 0.104726 | 0.0243952 | 0.0554661 | 0.1723281 | 0.3754462 | 0.1296958 | 0.3288255 | 0.2093315 |
| 321 | 1 | 0.7051744 | 0.7111053 | 0.5338514 | 1 | 1 | 0.6224827 | 0.6401627 |
| 322 | 1 | 1 | 1 | 3.1308027 | 3.0583185 | 2.7608813 | 1.2625619 | 1.1922039 |
| 323 | 1 | 1 | 0.6386409 | 0.5237172 | 0.4251976 | 1.2123743 | 0.9384236 | 0.6514757 |
| 324 | 1 | 0.6267458 | 0.683474 | 0.5897305 | 1.3156139 | 0.5952789 | 0.053629 | 1.0959024 |
| 325 | 1 | 0.001 | 1 | 0.3135738 | 0.7052823 | 1 | 0.2009172 | 0.6712008 |
| 326 | 1 | 0.9126915 | 0.6168632 | 0.4902169 | 0.5555827 | 1.3294294 | 1 | 0.7582777 |
| 327 | 1 | 2.0752702 | 1 | 1 | 3.5145933 | 1 | 1 | 2.3395009 |
| 328 | 1 | 0.4976276 | 1 | 0.6117492 | 2.6288334 | 2.195146 | 0.2385642 | 0.6849959 |
| 329 | 0.7150985 | 0.5364758 | 0.4860507 | 0.4628106 | 1 | 1 | 0.7518493 | 0.6568934 |
| 330 | 1.3504937 | 1.2105875 | 1.6957601 | 1.8426028 | 3.7530631 | 1 | 2.2806478 | 1.8467677 |
| 331 | 1 | 2.0569491 | 1 | 2.179228 | 1 | 1 | 1.9833421 | 1 |
| 332 | 1 | 1.4658859 | 1 | 2.2454805 | 2.1153668 | 1 | 1 | 1.818461 |
| 333 | 1 | 2.4712117 | 2.4347422 | 1 | 1 | 2.6440563 | 1 | 1 |
| 334 | 1 | 1 | 0.6227531 | 0.4794037 | 0.3663701 | 1 | 0.8725811 | 0.6540854 |
| 335 | 1 | 0.7539944 | 0.5543456 | 0.7489732 | 0.2188003 | 1.0618356 | 0.652433 | 0.6039631 |
| 336 | 1 | 3.468673 | 1 | 1 | 1 | 1.9491924 | 6.5427429 | 1 |
| 337 | 1 | 1 | 0.7647502 | 0.5378132 | 0.423722 | 1 | 0.9315447 | 1 |
| 338 | 1 | 0.6200782 | 1.4163252 | 0.5839836 | 4.8585352 | 2.2303315 | 0.0619125 | 0.7663892 |
| 339 | 1 | 1.4228926 | 2.2938909 | 1.6770037 | 2.1277559 | 1.2868618 | 1.3126567 | 1.305436 |
| 340 | 1 | 1000 | 1 | 1 | 1000 | 1000 | 1 | 1 |
| 341 | 1 | 2.3515508 | 0.6376019 | 4.185216 | 0.423548 | 1 | 1 | 1 |
| 342 | 1 | 1 | 1 | 1 | 2.4991861 | 1 | 1.6182484 | 1.6711507 |
| 343 | 1 | 2.2361437 | 1 | 1.0821007 | 2.126169 | 1.287682 | 0.2608976 | 1.6538357 |

Table 4

| SEQ ID NO | Patient ID | | | | | | | |
|--------------|------------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|
| | 392 | 393 | 413 | 452 | 505 | 517 | 534 | 546 |
| 344 | 0.5225996 | 0.1827658 | 0.2780375 | 0.7531279 | 1 | 0.5926342 | 1 | 0.6377243 |
| 345 | 1 | 0.2884782 | 0.5403894 | 1 | 1.1462935 | 1 | 0.3312983 | 1 |
| 346 | 1 | 0.7108429 | 0.6300878 | 0.5281767 | 0.3409028 | 1 | 0.8806048 | 0.6043225 |
| 347 | 1 | 0.7481479 | 0.5723697 | 0.4983553 | 0.2906921 | 1.1709183 | 1 | 0.6013694 |
| 348 | 1.943295 | 0.6331661 | 4.6861054 | 1.4844396 | 3.3079246 | 1.7721687 | 2.3501798 | 3.8169432 |
| 349 | 1 | 0.6641992 | 1.4645985 | 1.8456689 | 1 | 4.0654202 | 1 | 1.6780994 |
| 350 | 1 | 0.4064574 | 0.6835059 | 0.6300793 | 0.7855193 | 0.6531088 | 0.6629907 | 0.8178078 |
| 351 | 1 | 2.1013174 | 3.0057691 | 1 | 2.6991452 | 1.3235728 | 1.72883 | 1 |
| 352 | 1 | 1.8055187 | 1 | 1.6788967 | 3.9183049 | 1 | 1 | 1 |
| 353 | 1 | 0.8053766 | 2.4183769 | 3.1052499 | 3.2722189 | 1 | 0.3792691 | 1.4372972 |
| 354 | 1 | 0.5783611 | 1 | 1 | 1.7995763 | 1 | 1 | 1 |
| 355 | 1 | 0.1390999 | 0.3488403 | 1 | 0.5348414 | 0.4801709 | 0.8567764 | 1 |
| 356 | 1 | 1.6463269 | 1 | 1 | 1000 | 1 | 1 | 1 |
| 357 | 0.341755 | 0.2231771 | 0.6952522 | 0.1144915 | 0.5202528 | 0.5638956 | 0.4433055 | 0.2998214 |
| 358 | 1 | 2.0800285 | 0.6678598 | 1.7637873 | 0.382817 | 1 | 1 | 0.5639471 |
| 359 | 1.0623269 | 0.7563488 | 0.6368526 | 0.4797305 | 0.3883295 | 1.2161612 | 1 | 0.7067127 |
| 360 | 0.521027 | 0.5737611 | 0.3884422 | 0.5307254 | 0.6248365 | 0.6942736 | 0.6516159 | 0.271217 |
| 361 | 1 | 0.7473169 | 1 | 1.4408393 | 0.3928536 | 0.5861031 | 1 | 1.5572495 |
| 362 | 1 | 3.4836108 | 1 | 1 | 1000 | 2.0613338 | 1 | 1 |
| 363 | 1 | 1.6883408 | 3.2071567 | 1.2733011 | 1.5910005 | 2.0002076 | 1 | 2.7906167 |
| 364 | 1 | 1.2713577 | 2.2824403 | 1.6889495 | 2.2975774 | 3.2058514 | 1 | 1.7518983 |
| 365 | 1 | 1000 | 1 | 22.921204 | 1 | 1 | 1 | 1 |
| 366 | 1 | 1.6684567 | 4.1462948 | 1 | 4.7182944 | 1.1836203 | 1.7378763 | 3.275434 |
| 367 | 1 | 8.4351948 | 1.805811 | 2.8408959 | 0.3913433 | 0.2357429 | 0.469567 | 4.5122373 |
| 368 | 1 | 1.6817029 | 1 | 1.7333732 | 1.4024978 | 1.6857458 | 1 | 2.3327691 |
| 369 | 1 | 1.8676541 | 0.480375 | 0.7784364 | 0.3240174 | 1 | 0.5696938 | 0.4177726 |
| 370 | 0.7060869 | 0.7782906 | 1 | 0.5823466 | 1 | 0.3555575 | 1 | 1 |
| 371 | 1 | 1.2687065 | 1.739715 | 2.0400286 | 3.0960984 | 1.5287525 | 1 | 1.8383555 |
| 372 | 0.0463251 | 0.3258129 | 0.641647 | 0.0753491 | 1 | 0.0319353 | 0.0669031 | 0.0521309 |
| 373 | 1 | 1 | 1.9825546 | 3.0825775 | 4.0640929 | 2.9069127 | 2.2992921 | 1 |
| 374 | 1 | 4.7129942 | 4.999402 | 2.0744322 | 1.9783695 | 1 | 0.4043578 | 2.8052708 |
| 375 | 1 | 0.3904907 | 2.5492043 | 1 | 3.8263887 | 1.2009295 | 1.2555884 | 2.5107211 |
| 376 | 0.5870126 | 0.9293408 | 2.6796136 | 1.6453382 | 3.5769009 | 2.0793635 | 1.5246022 | 2.3271301 |
| 377 | 1 | 1.2547678 | 0.6916208 | 0.7524698 | 0.5530492 | 0.7514136 | 0.0949307 | 0.9023065 |
| 378 | 1 | 0.3059485 | 0.7821518 | 1 | 0.9262264 | 0.5936538 | 0.3104007 | 0.5460928 |
| 379 | 0.9176057 | 1 | 0.6250988 | 0.486402 | 0.6067192 | 1 | 1 | 0.6153065 |
| 380 | 1 | 0.5684487 | 0.4733098 | 1 | 0.4031895 | 1 | 1 | 0.4848396 |
| 381 | 0.909775 | 0.8261708 | 1 | 0.4906506 | 0.3860327 | 1.1672388 | 0.902854 | 0.7531611 |
| 382 | 1 | 2.0741325 | 3.0518494 | 0.7709985 | 5.1235093 | 1.7431235 | 1 | 2.2818539 |
| 383 | 1 | 0.3467951 | 0.5032243 | 0.7988871 | 0.3823507 | 0.5060043 | 0.3626946 | 0.594809 |
| 384 | 1 | 1.3522298 | 1.856211 | 1 | 2.3285085 | 1.8700979 | 1 | 1.5597989 |
| 385 | 1 | 1.8524888 | 1 | 4.9992389 | 5.0408015 | 1.848082 | 2.2093641 | 1.9941665 |
| 386 | 0.9028582 | 0.7941683 | 1 | 0.5432377 | 0.3902992 | 1.2053372 | 0.8737778 | 0.7913386 |
| 387 | 1 | 0.8428596 | 0.5049233 | 0.4167837 | 0.3363369 | 1.1561312 | 1 | 0.6696251 |
| 388 | 1 | 0.8530589 | 0.6610058 | 1 | 1 | 1 | 1 | 1 |
| 389 | 1 | 2.8838421 | 1 | 1.3213002 | 3.450671 | 1 | 1 | 3.1363778 |
| 390 | 0.3157677 | 0.6624482 | 0.5631106 | 0.4602684 | 0.3234397 | 0.4150126 | 0.4435511 | 0.4235567 |
| 391 | 1 | 0.4776544 | 0.3989308 | 0.6045046 | 0.4977714 | 1.290848 | 1 | 1 |
| 392 | 2.6952912 | 1.4102202 | 3.8430003 | 1.7591408 | 3.3630214 | 1.5239232 | 1 | 4.8834687 |

Table 4

| SEQ ID NO | Patient ID | | | | | | | |
|--------------|------------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|
| | 392 | 393 | 413 | 452 | 505 | 517 | 534 | 546 |
| 393 | 1 | 0.1913229 | 0.6055826 | 1 | 1 | 0.560216 | 0.2292769 | 1 |
| 394 | 1 | 0.8599442 | 0.5809258 | 0.4895898 | 0.3769705 | 1.1065725 | 1 | 0.675676 |
| 395 | 1.3140439 | 2.1717132 | 1.4593882 | 1.5906283 | 2.3718147 | 1 | 1 | 1.7204595 |
| 396 | 1 | 1 | 0.4604674 | 0.2502851 | 0.1537505 | 1 | 0.1205399 | 1 |
| 397 | 1 | 3.5882844 | 3.9869885 | 1 | 1.9840908 | 0.8931138 | 1 | 1.9594133 |
| 398 | 1 | 1 | 1.5887777 | 1 | 4.0526642 | 0.9201354 | 1 | 1.3457538 |
| 399 | 1 | 0.4393008 | 0.4311671 | 0.4950827 | 0.1417859 | 0.3369759 | 1 | 0.3051583 |
| 400 | 1 | 1 | 0.3738746 | 0.3480835 | 0.4973051 | 1 | 1 | 1 |
| 401 | 1 | 0.0916649 | 0.438266 | 1 | 0.3046263 | 0.3306594 | 0.171138 | 0.347942 |
| 402 | 1 | 0.2435559 | 1 | 1 | 1 | 1 | 1 | 1 |
| 403 | 1 | 1 | 0.432203 | 1.04993 | 0.2295747 | 0.5912621 | 0.3121178 | 1 |
| 404 | 1 | 0.329305 | 0.2666712 | 0.7006203 | 0.5660369 | 0.5078594 | 0.2202905 | 0.3459285 |
| 405 | 0.088035 | 0.0962847 | 0.1105014 | 0.450689 | 0.3191453 | 0.346696 | 0.0525506 | 0.253036 |
| 406 | 1 | 1.4547666 | 3.8872432 | 4.536571 | 2.8941139 | 2.9633091 | 1.2762914 | 3.6433021 |
| 407 | 0.2463422 | 0.3127151 | 0.7393921 | 0.4455765 | 0.2443164 | 1 | 0.6846295 | 0.4940985 |
| 408 | 1 | 1.1948978 | 2.1367254 | 1.7612714 | 3.4627121 | 1.2776783 | 2.4337854 | 2.5063634 |
| 409 | 1 | 0.1419193 | 1 | 0.2477363 | 0.3403042 | 0.6886699 | 1 | 1 |
| 410 | 1.9655324 | 2.0706009 | 3.4093009 | 3.9424084 | 4.8655928 | 3.201206 | 1.7181106 | 2.07075 |
| 411 | 0.3051851 | 0.2317639 | 0.5882319 | 0.403515 | 0.310988 | 0.5288557 | 0.2220942 | 0.3842845 |
| 412 | 0.8455557 | 0.8359942 | 0.504491 | 0.5614231 | 0.3347291 | 1.0943994 | 1 | 0.6713714 |
| 413 | 1 | 3.6691861 | 1 | 1.6535283 | 2.7563162 | 3.7968299 | 1 | 1 |
| 414 | 0.0344598 | 0.0915461 | 0.2068453 | 0.1183306 | 0.0232192 | 0.0205134 | 0.2042365 | 0.0561856 |
| 415 | 0.0052672 | 0.0114853 | 0.0462351 | 0.0322964 | 0.0105099 | 0.0088769 | 0.0703725 | 0.0180064 |
| 416 | 1 | 0.5998973 | 1 | 1.5808682 | 3.2886797 | 1.6096869 | 1.8411875 | 1.5802012 |
| 417 | 1 | 1.8025608 | 2.1615044 | 1.8255373 | 3.9909483 | 1.5600669 | 1 | 1.632654 |
| 418 | 1 | 1 | 1 | 1.2324388 | 3.2980203 | 1 | 1 | 1 |
| 419 | 1.9221745 | 1.6903095 | 2.8420039 | 2.9929127 | 1 | 1 | 0.6011551 | 1.3835898 |
| 420 | 1 | 1 | 1 | 6.1928681 | 0.5384537 | 0.2638223 | 0.4809704 | 1 |
| 421 | 1 | 1 | 0.5341683 | 1 | 0.5426577 | 0.5925039 | 0.449057 | 1 |
| 422 | 1 | 1 | 0.4028871 | 1.8941773 | 0.8799342 | 1 | 0.4449418 | 1 |
| 423 | 1.763854 | 1.3041319 | 1.9589749 | 1 | 3.8608625 | 1.6729594 | 1 | 1.1845028 |
| 424 | 1 | 0.532964 | 0.7301979 | 0.6813973 | 0.4255735 | 0.2697402 | 0.2135266 | 0.9347971 |
| 425 | 1 | 2.4219169 | 2.4439603 | 0.5659973 | 1.9369982 | 0.477143 | 1 | 2.5161211 |
| 426 | 1 | 0.3066212 | 0.4849525 | 0.3460422 | 1.0931316 | 1.300706 | 1 | 0.3889323 |
| 427 | 2.2680945 | 1.8251654 | 4.9453301 | 3.8435356 | 3.0169959 | 2.8603666 | 3.7169365 | 3.8782898 |
| 428 | 1 | 0.7785182 | 0.5696326 | 0.4868 | 0.4811784 | 1.0994051 | 0.8433602 | 0.5649813 |
| 429 | 1 | 1.8254226 | 2.7028787 | 1 | 2.9242375 | 1.4004673 | 1.5043748 | 2.0921729 |
| 430 | 1 | 3.4302501 | 1 | 4.9927548 | 4.8686901 | 2.20065 | 0.4005961 | 1.8983577 |
| 431 | 0.4542485 | 0.5504739 | 1 | 0.5255426 | 0.402403 | 0.2878542 | 0.1463613 | 1 |
| 432 | 0.1663482 | 0.0216648 | 0.3183316 | 0.0373459 | 0.4745314 | 0.1413093 | 0.0124537 | 0.0890977 |
| 433 | 1.7855043 | 1.4216857 | 1.761674 | 2.1017484 | 2.5421304 | 3.3403306 | 1 | 2.0434618 |
| 434 | 1 | 1 | 0.5597999 | 0.5429672 | 0.3091574 | 1.2134322 | 0.8596861 | 0.6618849 |
| 435 | 1 | 1 | 1000 | 1 | 1000 | 1 | 1 | 1 |
| 436 | 1 | 1 | 0.6432596 | 1 | 0.2657607 | 0.7272284 | 1 | 1 |
| 437 | 0.6483401 | 0.8110549 | 0.5539783 | 0.518144 | 0.6416106 | 1.0385472 | 0.629592 | 0.6810084 |
| 438 | 1 | 1.8415476 | 1 | 1 | 3.4961976 | 1.4080026 | 1 | 1 |
| 439 | 1.7221465 | 1 | 3.2977536 | 5.4325118 | 3.039004 | 1.277732 | 1.35135 | 3.0801415 |
| 440 | 1.8398507 | 1.7368838 | 2.1526531 | 1.8022097 | 2.1809039 | 1.3470144 | 1 | 2.0743288 |
| 441 | 2.1714763 | 2.1913896 | 2.0125974 | 1.6739579 | 2.0028415 | 1.7604019 | 1 | 1.6276509 |

Table 4

| SEQ ID | Patient ID | | | | | | | |
|--------|------------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|
| NO | 392 | 393 | 413 | 452 | 505 | 517 | 534 | 546 |
| 442 | 1 | 1.1323864 | 0.1891685 | 0.8263674 | 0.3683747 | 0.6919892 | 1 | 0.4105569 |
| 443 | 1 | 1 | 0.680254 | 0.4802234 | 0.3890047 | 1.1298072 | 0.7494968 | 0.672823 |
| 444 | 1 | 0.8273678 | 0.6061262 | 0.6085521 | 0.5013351 | 1.2270464 | 1 | 0.7055527 |
| 445 | 1.3582339 | 1.7779579 | 2.5923372 | 1 | 4.436755 | 0.6200544 | 1 | 1.6346176 |
| 446 | 0.5078911 | 0.5413331 | 0.4467159 | 0.4768188 | 0.3159923 | 0.3493177 | 0.2162539 | 0.5765526 |
| 447 | 1 | 1.5119656 | 1 | 1.8539305 | 2.8823651 | 1.3334692 | 1.4234595 | 1 |
| 448 | 1.633398 | 1.3543666 | 2.2629659 | 2.5127688 | 3.1935966 | 2.2492734 | 1.4487365 | 1.8602614 |
| 449 | 1 | 1 | 2.3186092 | 3.5716645 | 3.0798533 | 2.1453267 | 0.806567 | 2.2143867 |
| 450 | 1 | 0.2376203 | 0.4638836 | 0.4044727 | 0.6564497 | 0.4253153 | 0.2260747 | 0.2919655 |
| 451 | 1 | 1.4785781 | 1 | 1.8351619 | 1.427993 | 2.6368352 | 1 | 1.8138927 |
| 452 | 1 | 1.3635172 | 1 | 1 | 1 | 1.8045333 | 1 | 1 |
| 453 | 0.2547126 | 0.7471487 | 0.5278127 | 0.4129308 | 0.2507476 | 0.3685202 | 0.3225285 | 0.4866215 |
| 454 | 1 | 1 | 1 | 0.7937032 | 2.6950596 | 1.9336618 | 0.5967123 | 1 |
| 455 | 0.8466093 | 0.8443237 | 0.7475137 | 0.5053207 | 0.4487021 | 1.1476299 | 0.858945 | 0.6967653 |
| 456 | 1 | 1 | 0.5310534 | 1 | 0.4857094 | 0.7315365 | 1 | 0.6198792 |
| 457 | 1 | 1 | 0.5520172 | 0.3915611 | 0.3375271 | 1 | 1 | 0.5165619 |
| 458 | 1 | 2.2456109 | 2.1623562 | 1.9014975 | 1 | 1.6728368 | 3.0008447 | 2.7176653 |
| 459 | 1 | 1.4614144 | 1 | 1.8819209 | 1.8680993 | 2.857331 | 1 | 1.4043405 |
| 460 | 1 | 1000 | 1 | 1 | 1 | 1 | 0.1346263 | 1 |
| 461 | 0.8834366 | 1 | 0.555964 | 0.5503047 | 0.3254791 | 1.2468163 | 0.8056442 | 0.7325358 |
| 462 | 1 | 4.0368843 | 3.1038573 | 6.8423293 | 2.8226397 | 7.3786526 | 1.1035367 | 2.2723162 |
| 463 | 1 | 0.8834094 | 4.2344925 | 2.8228814 | 3.8994149 | 0.8345173 | 1.230773 | 4.3110199 |
| 464 | 1.3734209 | 1.1202087 | 2.4602612 | 1 | 3.4569491 | 1.0318244 | 1.4693509 | 3.2847471 |
| 465 | 1 | 1.7462719 | 2.5622245 | 2.0229385 | 2.078791 | 0.9529982 | 1.5833677 | 2.2947719 |
| 466 | 1 | 0.6491922 | 0.2750246 | 2.0836131 | 1 | 1.2375024 | 0.6054492 | 1 |
| 467 | 1.7823916 | 1.8709978 | 2.1873552 | 1 | 3.3889133 | 1.6372987 | 1.7432133 | 2.4396717 |
| 468 | 1 | 1.369067 | 1.8193584 | 2.2071583 | 2.7202763 | 3.1749511 | 1 | 2.3837313 |
| 469 | 1 | 1 | 1.5627025 | 1 | 2.0038368 | 1 | 1.3097746 | 1 |
| 470 | 0.8672783 | 0.7996982 | 0.6125162 | 0.6079528 | 0.4543747 | 1.0721383 | 0.7523324 | 0.6606169 |
| 471 | 0.064286 | 0.6397249 | 0.2902554 | 0.4347829 | 0.1975509 | 0.23989 | 0.0670295 | 0.3108465 |
| 472 | 1 | 0.8906706 | 0.528162 | 0.4449554 | 0.3319938 | 1.1435211 | 1 | 0.6931699 |
| 473 | 1 | 1 | 3.4737852 | 2.0835468 | 3.722494 | 1 | 1.8412599 | 3.596515 |
| 474 | 0.4888702 | 0.4056857 | 0.8755835 | 1 | 1.2401237 | 0.915191 | 0.3462031 | 0.6507738 |
| 475 | 1 | 1.7934497 | 1 | 1 | 3.4454161 | 1.6907745 | 1.4358767 | 1 |
| 476 | 1 | 1 | 2.9459564 | 1 | 3.8117584 | 1.6121399 | 2.9255752 | 3.3758135 |
| 477 | 0.7701661 | 1.245538 | 2.2442226 | 1 | 2.4714846 | 1.8869777 | 1 | 1.5215615 |
| 478 | 1 | 1 | 0.5825912 | 3.2834941 | 0.4349488 | 0.7069603 | 0.3312374 | 1 |
| 479 | 1 | 1.403147 | 2.6732491 | 1 | 3.6337099 | 1.7765918 | 1.2492079 | 2.7934846 |
| 480 | 1 | 1 | 1 | 1 | 0.8035393 | 0.3740625 | 0.1922563 | 1 |
| 481 | 1 | 0.4932946 | 0.5350245 | 1 | 1 | 1 | 1 | 0.4701998 |
| 482 | 1 | 1 | 1 | 2.2351266 | 2.2418333 | 1 | 1.400451 | 3.991692 |
| 483 | 1 | 0.8662161 | 1 | 0.5776584 | 0.3774438 | 1.1419037 | 0.8358712 | 0.7368107 |
| 484 | 0.4826631 | 0.2834231 | 0.4145218 | 0.686422 | 0.4499828 | 0.6922422 | 0.1942246 | 0.4594564 |
| 485 | 1 | 1.7044163 | 3.5028928 | 0.6889803 | 2.583105 | 1.5523322 | 1 | 2.3496719 |
| 486 | 0.0513533 | 0.0441111 | 0.0719252 | 0.0595294 | 0.0292815 | 0.0922795 | 0.0330242 | 0.139881 |
| 487 | 1.959076 | 2.5334659 | 2.8110631 | 2.1285466 | 2.5549372 | 1.6772216 | 1 | 2.1590853 |
| 488 | 1 | 0.8529798 | 0.6000034 | 0.7909117 | 0.4607015 | 1.1617118 | 1 | 0.7728688 |
| 489 | 1 | 1.7756035 | 2.4911183 | 1.8094853 | 2.9187251 | 1.5338042 | 1 | 3.2217683 |
| 490 | 1 | 1.5608351 | 1 | 1.6108317 | 4.5916121 | 1.8797567 | 1.7655588 | 2.2421613 |

Table 4

| SEQ ID | Patient ID | | | | | | | | |
|--------|------------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|
| | NO | 392 | 393 | 413 | 452 | 505 | 517 | 534 | 546 |
| 491 | | 1 | 0.3041283 | 0.5541812 | 0.6710078 | 0.8900404 | 0.6822844 | 1 | 0.6848994 |
| 492 | | 1 | 0.8799074 | 2.3999316 | 2.0132918 | 2.930627 | 1.3472444 | 2.6011432 | 3.1979116 |
| 493 | | 1 | 1 | 1 | 1 | 1.2199531 | 1.5240075 | 0.4601092 | 1.2385206 |
| 494 | | 2.0825919 | 1 | 1.9207014 | 2.1893622 | 3.5840212 | 1 | 1 | 1 |
| 495 | | 0.0499372 | 0.066409 | 0.0656933 | 0.2690935 | 1 | 0.1466139 | 0.3953323 | 0.2599723 |
| 496 | | 0.349268 | 0.4266778 | 1 | 0.4513231 | 0.5723359 | 0.6902491 | 0.400329 | 0.6280983 |
| 497 | | 1 | 1 | 0.5746514 | 0.3584341 | 0.4611887 | 0.5074761 | 0.3837822 | 0.7530322 |
| 498 | | 1 | 1 | 1 | 1.5840059 | 2.307085 | 1 | 1.3712135 | 2.0277694 |
| 499 | | 1 | 1.5705199 | 2.561178 | 1.540273 | 3.0117479 | 1.5473572 | 1 | 1.6206296 |
| 500 | | 1 | 1 | 0.0872628 | 0.2236379 | 0.5105155 | 1 | 3.0852642 | 1 |
| 501 | | 1.2181122 | 1.0564508 | 2.5810572 | 1.4597376 | 2.2615933 | 1.2487173 | 1 | 2.0692201 |
| 502 | | 0.1767746 | 0.2324959 | 0.3910323 | 0.3821896 | 1.498256 | 1 | 0.5743084 | 1 |
| 503 | | 1 | 1.6475635 | 3.1279662 | 1.6235 | 2.9368494 | 1.554011 | 1.5728117 | 2.3421096 |
| 504 | | 1 | 0.8134588 | 1.7835419 | 2.8035317 | 3.2487213 | 1.7119318 | 1.449768 | 1.6368178 |
| 505 | | 0.2681664 | 0.4230077 | 1 | 0.7410264 | 1.4828184 | 0.4679135 | 0.679065 | 1 |
| 506 | | 1 | 1 | 1 | 1.7183079 | 3.946946 | 1 | 1 | 3.4123337 |
| 507 | | 1.3585777 | 1.4168186 | 2.2998402 | 2.0820884 | 2.1633433 | 1 | 1.1280048 | 1.679197 |
| 508 | | 1 | 1.9686378 | 1 | 1.7497804 | 17.473868 | 1.5107995 | 1 | 1 |
| 509 | | 1 | 1.6246028 | 1 | 3.6130763 | 3.7570513 | 1 | 2.1030035 | 1 |
| 510 | | 1 | 1 | 0.4303702 | 0.5223294 | 0.3877936 | 0.2783104 | 0.4398248 | 0.444877 |
| 511 | | 14.999783 | 8.7151851 | 4.1293273 | 5.9334515 | 8.2446783 | 6.502365 | 1 | 3.9339227 |
| 512 | | 1 | 1 | 0.4843078 | 0.4446198 | 1 | 1 | 1 | 0.4231572 |
| 513 | | 0.8417766 | 0.635026 | 0.6417736 | 0.3813678 | 0.1428578 | 1.131486 | 1 | 0.6929931 |
| 514 | | 3.1651811 | 1 | 5.9716686 | 2.3992681 | 3.5883086 | 1.9611279 | 1 | 3.7628617 |
| 515 | | 1 | 1.2148512 | 1.7486206 | 2.1445906 | 1.1649468 | 2.2552833 | 0.7116 | 1 |
| 516 | | 1 | 1 | 2.3649551 | 1.9720953 | 1 | 1 | 1.8505733 | 1 |
| 517 | | 0.3032301 | 0.2640632 | 0.4917931 | 0.3333233 | 0.4981403 | 0.2938794 | 0.16176 | 0.1923998 |
| 518 | | 1 | 4.3803851 | 1 | 3.3321471 | 2.08177 | 7.1185788 | 1 | 1 |
| 519 | | 0.7693768 | 0.6989223 | 1 | 1.6102371 | 0.7127019 | 0.8331835 | 0.4095347 | 0.7371163 |
| 520 | | 1 | 1 | 0.2012579 | 0.1524045 | 0.396459 | 1 | 1 | 0.151661 |
| 521 | | 1 | 2.2351841 | 2.0476163 | 1 | 3.9621123 | 1.6120172 | 1 | 1.6311268 |
| 522 | | 0.3589048 | 1.7632476 | 1.4440012 | 1 | 1.6530505 | 1.1928958 | 1.6467581 | 1.9763835 |
| 523 | | 1 | 1 | 3.5523611 | 1.380708 | 2.7342315 | 2.1905543 | 3.2184243 | 1 |
| 524 | | 0.6957224 | 0.8381804 | 1 | 0.5326174 | 0.4424797 | 1 | 0.7855748 | 1 |
| 525 | | 1.5962151 | 3.9163825 | 4.0790586 | 2.9860843 | 1 | 1.5096343 | 1 | 2.1929491 |
| 526 | | 1.2023817 | 2.3947122 | 2.7560826 | 1 | 4.2756128 | 1 | 1 | 1.8615353 |
| 527 | | 0.6406331 | 1.6343866 | 2.7943311 | 1.6214886 | 1.5487313 | 0.4883502 | 0.8123595 | 1.9994731 |
| 528 | | 1 | 1 | 1 | 2.0780552 | 2.208334 | 1 | 1.5910064 | 1 |
| 529 | | 1 | 1 | 1 | 1 | 1 | 0.5296223 | 0.3916344 | 1 |
| 530 | | 1 | 1 | 0.3544473 | 1 | 1 | 0.5703501 | 0.2905247 | 0.5706184 |
| 531 | | 1 | 1.8123842 | 2.6700781 | 1 | 2.8403117 | 1 | 1.8954014 | 1.965539 |
| 532 | | 1 | 4.7064255 | 1 | 1 | 1 | 1 | 1 | 1 |
| 533 | | 0.2273055 | 0.2566141 | 1 | 0.1675261 | 0.1998408 | 0.1696033 | 0.0931112 | 0.4352027 |
| 534 | | 0.7875511 | 1.5335414 | 1.8474221 | 1.4788709 | 1.8940469 | 1 | 1.7250726 | 2.0855161 |
| 535 | | 1 | 2.0748547 | 0.5612063 | 1 | 1.5103737 | 1 | 1 | 1 |
| 536 | | 1 | 0.8783444 | 0.579461 | 0.528471 | 0.4339396 | 1.168335 | 1 | 0.7256055 |
| 537 | | 1 | 2.7497182 | 0.4993374 | 1 | 0.4382688 | 1 | 1 | 1.6538061 |
| 538 | | 1 | 1.9073334 | 2.4511936 | 3.3230101 | 2.7621627 | 9.2540551 | 1 | 2.7472324 |
| 539 | | 1 | 3.8652575 | 1 | 3.6556638 | 1 | 1.6516412 | 1 | 2.0685711 |

Table 4

| SEQ ID NO | Patient ID | | | | | | | |
|--------------|------------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|
| | 392 | 393 | 413 | 452 | 505 | 517 | 534 | 546 |
| 540 | 1 | 1 | 2.6000148 | 2.321639 | 2.1444882 | 1 | 1 | 1 |
| 541 | 1 | 1.6240389 | 2.033765 | 3.2311281 | 1.8151602 | 1 | 1.7820192 | 1.3888502 |
| 542 | 1 | 2.1660447 | 1.864767 | 1 | 3.3311716 | 1.7488191 | 1 | 2.3213434 |
| 543 | 1 | 0.8432059 | 0.5760504 | 0.4866443 | 0.4688171 | 1.0676615 | 1 | 0.6847573 |
| 544 | 0.1565236 | 0.331788 | 0.224652 | 0.2513155 | 0.5181787 | 0.5542215 | 0.1054357 | 0.320571 |
| 545 | 1 | 1 | 3.3305322 | 1.1799927 | 2.5576099 | 1 | 1 | 1.8614604 |
| 546 | 1 | 1 | 1.8377538 | 2.4381534 | 2.2779358 | 1 | 3.8270488 | 1 |
| 547 | 1 | 1.5638622 | 1.9854241 | 1.9721547 | 2.2393207 | 1.6389391 | 1 | 1.8471369 |
| 548 | 1.5678903 | 1.4029491 | 2.0407146 | 2.7530516 | 1.2870702 | 1 | 1 | 1.4644448 |
| 549 | 1 | 2.1390676 | 2.2972524 | 1.8882744 | 1.8687048 | 1.3955306 | 1 | 1.7406796 |
| 550 | 1 | 2.0251543 | 1 | 1.0839648 | 1.5176819 | 1 | 1 | 1 |
| 551 | 0.0780978 | 0.3395636 | 0.1438335 | 0.4702132 | 0.1497692 | 0.3335494 | 0.4438054 | 0.0160693 |
| 552 | 1 | 2.2446019 | 1 | 1 | 1 | 1 | 1 | 1 |
| 553 | 0.3296215 | 0.4692259 | 1 | 0.4693296 | 0.6460233 | 0.1943098 | 0.3514225 | 0.4659798 |
| 554 | 0.7667063 | 0.8507638 | 0.5400603 | 0.5040518 | 0.2837876 | 1.0651395 | 1 | 0.6583065 |
| 555 | 0.0472287 | 0.0487606 | 0.3320003 | 1 | 0.022032 | 0.0409654 | 0.2306211 | 0.0950272 |
| 556 | 1 | 1 | 1.9986681 | 1 | 2.3185155 | 0.7770553 | 1 | 2.0952085 |
| 557 | 0.3325582 | 0.4954215 | 0.7639317 | 1 | 1.5317642 | 0.4933559 | 0.6528377 | 1.3120708 |
| 558 | 1 | 3.1944698 | 1.8198864 | 1 | 1.6948361 | 2.2567398 | 0.2690101 | 1.7260182 |
| 559 | 1.4340371 | 1.3859339 | 1.9761728 | 1 | 2.788982 | 1 | 1 | 1 |
| 560 | 1 | 5.3550043 | 1 | 1 | 1000 | 1 | 1 | 1 |
| 561 | 1 | 0.6232142 | 1.5666066 | 1 | 2.0484382 | 1 | 1 | 1 |
| 562 | 2.1853119 | 1 | 2.7337682 | 1 | 1.8568907 | 1.803874 | 0.3860172 | 1.6933808 |
| 563 | 1 | 1 | 0.4905373 | 1 | 0.3271839 | 1.099934 | 1 | 0.6905337 |
| 564 | 1 | 2.1577151 | 2.5223968 | 1 | 2.1039822 | 1.7093254 | 1 | 1.8040142 |
| 565 | 1 | 1 | 0.4867298 | 1 | 0.3560014 | 1 | 0.8027716 | 0.756125 |
| 566 | 1.3269239 | 0.6459474 | 1.82117 | 1 | 3.0770042 | 1.4858247 | 2.3460002 | 2.9202365 |
| 567 | 1 | 7.3758356 | 1.4466186 | 1 | 0.4315617 | 3.195886 | 3.2618014 | 0.8015511 |
| 568 | 0.8840768 | 1 | 0.5024553 | 1 | 0.4011379 | 1 | 0.8362219 | 0.7362473 |
| 569 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 |
| 570 | 0.5247171 | 0.4220184 | 0.4324904 | 1 | 0.2135471 | 0.4994731 | 0.4404743 | 0.3891534 |
| 571 | 1 | 1 | 0.506146 | 1 | 0.4570678 | 1 | 1 | 1 |
| 572 | 1 | 0.6744084 | 2.2519944 | 1 | 2.3018763 | 1 | 1 | 2.2737138 |
| 573 | 1.1823848 | 1 | 2.7605025 | 1 | 3.3677764 | 1 | 1.3240693 | 3.1577028 |
| 574 | 1 | 0.7248607 | 1.3138404 | 1 | 1 | 0.6480495 | 0.2313817 | 1 |
| 575 | 1 | 1 | 0.5652934 | 1 | 0.4811641 | 1 | 1 | 0.7577679 |
| 576 | 1 | 0.7144141 | 0.5422988 | 1 | 0.440153 | 1 | 0.5395809 | 0.7356319 |
| 577 | 0.8250849 | 0.5872348 | 0.6786239 | 1 | 1 | 1 | 0.3553168 | 0.6565854 |
| 578 | 1.1991047 | 1.6352472 | 1.9234367 | 1 | 1.6840919 | 1.4270212 | 1.5995929 | 1.7074908 |
| 579 | 0.8336513 | 0.7969283 | 0.5111232 | 1 | 0.4251091 | 1 | 0.8012539 | 0.6882709 |
| 580 | 1 | 0.6879415 | 1.534862 | 1 | 1 | 0.3091801 | 0.7741467 | 0.8352506 |
| 581 | 3.1594987 | 1.3454236 | 1.9933584 | 1 | 2.8553427 | 2.2169932 | 1 | 3.0603545 |
| 582 | 1.4232761 | 0.8825982 | 2.8851551 | 1 | 2.7233961 | 1.8440116 | 1 | 3.3383776 |
| 583 | 1.3754622 | 1 | 2.2375303 | 1 | 2.2123211 | 1.3565736 | 1.8052729 | 3.0521679 |
| 584 | 1 | 1 | 2.4766412 | 1 | 2.0973884 | 1.5948001 | 1.148124 | 1.9027742 |
| 585 | 1 | 2.3881238 | 1 | 1 | 3.623963 | 1.6955425 | 1.7302353 | 1.5272188 |
| 586 | 1 | 1.2850491 | 2.0510607 | 1 | 3.0532477 | 1.6099322 | 3.4465268 | 1 |
| 587 | 0.2556905 | 0.4294873 | 0.3068104 | 1 | 0.8190378 | 1 | 0.354538 | 0.5052463 |
| 588 | 0.2015456 | 1.5887025 | 1.8903854 | 1 | 1 | 1 | 0.2436888 | 1 |

Table 4

| SEQ ID NO | Patient ID | | | | | | | |
|--------------|------------|-----------|-----------|-----|-----------|-----------|-----------|-----------|
| | 392 | 393 | 413 | 452 | 505 | 517 | 534 | 546 |
| 589 | 0.3078253 | 0.5929626 | 0.6908207 | | 0.2027571 | 0.1829339 | 0.2789872 | 0.2498443 |
| 590 | 1 | 1 | 0.437735 | | 0.4139911 | 1.4102794 | 1 | 1 |
| 591 | 0.6921697 | 1 | 0.5165729 | | 0.3916707 | 1 | 0.5441832 | 1 |
| 592 | 1 | 0.9086356 | 0.484233 | | 0.3741028 | 1.2179089 | 0.827994 | 0.8029718 |
| 593 | 4.3120761 | 1.1820473 | 2.2501474 | | 1.6825042 | 0.6257347 | 4.1303301 | 4.3432325 |
| 594 | 0.5060619 | 1 | 0.7461477 | | 1 | 0.649276 | 0.5790915 | 0.6518709 |
| 595 | 1 | 1.3310497 | 1.9097544 | | 3.0591524 | 1.6549834 | 1.1433447 | 2.103171 |
| 596 | 0.8754257 | 0.8191768 | 0.5153085 | | 0.4444789 | 1.1888483 | 0.68928 | 0.754785 |
| 597 | 1 | 3.2554973 | 3.0478232 | | 1 | 1 | 1 | 1 |
| 598 | 1 | 1 | 1.7628768 | | 2.2191632 | 1 | 1.6928023 | 2.3253735 |
| 599 | 1 | 1 | 1 | | 1 | 1 | 2.8115804 | 1 |
| 600 | 1 | 1 | 1.9110847 | | 1 | 4.590834 | 3.0432598 | 1 |
| 601 | 0.771622 | 0.7308556 | 1 | | 1 | 0.3084366 | 1 | 0.712933 |
| 602 | 1 | 1.4216758 | 2.0946149 | | 1 | 1 | 1.5702802 | 2.1466981 |
| 603 | 1.6114539 | 1 | 2.5244277 | | 1.900132 | 1 | 1 | 2.4405093 |
| 604 | 1 | 1 | 1 | | 2.5769867 | 1 | 1 | 2.8292306 |
| 605 | 1 | 1 | 1 | | 0.3643484 | 1.1315933 | 1 | 1 |
| 606 | 1.7757873 | 1.1616982 | 1 | | 1.7583769 | 1.2042564 | 1.6085765 | 2.9028094 |
| 607 | 1.7468059 | 1.3522001 | 2.2644836 | | 2.8473995 | 1.4434871 | 1.2838316 | 2.5471886 |
| 608 | 1.5314985 | 2.2032211 | 2.6712156 | | 1 | 1.9017418 | 0.489019 | 2.3500901 |
| 609 | 0.3603989 | 1.6124547 | 1 | | 1 | 0.3190765 | 0.6162003 | 1 |
| 610 | 0.213347 | 0.5913699 | 0.5021708 | | 0.5474941 | 1 | 0.2809211 | 0.3759418 |
| 611 | 0.4965194 | 1 | 1 | | 1 | 0.5481043 | 0.3644007 | 1 |
| 612 | 0.8946493 | 0.8697181 | 0.5727357 | | 0.3588648 | 1.0907199 | 0.8226703 | 0.704993 |
| 613 | 0.8398076 | 0.855077 | 0.5259943 | | 0.3229858 | 1 | 1 | 0.668337 |
| 614 | 1 | 0.8284659 | 0.5020732 | | 0.3182322 | 1.2449458 | 0.7272141 | 0.5818521 |
| 615 | 0.8499608 | 0.7822773 | 0.5768339 | | 0.4097238 | 1 | 0.6860386 | 0.6960569 |
| 616 | 1.9306438 | 1.225644 | 1.9127503 | | 2.2291847 | 1 | 1.7754993 | 2.6788303 |
| 617 | 0.1519274 | 0.1557491 | 0.296876 | | 0.3581023 | 0.4576262 | 0.2638961 | 0.1802466 |
| 618 | 0.1642791 | 0.1054057 | 0.2793175 | | 0.3274333 | 0.4566296 | 0.2622858 | 0.1633012 |
| 619 | 0.4032312 | 0.836469 | 0.6032026 | | 0.7533237 | 0.7677798 | 0.30498 | 1 |
| 620 | 0.3567366 | 0.38411 | 1.3028241 | | 0.7116024 | 0.4393588 | 0.2583308 | 1 |
| 621 | 0.4475242 | 0.1769589 | 1 | | 2.2203667 | 1 | 1 | 0.7523212 |
| 622 | 0.4216934 | 1 | 1 | | 2.4788744 | 1.546054 | 0.8918835 | 1.713601 |
| 623 | 2.1966248 | 2.5032539 | 2.4432802 | | 4.36923 | 1 | 2.0551954 | 2.8241297 |
| 624 | 2.5433179 | 2.0632111 | 1.9840332 | | 2.1429136 | 1 | 0.6263081 | 2.2879548 |
| 625 | 0.6993528 | 2.1295113 | 2.2613338 | | 2.829918 | 1 | 1.5144699 | 1 |
| 626 | 0.6720848 | 0.693234 | 0.6092939 | | 0.3746304 | 1 | 0.3029783 | 1 |
| 627 | 0.6511874 | 0.6664152 | 1 | | 0.728266 | 0.2155821 | 1 | 0.6643829 |
| 628 | 1 | 0.757437 | 1 | | 1 | 0.2216763 | 1 | 1 |
| 629 | 1 | 0.6396557 | 1.7272897 | | 3.3115346 | 1 | 2.1563109 | 2.2602569 |
| 630 | 12.35652 | 3.4429225 | 2.891522 | | 5.0312154 | 3.9650457 | 1 | 7.3676375 |
| 631 | 0.2112321 | 0.3227363 | 0.4048043 | | 1 | 1 | 0.5377592 | 1 |
| 632 | 0.3549614 | 0.5702492 | 0.4462776 | | 1 | 1 | 0.5854223 | 1 |
| 633 | 1.1483003 | 1.2432825 | 3.1808942 | | 1.7539459 | 1.1997949 | 1.6143713 | 2.7057308 |
| 634 | 1 | 1.7390701 | 1 | | 2.8287679 | 1.4346486 | 1 | 1.3127418 |
| 635 | 0.7179824 | 0.7316668 | 0.8324199 | | 0.699291 | 0.3232313 | 1 | 0.7352632 |
| 636 | 0.6973448 | 0.7709998 | 1 | | 1.7638132 | 1.4384048 | 1.6723393 | 1.471135 |
| 637 | 1.3259405 | 1.3657431 | 2.0388188 | | 2.8029089 | 1.5138734 | 1.7258991 | 1.9959322 |

Table 4

| SEQ ID NO | Patient ID | | | | | | | |
|--------------|------------|-----------|-----------|-----|-----------|-----------|-----------|-----------|
| | 392 | 393 | 413 | 452 | 505 | 517 | 534 | 546 |
| 638 | 0.4561458 | 0.5835943 | 1 | | 0.7254725 | 0.7067303 | 0.5356157 | 0.5481267 |
| 639 | 1.8120866 | 1.4347736 | 2.2777619 | | 3.8188211 | 1.7299538 | 1.3585635 | 2.1390465 |
| 640 | 1 | 1.4291942 | 1.8872157 | | 2.9664508 | 1.2306033 | 1.4721686 | 2.3396786 |
| 641 | 0.1174432 | 0.3861083 | 0.3053739 | | 0.7010166 | 0.4166377 | 0.3439351 | 0.655045 |
| 642 | 1 | 1 | 0.5054262 | | 0.3436585 | 1.1716925 | 1 | 0.7589502 |
| 643 | 0.8808922 | 1 | 0.4778388 | | 0.2794289 | 1 | 0.8956962 | 0.6658956 |
| 644 | 3.5831063 | 1 | 0.3789273 | | 2.5602087 | 1.4984884 | 1 | 1 |
| 645 | 0.3808372 | 1 | 1 | | 2.292475 | 1.447228 | 0.8589371 | 1.7347006 |
| 646 | 0.8504591 | 0.8128752 | 0.5552572 | | 0.3905783 | 1 | 0.8850484 | 0.7012911 |
| 647 | 1 | 0.8256168 | 0.5402065 | | 0.3829663 | 1 | 0.7242506 | 0.6545579 |
| 648 | 1 | 1 | 1 | | 2.6031055 | 1 | 1 | 1.3772599 |
| 649 | 1.5609371 | 1.407747 | 2.3662938 | | 2.1811919 | 1 | 1 | 2.6790633 |
| 650 | 0.7298041 | 1.1645869 | 1.6988447 | | 1.5221501 | 0.87339 | 1.1048384 | 1.4234613 |
| 651 | 1 | 1.6654988 | 1 | | 1 | 1 | 1 | 1 |
| 652 | 2.0954374 | 1 | 2.1315892 | | 4.1306727 | 1 | 1 | 3.2623688 |
| 653 | 0.7528187 | 1.9340533 | 0.3752602 | | 0.185701 | 1 | 0.1915842 | 0.3073514 |
| 654 | 0.2448717 | 0.3933596 | 0.5249124 | | 1 | 1 | 0.1959823 | 0.4530752 |
| 655 | 1.3623534 | 1.1111174 | 1.476347 | | 1.3966736 | 3.8311492 | 1 | 1 |
| 656 | 0.4908057 | 1 | 0.6585167 | | 1 | 1 | 0.2181544 | 1 |
| 657 | 1 | 1 | 0.6882698 | | 1 | 1 | 0.3152346 | 0.8007455 |
| 658 | 1.2102572 | 1.2038902 | 1.7382682 | | 1.7451942 | 1 | 1.351194 | 2.4141802 |
| 659 | 0.1987776 | 0.4404582 | 0.5219321 | | 0.3765314 | 1 | 0.1970113 | 0.4875585 |
| 660 | 1 | 2.4290989 | 1 | | 1 | 1 | 1.9699513 | 1 |
| 661 | 0.3864721 | 1 | 0.4371269 | | 0.5034928 | 1 | 0.2773523 | 1 |
| 662 | 1 | 1 | 1 | | 1 | 1 | 1 | 1 |
| 663 | 1 | 1 | 0.1631044 | | 1 | 1 | 1 | 1 |
| 664 | 1.6140463 | 1.2944273 | 3.9144558 | | 2.5010541 | 1.3153935 | 2.600421 | 4.9709362 |
| 665 | 2.2843103 | 4.040505 | 1 | | 1.7659613 | 3.0045198 | 0.1482947 | 2.1847066 |
| 666 | 2.4257377 | 1.3899503 | 1.5672498 | | 1.9326864 | 1.4734216 | 1 | 2.1342057 |
| 667 | 3.8555325 | 3.073414 | 2.1688201 | | 1 | 2.7146189 | 3.0613638 | 1.252808 |
| 668 | 1.6880269 | 3.0798739 | 2.6237933 | | 1 | 1.384285 | 1 | 1.8898177 |
| 669 | 2.223145 | 1.8627771 | 1 | | 1 | 1 | 1 | 2.4125416 |
| 670 | 1 | 2.9588973 | 1 | | 1.5834793 | 1 | 1 | 1 |
| 671 | 1 | 0.6870413 | 0.3097691 | | 1.9875449 | 1.5425584 | 0.4621092 | 1 |
| 672 | 2.0585512 | 2.5532214 | 1.8611694 | | 2.1905279 | 1.4416857 | 1 | 2.0306208 |
| 673 | 2.1472407 | 2.2447503 | 2.9450669 | | 1.9500136 | 1 | 1 | 2.2387938 |
| 674 | 5.2454533 | 3.1241928 | 1 | | 0.558979 | 1.5439306 | 0.4582833 | 1 |
| 675 | 4.879924 | 3.1896125 | 2.0964156 | | 1 | 1 | 4.0136861 | 2.3790065 |
| 676 | 1.1609292 | 1.6094671 | 2.2307643 | | 1.4253325 | 1 | 0.4811458 | 2.0226658 |
| 677 | 1 | 1 | 1 | | 2.6622489 | 1.9928255 | 2.2227345 | 3.7382051 |
| 678 | 0.7883607 | 1 | 0.5680698 | | 0.3212684 | 1.0650245 | 0.8600809 | 0.6646791 |
| 679 | 1.7015382 | 2.0585814 | 1.5971019 | | 1.4442012 | 1 | 0.4157225 | 1.7684924 |
| 680 | 1 | 1 | 1 | | 4.9489359 | 1 | 1 | 1 |
| 681 | 2.9803844 | 1 | 1 | | 1 | 1 | 2.3329107 | 1 |
| 682 | 0.2016804 | 0.3794703 | 1 | | 0.1965226 | 0.1328157 | 0.1915458 | 0.2588612 |
| 683 | 1.6497894 | 1 | 1 | | 3.3218076 | 1.9923426 | 1 | 2.1154953 |
| 684 | 0.3869694 | 0.2816127 | 0.6601012 | | 1 | 1 | 0.5042417 | 0.4037379 |
| 685 | 0.3531677 | 0.4162906 | 1 | | 1 | 0.5766513 | 0.3955928 | 0.7355851 |
| 686 | 0.28481 | 0.4131942 | 0.5961733 | | 1 | 1 | 0.7556587 | 1 |

Table 4

| SEQ ID NO | Patient ID | | | | | | | |
|--------------|------------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|
| | 392 | 393 | 413 | 452 | 505 | 517 | 534 | 546 |
| 687 | 0.1068421 | 1 | 1 | | 1 | 2.4545835 | 0.001 | 1 |
| 688 | 1 | 0.8896714 | 0.6810456 | | 0.493497 | 1 | 0.8394221 | 0.6928944 |
| 689 | 0.7495964 | 0.6004315 | 0.8123016 | | 1.3656791 | 0.2352063 | 0.5888489 | 1 |
| 690 | 1 | 2.5592262 | 1 | | 1 | 1 | 1 | 1 |
| 691 | 1 | 1 | 1000 | | 1 | 1 | 1 | 1 |
| 692 | 1 | 0.6762286 | 1 | | 1.5149936 | 1.3967724 | 1 | 2.1085933 |
| 693 | 0.8402743 | 0.8090665 | 0.5550887 | | 0.4240136 | 1 | 0.8104475 | 0.8053859 |
| 694 | 1 | 1.5758323 | 2.2015071 | | 1.8387402 | 1 | 1 | 2.0732585 |
| 695 | 1.3644486 | 1.4443991 | 2.0283143 | | 1 | 1 | 2.3093267 | 1 |
| 696 | 0.1542138 | 0.061532 | 0.2297415 | | 0.7498501 | 0.456461 | 0.0315165 | 0.070319 |
| 697 | 1.4383216 | 2.756178 | 1 | | 0.6731839 | 2.3478311 | 0.8717851 | 1 |
| 698 | 1.311812 | 1.4456753 | 1.4045646 | | 2.1894254 | 1.8686567 | 1.4717984 | 1.9736823 |
| 699 | 1 | 1 | 0.505866 | | 0.3213455 | 1.0955723 | 1 | 0.6915309 |
| 700 | 1 | 3.4261249 | 1.3658846 | | 1 | 1 | 1.7013818 | 1 |
| 701 | 1 | 1 | 0.4643719 | | 0.3093195 | 1.1584922 | 0.7953141 | 0.6450552 |
| 702 | 3.5569878 | 1 | 1.5678656 | | 2.8763466 | 1.4583355 | 1 | 1.5748696 |
| 703 | 0.7706028 | 0.8389323 | 0.4578904 | | 1 | 1.2536157 | 0.6981533 | 0.7873006 |
| 704 | 2.3225617 | 1.4806852 | 2.5436647 | | 2.5352165 | 1.1465184 | 2.5555079 | 4.0697365 |
| 705 | 0.8479601 | 0.6035081 | 1 | | 1.193877 | 0.2665283 | 1 | 1 |
| 706 | 0.9317015 | 1 | 0.5456221 | | 0.2870344 | 1 | 1 | 0.7411894 |
| 707 | 1 | 1 | 0.5396918 | | 0.3011632 | 1.133801 | 1 | 0.6995288 |
| 708 | 1 | 0.3373674 | 1 | | 1 | 1 | 0.2610998 | 1 |
| 709 | 1 | 0.6829358 | 2.6291366 | | 3.424613 | 1 | 1.2012693 | 3.6849938 |
| 710 | 2.1235821 | 1.6075776 | 2.9565722 | | 6.2138947 | 2.3409014 | 1.373526 | 2.5669985 |
| 711 | 1 | 1.7525834 | 1.3612886 | | 1 | 1.3779915 | 0.9129483 | 1 |
| 712 | 1 | 2.3982637 | 1 | | 1 | 1 | 1 | 1.7595363 |
| 713 | 2.1830899 | 1.7270506 | 1 | | 3.5923527 | 2.1206432 | 0.5435736 | 2.0627543 |
| 714 | 1 | 1 | 1 | | 1 | 1 | 1 | 1 |
| 715 | 0.8223104 | 1 | 0.4769199 | | 0.2870782 | 1 | 0.7867361 | 0.6760517 |
| 716 | 1 | 1 | 0.3319864 | | 1 | 1 | 1 | 1 |
| 717 | 0.7411916 | 0.8303851 | 0.4895717 | 0.5006123 | 0.3650191 | 1 | 0.7365937 | 0.6767943 |
| 718 | 1.5077308 | 0.6700557 | 1.6371918 | 1 | 2.435078 | 0.7979596 | 1 | 2.0577482 |
| 719 | 18.238778 | 8.3950803 | 2.8865781 | 5.6374946 | 7.5001977 | 6.1764046 | 1 | 3.3279192 |
| 720 | 17.931092 | 9.8917025 | 2.2560455 | 5.4651776 | 5.1806352 | 5.4141671 | 1 | 2.5520419 |
| 721 | 1.5273368 | 1 | 4.4403166 | 1.7344298 | 3.6408346 | 0.8340727 | 1 | 2.762176 |
| 722 | 1 | 0.6417628 | 3.1552852 | 2.5684919 | 3.2437822 | 1.4019161 | 1.654876 | 3.9637865 |
| 723 | 1 | 1.705554 | 2.5747741 | 1.9083735 | 1.3337006 | 0.6092304 | 1 | 2.6153049 |
| 724 | 1 | 1.9243684 | 1.3899761 | 1.6353877 | 4.7487094 | 0.7752002 | 1.2010382 | 1.4709243 |
| 725 | 0.3821455 | 0.3607041 | 0.3466214 | 0.2861968 | 0.3895923 | 0.3033695 | 0.5952182 | 0.3145537 |
| 726 | 1 | 5.0311205 | 2.9844132 | 2.8471997 | 0.5043575 | 2.2092049 | 0.3582497 | 1.7201393 |
| 727 | 1 | 1.5815601 | 1.5491627 | 1.7986927 | 1.7902627 | 1 | 1.8709048 | 1.939267 |
| 728 | 0.4747464 | 1.3033207 | 0.7204601 | 0.6335441 | 0.4455344 | 2.8849121 | 0.4522946 | 0.4027983 |
| 729 | 0.5744789 | 1.4162547 | 0.657417 | 0.6122242 | 0.4728835 | 2.2317497 | 0.6462698 | 0.4791363 |
| 730 | 0.1759149 | 0.2265109 | 0.311933 | 1.2186 | 0.8461715 | 8.5052785 | 0.6866472 | 0.4000279 |
| 731 | 0.4479593 | 1 | 1 | 1.3468354 | 1 | 3.420552 | 0.5317023 | 0.2464655 |
| 732 | 1.6532193 | 2.1663019 | 1.5384932 | 1.8793807 | 1.9276015 | 1.6690346 | 2.2876109 | 3.305069 |
| 733 | 3.9162939 | 2.2546627 | 1 | 1.7794224 | 2.2031475 | 0.0861393 | 4.0956518 | 1.2045414 |
| 734 | 1.1875907 | 0.4828876 | 2.1446597 | 1.9716199 | 3.5375773 | 1.3829129 | 2.3492955 | 2.5890031 |
| 735 | 0.3058886 | 0.3366156 | 0.5385363 | 1 | 1.7542111 | 0.7055651 | 0.5231461 | 0.3960135 |

Table 4

| SEQ ID NO | Patient ID | | | | | | | |
|--------------|------------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|
| | 392 | 393 | 413 | 452 | 505 | 517 | 534 | 546 |
| 736 | 2.0018918 | 3.3606556 | 1.7138688 | 4.7150398 | 1.4600762 | 1.8230689 | 2.1445599 | 1.4630538 |
| 737 | 0.2194438 | 4.4009321 | 1.4966075 | 1.3632205 | 1.3389088 | 0.3649557 | 0.1472849 | 1 |
| 738 | 2.3985309 | 1 | 3.1150912 | 5.2023243 | 3.5561943 | 2.4340854 | 2.2432843 | 4.2788854 |
| 739 | 0.5477328 | 1 | 0.6586501 | 1 | 1 | 0.6584901 | 0.6472345 | 0.4140999 |
| 740 | 2.5925149 | 2.1821499 | 1.8065913 | 1.6762734 | 1 | 2.7161904 | 1 | 2.6730194 |
| 741 | 1.6697013 | 1 | 1 | 2.4797286 | 2.4142993 | 2.6979997 | 1.4581645 | 1.9476038 |
| 742 | 2.5292962 | 1.4350605 | 2.1013835 | 1.4666735 | 2.3364161 | 1 | 2.6656999 | 3.682938 |
| 743 | 0.046754 | 1 | 0.0878287 | 0.4683924 | 0.2353855 | 0.1480627 | 1 | 0.1030335 |
| 744 | 1.3193733 | 1.7278618 | 1.7698069 | 3.5275746 | 1.6304014 | 2.3673863 | 1.3921868 | 1.2558382 |
| 745 | 1.6298518 | 1 | 1.8300154 | 1.8969226 | 2.6297591 | 1.5239998 | 2.2073334 | 2.402757 |
| 746 | 0.0055733 | 0.0560218 | 0.0873693 | 0.0488687 | 0.0152466 | 0.1212482 | 0.5558815 | 0.0544671 |
| 747 | 1 | 1.0861781 | 2.397965 | 1.7456263 | 3.2724545 | 1.2016347 | 1 | 2.2816285 |
| 748 | 0.4150096 | 0.5221316 | 0.6267276 | 1 | 0.493102 | 1.5896411 | 0.1404774 | 0.2901288 |
| 749 | 0.0175625 | 1 | 0.0502156 | 0.0696339 | 0.1782898 | 0.0445223 | 1 | 0.0424618 |
| 750 | 0.3349603 | 1 | 0.3210405 | 0.2999745 | 0.4366188 | 0.2758727 | 0.1312039 | 0.3725502 |
| 751 | 2.5048637 | 1.790482 | 2.5370488 | 2.5050736 | 3.6669214 | 1.7336103 | 1 | 2.9080156 |
| 752 | 1 | 1 | 1 | 4.1697488 | 0.5668917 | 0.1946165 | 16.878602 | 1 |
| 753 | 2.0952329 | 2.0496385 | 2.6534532 | 3.868529 | 4.6469378 | 3.0485209 | 1.6343442 | 1.918216 |
| 754 | 1 | 1 | 0.5148431 | 0.5842391 | 0.3590185 | 1 | 1 | 0.6552401 |
| 755 | 0.0143326 | 0.0598799 | 0.1127471 | 0.1152653 | 0.0224096 | 0.0554766 | 0.1479111 | 0.0615376 |
| 756 | 1 | 1 | 1 | 4.4730032 | 0.4673868 | 0.001 | 17.00733 | 1 |
| 757 | 1.6885048 | 1.1171716 | 1.6256412 | 2.7686595 | 2.3671678 | 0.8151231 | 1.5472192 | 2.7467425 |
| 758 | 2.86704 | 1 | 2.3744219 | 1.5697195 | 2.9773638 | 1.2024779 | 1.3441355 | 2.188535 |
| 759 | 1.6032235 | 1 | 1 | 1 | 2.0383598 | 1 | 1.355712 | 1.557827 |
| 760 | 1.498199 | 0.469315 | 4.1695321 | 1 | 4.0400415 | 1.3927556 | 2.1034286 | 2.5659294 |
| 761 | 1.379049 | 0.5423619 | 2.8604314 | 2.0860707 | 2.5487708 | 1.4057719 | 1 | 2.5214756 |
| 762 | 1.2976206 | 2.8073525 | 1.3909671 | 1.9291326 | 0.7569201 | 2.1815547 | 1.2990744 | 1 |
| 763 | 0.1233318 | 1 | 0.4165002 | 1 | 1.4072064 | 0.3276468 | 0.3119816 | 0.3943979 |
| 764 | 1.8651027 | 3.8152504 | 1 | 0.6000645 | 1.7182668 | 2.0282027 | 0.2499136 | 1.6090051 |
| 765 | 1 | 1 | 1 | 1 | 1 | 1.7316709 | 1 | 1 |
| 766 | 1 | 1 | 1.55915 | 2.0791116 | 2.47438 | 1.3343661 | 2.5076807 | 2.3860083 |
| 767 | 2.1108468 | 1.0840413 | 2.5831837 | 2.5181836 | 2.3332049 | 1.3918894 | 2.1533859 | 2.6902933 |
| 768 | 1.3995078 | 1.2873244 | 1 | 1.588736 | 3.6145531 | 1 | 2.3287922 | 2.3273645 |
| 769 | 1 | 1 | 2.0803692 | 2.4059722 | 2.8695871 | 1.3485552 | 1.430744 | 2.2609204 |
| 770 | 1 | 1 | 1.4041153 | 0.6520985 | 1.2027066 | 0.2510129 | 0.5123177 | 1 |
| 771 | 8.892764 | 1 | 1 | 1 | 1 | 2.6266092 | 2.9813581 | 1 |
| 772 | 1 | 1 | 2.7306221 | 1 | 3.7057733 | 1.6683064 | 1 | 2.8979852 |
| 773 | 0.7298388 | 1 | 1 | 0.3675374 | 1 | 0.485008 | 1 | 0.6263913 |
| 774 | 1.7598926 | 1 | 1 | 0.1953708 | 1 | 0.7118586 | 1 | 0.7510007 |
| 775 | 2.616016 | 1 | 1 | 2.9274419 | 3.8242766 | 1.9716146 | 3.4972318 | 3.6456016 |
| 776 | 1.3704579 | 1 | 1.9256306 | 2.2261545 | 2.7391513 | 1.3566655 | 2.5481381 | 3.0593414 |
| 777 | 1 | 1 | 0.5586066 | 0.5793153 | 0.3953931 | 1 | 0.8901543 | 0.6846458 |
| 778 | 4.6828112 | 1 | 1 | 11.093412 | 6.3372334 | 3.0065666 | 6.2753343 | 2.1381558 |
| 779 | 0.7593148 | 0.474934 | 1 | 1.6238223 | 2.7801811 | 1.1424709 | 1.098064 | 1.9166645 |
| 780 | 0.0771927 | 1 | 0.2718901 | 0.5265109 | 0.3775404 | 0.396293 | 0.2467226 | 0.11592 |
| 781 | 1 | 1 | 3.6534812 | 5.1257176 | 2.8734966 | 3.3188897 | 3.5850475 | 4.210654 |
| 782 | 0.0435023 | 1 | 0.5165729 | 0.0390744 | 0.0329749 | 0.0368949 | 0.1906723 | 0.134062 |
| 783 | 2.460542 | 1.2534521 | 3.2757276 | 4.0795485 | 3.6188756 | 3.0789997 | 1.2944243 | 3.4492664 |
| 784 | 0.7902759 | 1.2369513 | 2.8944774 | 1 | 2.9308504 | 1.2538457 | 2.0154802 | 2.7719518 |

Table 4

| SEQ ID NO | Patient ID | | | | | | | |
|--------------|------------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|
| | 392 | 393 | 413 | 452 | 505 | 517 | 534 | 546 |
| 785 | 0.1269542 | 1 | 0.3478934 | 0.0892982 | 0.5132992 | 0.1131072 | 1 | 0.0780113 |
| 786 | 1.2261819 | 1.6126327 | 2.3952825 | 1.5920601 | 2.8988686 | 1.8312865 | 1 | 1.8205745 |
| 787 | 0.7573756 | 1.2484267 | 1.9981677 | 1.8968677 | 1.7175884 | 1 | 1 | 1.7783953 |
| 788 | 4.118524 | 3.8978833 | 1 | 1.5870407 | 1 | 1.5947234 | 1 | 2.434787 |
| 789 | 0.027289 | 1 | 0.0922157 | 0.0773622 | 0.0502925 | 0.0246069 | 1 | 0.0771007 |
| 790 | 1.6091833 | 1.3199898 | 1.5802552 | 2.5888139 | 2.587525 | 2.3467273 | 2.234134 | 1.6615066 |
| 791 | 0.4136472 | 1.4499291 | 1.3586972 | 1 | 2.9697416 | 1.2378781 | 1 | 1.6172265 |
| 792 | 1.4389192 | 0.732755 | 0.8149181 | 0.5130258 | 0.501483 | 0.571109 | 1 | 0.7975324 |
| 793 | 0.0909437 | 0.175564 | 0.3449476 | 0.2297754 | 0.6322726 | 0.1142264 | 0.1680022 | 0.6427762 |
| 794 | 2.6494595 | 1.2745135 | 3.4440761 | 2.003246 | 3.1787465 | 1 | 1 | 3.1834813 |
| 795 | 0.5084588 | 1.4047199 | 1 | 0.6944714 | 0.3627854 | 2.4577878 | 0.5830389 | 0.592981 |
| 796 | 1 | 1.7105497 | 1 | 0.5501104 | 1 | 0.6802454 | 1 | 0.6532116 |
| 797 | 1.9425566 | 1.4749871 | 2.6742263 | 1.9623377 | 6.7522152 | 1.2394955 | 2.2794267 | 2.3084136 |
| 798 | 2.7393771 | 1.6612252 | 1.992725 | 2.3309837 | 4.1301824 | 1.2922891 | 3.8851522 | 2.3474637 |
| 799 | 1 | 1.3613903 | 2.0233123 | 3.0811261 | 4.0660027 | 3.1409614 | 2.4260942 | 0.6671502 |
| 800 | 0.7516275 | 1.3053586 | 2.0548052 | 2.9197357 | 3.5291469 | 1.1640498 | 2.3341316 | 2.5268529 |
| 801 | 0.7356352 | 0.8161892 | 1 | 0.3355917 | 0.7486322 | 0.3009319 | 1.1945586 | 0.5670056 |
| 802 | 1.2765735 | 1.7342821 | 3.5417557 | 2.5090115 | 5.5797526 | 1.4061475 | 2.7329841 | 3.876663 |
| 803 | 1 | 0.6497165 | 1.4927141 | 0.5120904 | 1 | 0.240028 | 0.5646416 | 0.7604552 |
| 804 | 0.3450359 | 0.2397077 | 1 | 1 | 0.5440193 | 0.271373 | 0.2206293 | 1 |
| 805 | 1.4661966 | 1.4458237 | 1 | 2.5759737 | 2.94586 | 1.4525249 | 2.3122344 | 2.3368981 |
| 806 | 1.7018619 | 1 | 2.578404 | 3.976909 | 4.0935032 | 3.7464663 | 2.2913606 | 3.583129 |
| 807 | 1.3733682 | 1 | 2.0704582 | 1.8355222 | 3.6218887 | 1 | 1 | 1.928181 |
| 808 | 2.0679094 | 1 | 2.2215629 | 2.7791242 | 2.2146441 | 1 | 2.2031795 | 3.2924704 |
| 809 | 2.4643829 | 1 | 4.0724358 | 3.4782628 | 2.3425496 | 1.5512897 | 0.6432605 | 2.06211 |
| 810 | 1.2626104 | 1 | 2.3940414 | 1.8993451 | 5.4164852 | 1.619269 | 2.4670573 | 2.4607835 |
| 811 | 1.439556 | 1 | 3.9284691 | 1.8185871 | 4.2842444 | 1 | 1 | 2.4862036 |
| 812 | 1 | 1 | 2.8255391 | 3.2007844 | 3.6651835 | 1.6633007 | 3.0165018 | 3.3316383 |
| 813 | 1.5607555 | 1 | 1.9088824 | 1 | 2.8866056 | 1.5354447 | 2.8152989 | 2.5784573 |
| 814 | 1 | 0.6080191 | 2.7672025 | 1.7437192 | 3.9530774 | 1 | 1 | 2.5762292 |
| 815 | 1.3681175 | 1.4849687 | 2.7921981 | 1.6581791 | 4.2471219 | 1 | 1 | 2.807657 |
| 816 | 1 | 1 | 0.5294712 | 0.7206418 | 0.3429506 | 1.1198188 | 1 | 0.7175884 |
| 817 | 1 | 1 | 0.5587417 | 0.8173058 | 0.3566801 | 1.1387377 | 1 | 0.7023356 |
| 818 | 1 | 1 | 0.5656139 | 1 | 0.4027697 | 1.1516468 | 0.8724023 | 0.6849096 |
| 819 | 0.7412069 | 0.6461057 | 0.6220779 | 0.4811838 | 0.6124173 | 0.59961 | 0.7681027 | 0.6226774 |
| 820 | 1 | 1 | 0.6115903 | 0.5002334 | 0.3980022 | 0.8583882 | 1 | 0.6964975 |
| 821 | 1 | 1 | 2.2983951 | 2.3013095 | 3.0680523 | 1.5352607 | 1 | 2.1619642 |
| 822 | 2.7198745 | 1 | 2.4648894 | 1 | 2.8392688 | 1.4273968 | 1 | 3.7536918 |
| 823 | 1.4995383 | 0.6593815 | 2.5559583 | 1.8394951 | 2.4495613 | 1.3227295 | 1.6838547 | 3.2923531 |
| 824 | 0.3851521 | 0.1439176 | 0.4261212 | 0.8401597 | 1 | 0.5545281 | 0.1122368 | 0.4866728 |
| 825 | 0.2464541 | 1 | 0.4909598 | 0.4131368 | 0.346128 | 0.45387 | 0.494725 | 0.4346869 |
| 826 | 2.2930931 | 1.455281 | 4.9553793 | 4.9158682 | 2.9286306 | 4.3803419 | 1.8401023 | 2.5037832 |
| 827 | 1 | 0.8963193 | 0.4937376 | 0.5945851 | 0.3783634 | 1.1443567 | 0.9069544 | 0.6648321 |
| 828 | 0.1340896 | 1 | 0.5502629 | 0.8088104 | 0.3595508 | 0.2370537 | 1 | 0.4622716 |
| 829 | 0.5710199 | 0.6894847 | 2.2517634 | 2.2645179 | 3.498107 | 1.3213267 | 1.9980238 | 1.544575 |
| 830 | 0.0344993 | 0.0332391 | 0.0999094 | 0.049404 | 0.3996752 | 0.0317513 | 0.0457174 | 0.102554 |
| 831 | 0.0858248 | 1 | 0.2124152 | 0.386127 | 0.2599469 | 0.1187721 | 0.4064706 | 0.1600329 |
| 832 | 4.3758793 | 1.9509795 | 3.2514629 | 2.6798819 | 3.5028603 | 1.2817028 | 1.7364585 | 2.8003407 |
| 833 | 0.0237992 | 1 | 0.0524628 | 0.0438766 | 0.4358587 | 0.0151321 | 0.0298754 | 0.0660038 |

Table 4

| SEQ ID | Patient ID | | | | | | | | |
|--------|------------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|
| | NO | 392 | 393 | 413 | 452 | 505 | 517 | 534 | 546 |
| 834 | | 1 | 1 | 0.5247806 | 0.7000432 | 0.4021786 | 1.1010762 | 1 | 0.6578566 |
| 835 | 0.3601015 | 0.1851302 | | 0.387554 | 1 | 1 | 0.4088187 | 0.2294768 | 0.4222485 |
| 836 | | 1 | 1 | 0.5712896 | 1 | 0.3727924 | 1.1160933 | 1 | 0.7247633 |
| 837 | 0.9153446 | 0.8695499 | | 0.4937681 | 1 | 0.3988232 | 1.1368903 | 0.8957561 | 0.7029232 |
| 838 | 1.786039 | 1.1219893 | | 1.4943657 | 2.5885067 | 2.5040234 | 1.7712872 | 1.2503586 | 2.3012287 |
| 839 | 1.9784278 | 1.5940149 | | 2.1628889 | 2.8450953 | 4.1575673 | 2.8732526 | 1 | 1.5486903 |
| 840 | 0.6791943 | 1.3718864 | | 1.7375114 | 1 | 2.0997295 | 0.8938957 | 1.6146218 | 1.9457177 |
| 841 | 3.792604 | 1.9697755 | | 1 | 3.6961331 | 2.6325441 | 2.1967021 | 1.5529915 | 1.4597031 |
| 842 | 1.8970392 | 1.5140431 | | 1.866829 | 2.2057448 | 4.4499606 | 1.843222 | 1.8449958 | 1.9369909 |
| 843 | 0.5944497 | 0.5903213 | | 0.8756184 | 0.3316879 | 0.6348505 | 0.5740603 | 0.2728692 | 0.4662267 |
| 844 | 3.1480103 | | 1 | 3.2851663 | | 1 | 4.0407451 | 1.5476101 | 2.5094948 |
| 845 | 1.4385529 | 1.653687 | | 1 | 4.0347763 | 3.6951494 | 3.2928033 | 2.0324501 | 2.6268267 |
| 846 | 0.071704 | | 1 | 0.691109 | 0.2230472 | 0.4057517 | 0.0747481 | 0.2159508 | 0.2492298 |
| 847 | 1.9898693 | 2.5520442 | | 1 | 1.3225019 | 2.3515722 | 1.8128659 | | 1 |
| 848 | 1.3666719 | 0.4133525 | | 0.8365127 | 2.1737265 | 1.4810792 | 1.8875143 | 0.0649838 | 0.6281752 |
| 849 | | 1 | 1 | 0.4960307 | 0.7666089 | 0.3802423 | 1.1493317 | 0.8678914 | 0.6883325 |
| 850 | | 1 | 0.5957325 | 1.5541816 | 2.5022957 | 3.1684724 | | 1 | 2.3105801 |
| 851 | 0.1832836 | 0.2813654 | | 0.3899624 | 0.3458246 | 0.2769208 | 0.2008793 | 0.2828281 | 0.2808792 |
| 852 | 1.6494599 | 0.558665 | | 2.2823809 | | 1 | 2.4923668 | 1.295984 | 0.8265545 |
| 853 | | 1 | 1.1577412 | | 1 | 1.7610344 | 3.2744559 | 1.9678431 | 1.9802809 |
| 854 | | 1 | 1.2878091 | 2.7144116 | 2.0577981 | 2.164842 | 1.7560325 | 2.0642547 | 2.3124567 |
| 855 | 0.4575338 | | 1 | 0.390004 | | 1 | 0.7281745 | 0.4919684 | 1 |
| 856 | 1.4010421 | 1.6509963 | | 1.9944 | 1.3207669 | 1.8726783 | | 1 | 2.1335679 |
| 857 | 0.4955911 | 1.3525364 | | 0.5237443 | 0.4382067 | 0.3483314 | 2.3908893 | 0.6691675 | 0.4516692 |
| 858 | 0.0671074 | | 1 | 0.8162593 | 0.272382 | 1.1154855 | 0.0741195 | 0.0641344 | 0.13732 |
| 859 | 0.3128753 | 0.8098184 | | 0.7020183 | 0.6017198 | 0.4660411 | 0.3877074 | 0.4336001 | 0.538576 |
| 860 | 0.287334 | 0.1226584 | | 0.2773006 | | 1 | 1 | 0.3119091 | 0.0895228 |
| 861 | 2.0854238 | 1.9993939 | | 2.0554307 | 1.6669223 | | 1 | 1.5002515 | 2.5956646 |
| 862 | 2.0854238 | 1.9993939 | | 2.0554307 | 1.6669223 | | 1 | 1.5002515 | 2.5956646 |
| 863 | | 1 | | 1 | 0.5258683 | 0.764674 | 0.3551676 | | 1 |
| 864 | 0.1901155 | | 1 | 0.7317804 | 1.1536163 | 0.5331717 | 1.2746427 | 0.2136103 | 0.4258146 |
| 865 | 0.0957499 | | 1 | 0.7779929 | | 1 | 0.8419746 | 0.1522635 | 0.1808312 |
| 866 | 1.3129993 | 1.332959 | | 2.7648494 | 2.8239778 | 2.8114002 | 1.6775665 | 2.6318421 | 4.9327309 |
| 867 | 1.2244756 | 0.4861126 | | 1 | | 1 | 4.4878351 | 1.386623 | 2.8254907 |
| 868 | | 1 | 1 | 0.5087919 | | 1 | 0.3521344 | 1.1127817 | 0.941906 |
| 869 | 1.1654538 | 1.2235962 | | 2.09842 | 4.0000023 | 3.2422711 | 1.9005153 | 2.3603076 | 2.5574797 |
| 870 | 1.420207 | | 1 | 4.4233133 | 2.119584 | 3.0578084 | | 1 | 2.114016 |
| 871 | 1.2030824 | 1.7407914 | | 2.3802803 | 2.3342264 | 4.3879608 | 1.4203444 | 2.3874424 | 3.1089463 |
| 872 | 1.8769726 | 1.2463888 | | 2.7328321 | 1.7911602 | 2.4790509 | 1.1138013 | 1.9430597 | 2.8834283 |
| 873 | 1.1985826 | 0.5006448 | | 3.3655166 | 1.9450152 | 4.4079692 | 1.3954922 | 2.9852542 | 3.1105158 |
| 874 | 1.4893239 | 1.1452369 | | 2.1006796 | 1.8853367 | 3.117803 | 1.3166123 | 2.5466831 | 2.7143928 |
| 875 | 2.2670407 | 1.697808 | | 1.4954603 | 1.7246024 | 2.0793426 | 1.4250128 | 2.3208287 | 1.3408726 |
| 876 | 1.6789454 | | 1 | 1 | 2.6018861 | 2.1866053 | 1.7651776 | 2.4520084 | 2.8199934 |
| 877 | 0.079803 | 0.1649789 | | 0.2139746 | 0.4918122 | 0.1514502 | 0.1885912 | 0.2769398 | 0.033406 |
| 878 | 1.8237848 | 0.7244947 | | 1 | 0.1804088 | 0.4631816 | 0.5571268 | | 1 |
| 879 | | 1 | 1 | 1 | 2.5686936 | 2.4013882 | 1.4324638 | 2.7516927 | 2.203143 |
| 880 | 0.8107348 | | 1 | 0.5554786 | 0.5884366 | 0.4477528 | | 1 | 0.6532763 |
| 881 | 0.1010919 | | 1 | 0.2324318 | 0.3802708 | 0.2226382 | 0.1532141 | 0.397259 | 0.1150321 |
| 882 | 0.4932797 | 0.2832747 | | 0.5347345 | 0.4447165 | 0.3887762 | 0.3532962 | 0.6131466 | 0.3781847 |

Table 4

| SEQ ID NO | Patient ID | | | | | | | |
|--------------|------------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|
| | 392 | 393 | 413 | 452 | 505 | 517 | 534 | 546 |
| 883 | 0.0723366 | 1 | 0.116062 | 0.185201 | 0.1865841 | 0.1067064 | 0.1657723 | 0.0665574 |
| 884 | 1.8598037 | 1.483287 | 5.2134628 | 2.5829894 | 4.0860534 | 1.6706597 | 3.4618135 | 5.4275103 |
| 885 | 1 | 1 | 2.4393426 | 1 | 3.187189 | 1 | 1.9679645 | 2.933957 |
| 886 | 1.792271 | 1.2891644 | 3.9169009 | 2.4251422 | 3.4251186 | 1.0626021 | 1.9020992 | 2.9966488 |
| 887 | 0.8493018 | 0.7762824 | 2.9032839 | 2.3042267 | 4.467957 | 1.5598292 | 2.4493793 | 1.8211485 |
| 888 | 1.8504429 | 1.4408378 | 1 | 2.3610072 | 2.6240088 | 1.4491214 | 2.2565259 | 4.229732 |
| 889 | 0.2725758 | 1 | 0.5910159 | 1 | 1 | 1.702526 | 0.6816796 | 0.5125398 |
| 890 | 1.2349981 | 1 | 2.3446171 | 3.1838103 | 3.3712019 | 1.6308825 | 2.895368 | 3.1514576 |
| 891 | 1 | 1 | 0.4898694 | 0.6572859 | 0.3790165 | 1.1587375 | 0.8506909 | 0.6758935 |
| 892 | 1 | 1 | 0.5582124 | 0.6090051 | 0.3865845 | 1.1270399 | 1 | 0.6810987 |
| 893 | 3.6436699 | 2.3984912 | 1.9363337 | 1 | 2.1428476 | 1.1371893 | 1 | 2.602344 |
| 894 | 1.2478606 | 2.2555134 | 1 | 2.7144532 | 1 | 1.7561551 | 2.7290025 | 3.3174071 |
| 895 | 5.6504788 | 1 | 1.8931983 | 0.8524279 | 1.2660403 | 1.2082425 | 1.3991957 | 1.9747787 |
| 896 | 1.6466515 | 0.69545 | 4.3269505 | 1.7751265 | 3.0142408 | 1.1316776 | 1 | 2.710174 |
| 897 | 0.8395974 | 1.505763 | 1 | 1.1548989 | 2.888882 | 1.2557928 | 2.1752918 | 2.8803729 |
| 898 | 1.1556429 | 1 | 1.6568433 | 1.8024083 | 2.4057874 | 1.2780846 | 1.9400009 | 1.6908713 |
| 899 | 1.2229133 | 0.7859079 | 2.3143915 | 2.2335246 | 3.1822346 | 1.5214165 | 2.1377072 | 2.4730311 |
| 900 | 0.7674737 | 1.3997241 | 1 | 1.3110032 | 3.5150666 | 1.293071 | 2.6188168 | 2.7068402 |
| 901 | 1.3161382 | 1 | 1 | 2.1199273 | 3.1788917 | 1.2040187 | 1 | 3.489509 |
| 902 | 0.6882955 | 1.4721677 | 2.7661562 | 1.4528348 | 3.7264072 | 1.363396 | 2.3548479 | 3.3298377 |
| 903 | 1 | 1 | 0.4976926 | 0.607349 | 0.348293 | 1.1023257 | 0.9617729 | 0.6600555 |
| 904 | 1.1395243 | 1.1781595 | 1.6080725 | 1.8029048 | 3.0609013 | 0.8838843 | 1.5991832 | 2.811244 |
| 905 | 0.8150063 | 0.8479939 | 1 | 0.2303083 | 0.6839803 | 0.2608633 | 1 | 0.5333144 |
| 906 | 1.5471472 | 1.2709818 | 3.6431713 | 1 | 3.7258088 | 1 | 2.3950127 | 3.036524 |
| 907 | 0.1151495 | 0.0609285 | 0.1400234 | 0.279018 | 2.6203537 | 0.8619145 | 0.3617742 | 0.1768107 |
| 908 | 0.2833973 | 0.4830162 | 0.5688132 | 0.7237981 | 0.8167312 | 0.5251225 | 0.380774 | 0.5812593 |
| 909 | 0.6126116 | 0.5156123 | 0.6739559 | 0.2414459 | 0.5777524 | 0.6926868 | 0.4320321 | 0.4825587 |
| 910 | 0.2663434 | 0.1421369 | 0.3510007 | 0.1380329 | 0.4997977 | 0.3774354 | 0.1767211 | 0.2402638 |
| 911 | 0.3048039 | 0.1986731 | 0.433749 | 0.1379692 | 1 | 0.5793189 | 0.1911806 | 0.2297333 |
| 912 | 0.6484067 | 0.8389224 | 1 | 0.3026451 | 0.8488753 | 0.3077007 | 1 | 0.6692129 |
| 913 | 1 | 1 | 1 | 0.5710649 | 0.3637543 | 1.1694005 | 0.8607132 | 0.7777075 |
| 914 | 1 | 0.8641683 | 0.5209472 | 1 | 0.4276505 | 1.1372429 | 1 | 0.7165925 |
| 915 | 0.057341 | 0.0658254 | 0.6088122 | 0.0769761 | 0.0470733 | 0.0496813 | 1 | 0.116196 |
| 916 | 1 | 1 | 1 | 0.6374195 | 1 | 0.3424645 | 1 | 0.8284894 |
| 917 | 0.7576375 | 0.8057822 | 2.7779729 | 2.3606665 | 4.2098732 | 1.5396685 | 2.3347717 | 1.9592056 |
| 918 | 1 | 0.8614874 | 0.5131098 | 0.7280418 | 0.3622322 | 1.1427469 | 0.9089083 | 0.6923131 |
| 919 | 1.3408119 | 1 | 2.3076387 | 3.2362414 | 3.2815575 | 1.2648689 | 1 | 3.3512091 |
| 920 | 3.6814049 | 2.3136522 | 1 | 2.8753476 | 4.0988066 | 2.1767484 | 1 | 5.386388 |
| 921 | 0.3175517 | 0.7203991 | 0.7762182 | 0.6190056 | 0.4347995 | 0.3475316 | 0.4392637 | 0.5072317 |
| 922 | 1.2014532 | 1.5327401 | 1 | 1.6829121 | 2.4441421 | 1.8418422 | 1.1326839 | 2.022356 |
| 923 | 2.9505675 | 1 | 1 | 3.1691625 | 2.2093015 | 1.7614445 | 1.7040749 | 2.079884 |
| 924 | 0.036904 | 0.0286885 | 0.5833073 | 0.0767104 | 0.0290993 | 0.0438094 | 0.4751364 | 0.0976475 |
| 925 | 1.270831 | 1 | 1 | 1.9693652 | 2.9140395 | 1.4890826 | 2.1286703 | 3.5686016 |
| 926 | 1 | 1 | 0.5283463 | 0.8190345 | 0.3780797 | 1 | 0.7527678 | 0.6645262 |
| 927 | 2.2782506 | 1.6875791 | 2.0095108 | 3.0037656 | 1 | 1 | 0.5667052 | 1.3412618 |
| 928 | 0.7122235 | 3.2077852 | 1 | 1 | 1 | 1.4309537 | 0.7534399 | 0.6446143 |
| 929 | 0.1560615 | 1 | 0.7193325 | 0.8725222 | 0.8399628 | 0.1928687 | 0.2470747 | 0.5903636 |
| 930 | 1 | 1 | 0.5627243 | 0.4350806 | 0.3640606 | 0.1074116 | 0.2445925 | 0.3171867 |
| 931 | 1.4493513 | 1.1498865 | 3.3113118 | 2.26006 | 3.5354211 | 1.2827223 | 1.6159311 | 4.0481667 |

Table 4

| SEQ ID | Patient ID | | | | | | | |
|--------|------------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|
| NO | 392 | 393 | 413 | 452 | 505 | 517 | 534 | 546 |
| 932 | 11.829581 | 6.4598597 | 2.7760403 | 7.8230768 | 1 | 4.0752476 | 3.6255706 | 2.7601136 |
| 933 | 1.6553862 | 1.2544117 | 4.2782407 | 1 | 2.8301482 | 1.3934838 | 2.2924262 | 3.1269335 |
| 934 | 1 | 0.780101 | 1.9279988 | 2.0776594 | 2.5958242 | 1.2315539 | 1 | 1.7768908 |
| 935 | 1 | 1 | 1.6991406 | 1 | 2.4762286 | 1.6222816 | 1 | 1 |
| 936 | 0.2047249 | 1 | 0.3255575 | 1 | 1.5901358 | 0.367838 | 0.5171322 | 0.506695 |
| 937 | 0.1717955 | 0.2386393 | 0.472548 | 0.6222902 | 1 | 0.6936526 | 0.3031773 | 0.4174612 |
| 938 | 1 | 0.5457254 | 2.8961007 | 2.3504916 | 3.5438816 | 1.2760072 | 1.2702847 | 3.5018053 |
| 939 | 1 | 1 | 4.0862735 | 1.428853 | 2.8634482 | 0.7652655 | 1 | 2.8438564 |
| 940 | 1 | 1 | 0.5551449 | 0.5846567 | 0.3384661 | 1 | 0.8892669 | 0.6921368 |
| 941 | 1.6537032 | 1 | 1 | 1 | 3.1468412 | 0.0881324 | 0.1102023 | 1 |
| 942 | 0.0531413 | 1 | 0.1028306 | 0.3009803 | 0.348511 | 0.216019 | 0.0868362 | 0.0590726 |
| 943 | 0.117507 | 0.1195323 | 0.3062752 | 0.4927417 | 0.6732425 | 0.4665107 | 0.2667621 | 0.1835023 |
| 944 | 1.4863134 | 1 | 3.6418111 | 1 | 3.1011332 | 1.3720352 | 2.3553216 | 2.8307037 |
| 945 | 2.2792664 | 2.1125752 | 5.8004294 | 3.1787068 | 5.1181583 | 1.2674753 | 4.5232959 | 4.8070137 |
| 946 | 0.0538875 | 1 | 0.5285054 | 0.0682487 | 0.0437545 | 0.0397159 | 0.2195443 | 0.1050739 |
| 947 | 2.2607389 | 0.6123224 | 3.880885 | 1.9206397 | 3.4439304 | 1.890366 | 1.5668389 | 2.6889626 |
| 948 | 3.2927475 | 1.5433252 | 1 | 2.6045786 | 2.9063736 | 3.5011107 | 1 | 3.0920956 |
| 949 | 1.101366 | 1 | 2.2935913 | 2.0941482 | 2.9174596 | 1.3385745 | 1.222053 | 2.7397399 |
| 950 | 1.8398507 | 1.883235 | 1.5408695 | 3.2777379 | 2.3749218 | 2.182214 | 1.6267367 | 2.2647433 |
| 951 | 1 | 1 | 0.5292063 | 0.5284539 | 0.3020533 | 1.1609376 | 1 | 0.6989151 |
| 952 | 3.5748734 | 0.7904387 | 3.0760161 | 2.1802444 | 1.6614192 | 1.577514 | 1 | 2.9432071 |
| 953 | 1.9702942 | 2.192547 | 1.7776551 | 1.7380229 | 2.2354135 | 1.3399313 | 1.6706092 | 2.5073154 |
| 954 | 0.3005517 | 0.2686336 | 0.7950003 | 0.6359514 | 0.6170922 | 2.1293437 | 0.1110737 | 0.2011248 |
| 955 | 1 | 1 | 0.3052486 | 0.2861755 | 1 | 0.2523544 | 0.2507137 | 0.459614 |
| 956 | 5.2956515 | 2.4716173 | 1.2307342 | 1 | 1.4168889 | 3.3219406 | 2.6173531 | 1 |
| 957 | 1 | 0.5780446 | 1 | 2.2807764 | 3.099062 | 1.5447278 | 1 | 2.4624226 |
| 958 | 1.6380086 | 1.3515076 | 1 | 2.2992073 | 1.747341 | 1.5097416 | 1 | 2.3283026 |
| 959 | 1.9379978 | 1.1509648 | 1.5343255 | 2.2366545 | 1.7132759 | 1.1743755 | 2.3782881 | 2.5881331 |
| 960 | 1.1902504 | 1 | 1.3970321 | 1.8970326 | 1.424195 | 1.5924007 | 1.8077469 | 1.6447703 |
| 961 | 2.5729424 | 1.2409775 | 2.4295539 | 2.2311639 | 2.3076766 | 1 | 2.2382986 | 3.8485735 |
| 962 | 1.6585831 | 1.3996549 | 3.2429352 | 2.0375514 | 2.2608275 | 1.3261254 | 2.0387767 | 2.6808506 |
| 963 | 1.3810359 | 1 | 2.0355569 | 1.5801429 | 2.4974644 | 1.3693752 | 1.7968913 | 2.9395561 |
| 964 | 1 | 2.1966524 | 1 | 1.4697369 | 1.4280815 | 1.3301653 | 1 | 2.606307 |
| 965 | 0.7200725 | 1 | 1 | 1.5560584 | 1.9292578 | 1.3380303 | 1 | 2.0392684 |
| 966 | 1.2561983 | 1.3288436 | 3.593512 | 1 | 2.0037377 | 1.3171336 | 1.9814959 | 2.8052708 |
| 967 | 0.2876404 | 0.325803 | 0.7052272 | 0.6703892 | 1.6323515 | 0.7576611 | 0.5081235 | 0.4696932 |
| 968 | 1 | 1 | 1.5559996 | 1 | 2.5046542 | 1.235356 | 1 | 2.7880911 |
| 969 | 1 | 1 | 0.562995 | 0.4903492 | 0.3340044 | 1 | 1 | 0.6607917 |
| 970 | 1 | 0.6202761 | 2.1242136 | 2.3894562 | 2.7642811 | 1.605762 | 1.9711536 | 3.04042 |
| 971 | 2.573806 | 1 | 1 | 2.0771977 | 1.9591802 | 1.2286946 | 1.5830198 | 2.5053443 |
| 972 | 0.293695 | 1 | 0.4916444 | 0.4043827 | 0.5941258 | 0.1490286 | 0.2439008 | 0.2913773 |
| 973 | 0.7601374 | 1 | 1 | 0.3643959 | 0.7158694 | 0.4896074 | 1 | 0.6137089 |
| 974 | 1 | 0.8610027 | 0.6125718 | 0.4942974 | 0.4459769 | 1 | 1 | 0.6705239 |
| 975 | 1 | 1 | 1 | 0.3814678 | 1 | 0.6326414 | 1 | 0.6640917 |
| 976 | 1 | 0.5900245 | 0.6850152 | 0.7856513 | 0.6103015 | 0.5094615 | 1 | 0.566585 |
| 977 | 1.1629666 | 2.1080345 | 3.1695249 | 1.7573928 | 3.7938425 | 1.6593452 | 2.245005 | 6.5592367 |
| 978 | 1.4906474 | 0.7232284 | 3.4741976 | 1.4978264 | 3.4175505 | 0.8561115 | 3.0285971 | 3.0591389 |
| 979 | 2.5304289 | 1 | 1 | 3.4740159 | 2.0966934 | 1.9526037 | 1.4803592 | 2.1878615 |
| 980 | 2.8297076 | 3.4994093 | 4.2064925 | 2.3451848 | 1.5852104 | 0.8004357 | 1 | 2.3699168 |

Table 4

| SEQ ID | Patient ID | | | | | | | |
|--------|------------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|
| | 392 | 393 | 413 | 452 | 505 | 517 | 534 | 546 |
| 981 | 0.3313061 | 0.2936322 | 0.5744559 | 1.6460004 | 0.7364806 | 0.9007948 | 0.5403342 | 0.4906465 |
| 982 | 1 | 0.8023791 | 1.3957661 | 1.504853 | 2.2916447 | 1.5355673 | 2.4174526 | 1.8902815 |
| 983 | 1 | 1 | 2.4108722 | 1 | 2.7371047 | 1.2457814 | 2.0125352 | 3.1842491 |
| 984 | 1.5184578 | 1 | 4.6758721 | 2.5556525 | 3.8875019 | 1 | 1 | 3.5680505 |
| 985 | 0.0551704 | 1 | 0.583009 | 0.0721513 | 0.0546387 | 0.0379988 | 0.2027584 | 0.138121 |
| 986 | 1.6873636 | 1.3419711 | 2.850401 | 1.9114393 | 2.4897812 | 1.4115825 | 2.6977177 | 2.3198867 |
| 987 | 0.1776748 | 0.2095946 | 0.447048 | 0.3099617 | 0.5346174 | 0.3671557 | 0.154412 | 0.2471457 |
| 988 | 1 | 1 | 0.553308 | 0.5279168 | 0.3893722 | 1 | 1 | 0.6634719 |
| 989 | 1.0692468 | 0.5870765 | 1.5962888 | 0.5621175 | 1 | 0.1722096 | 0.5121188 | 0.8560545 |
| 990 | 1 | 1.6487012 | 1.4455467 | 2.0359032 | 1.6240861 | 1 | 1.7912553 | 1.5402761 |
| 991 | 0.151752 | 0.7246925 | 0.4467773 | 1 | 1.6409335 | 1 | 0.3661243 | 0.6796112 |
| 992 | 1 | 1 | 0.5778742 | 0.5277465 | 0.3579568 | 1 | 1 | 1 |
| 993 | 0.1058262 | 1 | 1 | 1 | 1 | 0.2282075 | 0.2212762 | 0.310994 |
| 994 | 1 | 1 | 1 | 1.4989586 | 1 | 1.8455677 | 1 | 2.7048597 |
| 995 | 1 | 0.8898693 | 1 | 0.4694306 | 0.380498 | 1 | 1 | 0.7165702 |
| 996 | 1.2148728 | 1.3248272 | 2.2728673 | 1.5334514 | 3.2124912 | 1 | 1 | 2.2685234 |
| 997 | 4.0567376 | 1.3703728 | 1 | 11.203567 | 0.6270266 | 0.2311281 | 0.5208709 | 1 |
| 998 | 2.169984 | 0.6610039 | 1 | 2.9066375 | 1 | 1 | 2.1662858 | 1.3793153 |
| 999 | 0.6862759 | 1 | 0.6057456 | 0.6644401 | 0.7697104 | 0.659456 | 0.4994047 | 0.5739174 |
| 1000 | 1 | 1.6539344 | 1 | 0.5895764 | 1 | 0.6155853 | 1 | 1 |
| 1001 | 0.1821452 | 0.0699407 | 0.2862773 | 0.0693357 | 1 | 0.5042949 | 0.0760653 | 0.1016208 |
| 1002 | 0.6100772 | 0.2917329 | 0.5342789 | 0.2997684 | 0.7557038 | 0.5218646 | 0.3638981 | 0.3507933 |
| 1003 | 1 | 1 | 1.9764397 | 1 | 2.8229167 | 1.7276234 | 1 | 2.466168 |
| 1004 | 1 | 1.5882376 | 1.601034 | 1.6446353 | 1.603655 | 1 | 1.7596544 | 2.0833066 |
| 1005 | 1 | 0.8617743 | 0.5663291 | 0.7033236 | 0.4055578 | 1.1706423 | 0.8999305 | 0.6669239 |
| 1006 | 1.690286 | 1 | 3.3335675 | 0.3074597 | 1.3017962 | 0.4585844 | 1 | 1.8742197 |
| 1007 | 0.1583816 | 1 | 0.326869 | 0.313846 | 0.1744499 | 0.1288602 | 0.2481687 | 0.2466063 |
| 1008 | 1 | 0.8720626 | 0.5945059 | 0.6970753 | 0.3719199 | 1 | 1 | 0.6967495 |
| 1009 | 1 | 1 | 0.576247 | 0.5870694 | 0.3751999 | 1 | 1 | 0.6515859 |
| 1010 | 1.5561854 | 0.9156197 | 2.0757945 | 1.5575769 | 2.0417681 | 1.5033791 | 1.6394364 | 1.6650688 |
| 1011 | 0.8761544 | 0.868343 | 0.5028583 | 0.6694975 | 0.4186854 | 1.0994971 | 1 | 0.7372927 |
| 1012 | 2.3624799 | 2.4002125 | 3.2024769 | 1.7284743 | 2.8712443 | 1.3962281 | 1 | 3.4085581 |
| 1013 | 1.3704054 | 1.5254097 | 1.8710863 | 1 | 3.449905 | 2.2092355 | 1.4417784 | 2.3840387 |
| 1014 | 1 | 1 | 0.5389992 | 0.5780309 | 0.4558107 | 0.8998596 | 1 | 0.6785085 |
| 1015 | 1.3217124 | 1 | 2.9363983 | 2.3723051 | 3.3560844 | 1.5719563 | 2.1062194 | 2.6556606 |
| 1016 | 1 | 0.84006 | 0.6281986 | 0.589906 | 0.4205879 | 1 | 0.8189585 | 0.6817871 |
| 1017 | 1.3241742 | 1 | 2.0129204 | 1.4970383 | 2.3133524 | 1.6368847 | 1 | 2.0111339 |
| 1018 | 1.8035624 | 0.7955433 | 1 | 0.2214141 | 0.3408329 | 0.4952877 | 1 | 1 |
| 1019 | 0.8019051 | 1 | 2.5762853 | 0.9034187 | 1 | 0.5825768 | 0.3464862 | 1.4802301 |
| 1020 | 1.5183719 | 1.8972132 | 1 | 1.9426479 | 4.241428 | 2.3022663 | 0.150555 | 3.7549118 |
| 1021 | 1 | 1 | 2.4038088 | 4.1647067 | 3.3957084 | 1.1741839 | 1.5855657 | 2.7782848 |
| 1022 | 1.5776136 | 2.6486751 | 2.0705559 | 1 | 0.7006355 | 2.231857 | 2.1308981 | 1 |
| 1023 | 1 | 0.8833995 | 0.5420142 | 0.6649599 | 0.3811919 | 1.1413671 | 1 | 0.6726174 |
| 1024 | 0.4646048 | 1 | 0.8015769 | 0.6688065 | 0.5682942 | 0.5255978 | 0.6684082 | 0.5648018 |
| 1025 | 1.7153771 | 0.6491427 | 2.8084551 | 1.7288396 | 2.3596242 | 1.8621179 | 1 | 3.3371721 |
| 1026 | 1.6629765 | 1.3998231 | 3.9205743 | 1 | 2.6480686 | 1.3387585 | 1.8840015 | 2.7511578 |
| 1027 | 1.4212223 | 1 | 4.6533181 | 3.4433063 | 3.7266068 | 1.3955459 | 2.3673474 | 3.8385034 |
| 1028 | 1 | 0.7108429 | 1.4359706 | 3.3440665 | 1.8973866 | 2.3470492 | 3.6000678 | 3.7875352 |
| 1029 | 2.4332702 | 1.2759479 | 1.86042 | 2.0186328 | 1.852936 | 1.4681016 | 1 | 1.729539 |

Table 4

| SEQ ID NO | Patient ID | | | | | | | |
|--------------|------------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|
| | 392 | 393 | 413 | 452 | 505 | 517 | 534 | 546 |
| 1030 | 0.4384028 | 0.4227208 | 0.5922959 | 1 | 0.5551359 | 2.4106514 | 0.4616149 | 0.3059919 |
| 1031 | 1.5731978 | 1.787257 | 4.2338799 | 3.9728046 | 4.1498828 | 3.2734475 | 2.8083768 | 3.7457806 |
| 1032 | 0.2632418 | 0.3249126 | 0.2690231 | 0.3594737 | 0.5655237 | 0.5588285 | 0.1389572 | 0.2360209 |
| 1033 | 1.8591595 | 1.2952286 | 2.5960168 | 1 | 2.2018929 | 1.3916364 | 2.7899721 | 2.9091141 |
| 1034 | 1 | 1.2469626 | 2.9203785 | 2.3837117 | 2.7089804 | 1 | 1.4180714 | 4.0453316 |
| 1035 | 1 | 1.4515911 | 1.7856823 | 1 | 1 | 1.2579315 | 1.5824314 | 1.5402504 |
| 1036 | 0.6193266 | 0.13725 | 1.8412227 | 0.3955539 | 1 | 0.5522514 | 0.2099628 | 0.3762111 |
| 1037 | 0.8252308 | 0.7763418 | 1 | 0.4183744 | 0.8054929 | 0.2858075 | 1 | 0.7485615 |
| 1038 | 1 | 1.2045233 | 1 | 2.1368873 | 1.4886182 | 1 | 2.0100301 | 1 |
| 1039 | 3.1323038 | 1.7130624 | 1 | 3.050391 | 1 | 2.1634101 | 2.6679779 | 3.2011238 |
| 1040 | 1.6596343 | 1 | 2.4511936 | 2.8300842 | 1 | 1.4324562 | 2.0028519 | 2.5069073 |
| 1041 | 1 | 1 | 1 | 1.9586961 | 1 | 1 | 1.8502077 | 1 |
| 1042 | 1.2484411 | 1 | 2.1694096 | 2.3889328 | 2.8224588 | 1.5857163 | 1 | 2.7512397 |
| 1043 | 1 | 1 | 2.9057824 | 1 | 4.1865765 | 1.8156409 | 1 | 3.0420212 |
| 1044 | 1 | 0.8515849 | 1.6816945 | 1.9707886 | 2.7042441 | 1.1474843 | 2.1148752 | 2.5960575 |
| 1045 | 5.2189328 | 6.1858346 | 1.9666988 | 3.1184197 | 4.5718493 | 5.5151318 | 1 | 2.035675 |
| 1046 | 0.4194641 | 0.2135022 | 0.5238537 | 0.2671502 | 0.2859942 | 0.2456699 | 0.2887023 | 0.4137088 |
| 1047 | 0.0768573 | 0.0744913 | 0.6900876 | 0.0726062 | 0.0489319 | 0.0534835 | 1 | 0.1158517 |
| 1048 | 0.1309856 | 1 | 0.7287129 | 0.3937001 | 0.099376 | 0.0437941 | 0.0404345 | 0.1187173 |
| 1049 | 1.7067592 | 1 | 1 | 2.1523496 | 1.6629276 | 1.5143487 | 0.8308291 | 2.158934 |
| 1050 | 2.0405521 | 1 | 2.6867483 | 1 | 2.6466588 | 1.4493207 | 1 | 3.4188978 |
| 1051 | 0.0950217 | 1 | 0.1971022 | 0.4928753 | 0.683443 | 0.3353048 | 0.1660721 | 0.1850425 |
| 1052 | 1 | 0.8362019 | 0.5543456 | 0.4704464 | 0.4044596 | 1 | 0.8284261 | 0.6899511 |
| 1053 | 1 | 0.8456296 | 1 | 0.4029609 | 0.7410521 | 0.5106344 | 1.6587154 | 0.646825 |
| 1054 | 1 | 0.5258017 | 0.5655775 | 0.3243797 | 0.6053018 | 0.4952953 | 1 | 0.5444681 |
| 1055 | 1 | 1 | 0.6195011 | 0.4219161 | 0.7583634 | 0.6737525 | 1 | 0.6622928 |
| 1056 | 0.8008105 | 1 | 1 | 0.3345622 | 0.6983158 | 0.5122135 | 1 | 0.6908899 |
| 1057 | 1 | 1 | 1 | 0.4094737 | 0.7581156 | 0.583673 | 1 | 0.657211 |
| 1058 | 1 | 1 | 1 | 0.3454157 | 1 | 0.6843695 | 1 | 0.7290858 |
| 1059 | 1.2228576 | 1 | 2.9064559 | 3.0011482 | 3.0920406 | 0.8732137 | 1 | 3.9071466 |
| 1060 | 0.2862026 | 0.3645919 | 0.4653762 | 0.5414891 | 0.5131592 | 0.4131038 | 0.4174475 | 0.4167816 |
| 1061 | 2.107118 | 1.6941478 | 2.087989 | 2.9856756 | 1 | 1 | 0.567354 | 1.4653968 |
| 1062 | 2.9381315 | 1.7897895 | 1.594665 | 1.5543583 | 1.5971416 | 1 | 0.7059574 | 1.6464698 |
| 1063 | 1.7263005 | 1.4338932 | 1.8172117 | 3.3077253 | 8.1682707 | 1.1927578 | 1 | 1.7574953 |
| 1064 | 1 | 0.8267446 | 2.2210008 | 2.8871454 | 2.9891275 | 1.5136741 | 3.0249779 | 3.0204473 |
| 1065 | 2.2088278 | 1.3009465 | 2.4042696 | 3.6607763 | 6.120995 | 2.0065165 | 1.5505747 | 4.2150709 |
| 1066 | 1 | 0.8830929 | 0.5747417 | 0.7326717 | 0.4041238 | 1.1335864 | 1 | 0.7571781 |
| 1067 | 8.0060741 | 7.1268684 | 3.2670723 | 4.1344476 | 6.1605447 | 7.2834371 | 1 | 3.1138694 |
| 1068 | 2.7158149 | 1 | 6.6861766 | 2.548685 | 4.2671715 | 1.5028502 | 2.8714892 | 5.3857602 |
| 1069 | 0.7131508 | 0.7743039 | 0.5783844 | 0.5814463 | 0.4775131 | 1 | 0.5446325 | 0.5822774 |
| 1070 | 1.6683779 | 1 | 2.4223807 | 2.1387031 | 2.1360084 | 1.4173165 | 1.3305399 | 2.2508986 |
| 1071 | 1 | 0.7706733 | 1 | 0.3517166 | 0.7652421 | 0.3068728 | 1 | 0.6598717 |
| 1072 | 1.9526264 | 1.6147596 | 1.9801398 | 2.434163 | 1.9958087 | 1.6952512 | 1 | 2.4875419 |
| 1073 | 1.4900474 | 0.8652268 | 3.8953498 | 3.7581139 | 3.249082 | 1.165744 | 1 | 1.94163 |
| 1074 | 0.3763843 | 0.2633411 | 0.6499941 | 0.6023124 | 1 | 0.5303199 | 0.3154449 | 0.8148587 |
| 1075 | 0.0447268 | 1 | 0.0644198 | 0.0861443 | 0.1370881 | 0.0609652 | 0.0495569 | 0.0233787 |
| 1076 | 2.3400276 | 6.1211271 | 1 | 1.6163222 | 1 | 1 | 0.7768564 | 3.7878456 |
| 1077 | 1.2448797 | 1 | 4.1019297 | 3.8153007 | 2.5181561 | 2.4782245 | 3.127713 | 3.9096258 |
| 1078 | 1 | 0.7804175 | 1.6285664 | 4.2388935 | 2.6049566 | 1.1345523 | 1 | 2.6038104 |

Table 4

| SEQ ID NO | Patient ID | | | | | | | |
|--------------|------------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|
| | 392 | 393 | 413 | 452 | 505 | 517 | 534 | 546 |
| 1079 | 2.450936 | 1 | 2.438394 | 1 | 2.4259118 | 1.3730778 | 1 | 4.6446701 |
| 1080 | 1.9042402 | 1.8015122 | 4.1398425 | 3.0646765 | 3.7266068 | 1.2946271 | 1 | 4.7001803 |
| 1081 | 0.170298 | 0.4447813 | 0.414424 | 1 | 0.3122377 | 0.451371 | 0.5645123 | 0.0936469 |
| 1082 | 1.2137053 | 0.4778622 | 2.3375003 | 1.5117013 | 3.2658518 | 1.3100275 | 1.9528234 | 2.6122741 |
| 1083 | 1.7896119 | 1.4526496 | 3.1777854 | 1.8884379 | 6.507277 | 1.2531404 | 2.6879625 | 2.5208566 |
| 1084 | 1.9837654 | 1.8858565 | 2.6848584 | 2.7268955 | 1 | 1.9052604 | 1.9719837 | 3.3508446 |
| 1085 | 0.0897209 | 0.2120084 | 0.2353089 | 0.5152272 | 0.1700056 | 0.2126385 | 0.2649187 | 0.0394065 |
| 1086 | 3.6164207 | 0.6892572 | 1.8612878 | 0.8241403 | 1.7832907 | 1.282592 | 1.4092592 | 1.7504384 |
| 1087 | 0.1683062 | 0.0810501 | 0.3222212 | 0.2065677 | 0.3547078 | 0.4222413 | 0.4548117 | 0.2095185 |
| 1088 | 0.5478614 | 1.2973357 | 0.6468714 | 0.5866589 | 0.4237168 | 1.9956005 | 0.7760325 | 0.4863629 |
| 1089 | 0.3166712 | 0.2017102 | 0.5039899 | 0.2018427 | 0.7727698 | 0.4921601 | 0.2157891 | 0.3044577 |
| 1090 | 2.0087091 | 1.6771424 | 1.959587 | 1.6058511 | 3.0156774 | 1.605739 | 1 | 3.192609 |
| 1091 | 0.3637349 | 0.4244025 | 1 | 0.8211619 | 0.6374495 | 0.6111622 | 0.682972 | 0.7083974 |
| 1092 | 2.584588 | 1.8686236 | 2.6472122 | 2.7361307 | 2.0766129 | 1.0927973 | 1 | 1.5152997 |
| 1093 | 1.1504785 | 1.3665641 | 1.9704951 | 2.9577418 | 3.4715863 | 2.6941439 | 2.2919774 | 0.8056738 |
| 1094 | 0.7308325 | 1.3839949 | 3.0446521 | 3.0272488 | 3.583475 | 1 | 2.5510531 | 3.1762603 |
| 1095 | 0.8838948 | 0.8935889 | 0.5478728 | 0.767382 | 0.4061542 | 1.0531503 | 1 | 0.6807475 |
| 1096 | 1 | 1.3494697 | 1.8696916 | 3.854629 | 1.7554499 | 1.9801695 | 3.6299265 | 3.1428839 |
| 1097 | 1 | 0.8899682 | 0.5182654 | 0.5342306 | 0.3307333 | 1 | 1 | 0.6771861 |
| 1098 | 2.1957262 | 2.0034202 | 1.6710669 | 1.5315493 | 1.8849005 | 2.3363173 | 1 | 2.8946268 |
| 1099 | 2.2365302 | 1 | 4.7646947 | 3.1446438 | 3.6758296 | 2.0041018 | 2.5626399 | 4.9607968 |
| 1100 | 1 | 1 | 1.8630257 | 1 | 2.6218343 | 1.1760313 | 1 | 3.098523 |
| 1101 | 1.7937683 | 1.722134 | 1.9963048 | 2.5329013 | 2.5293202 | 1.1674764 | 1.5877698 | 3.0813738 |
| 1102 | 1.2995055 | 1.2810525 | 1 | 3.6501582 | 1.669389 | 2.2568471 | 1.9608777 | 1.7482199 |
| 1103 | 2.4731828 | 1 | 2.5587892 | 2.9768474 | 1.8136341 | 1.8184542 | 0.4975952 | 1.6857823 |
| 1104 | 1 | 2.1079455 | 1.5109549 | 1.651692 | 2.6905499 | 1.2239725 | 2.4286105 | 1.3398423 |
| 1105 | 0.457887 | 0.4323067 | 0.776177 | 1 | 0.6605846 | 0.6509701 | 0.734232 | 0.7203907 |
| 1106 | 1 | 0.7804571 | 2.710138 | 1.4067378 | 1.9587391 | 1.2337003 | 1.4634047 | 2.1769361 |
| 1107 | 1.4355712 | 1.5360838 | 1 | 1 | 1 | 2.1475191 | 4.3388939 | 3.1308528 |
| 1108 | 0.6583839 | 1.1185368 | 2.1691952 | 1.8997862 | 1 | 1.55917 | 1 | 1.6388496 |
| 1109 | 0.1529556 | 0.1331841 | 0.553863 | 1 | 0.352318 | 0.2315497 | 0.2378687 | 0.3813085 |
| 1110 | 0.8041035 | 0.6284968 | 2.4630222 | 2.8028113 | 3.6421682 | 1.4367106 | 1 | 3.8119054 |
| 1111 | 1.7578466 | 1.4702881 | 1.674669 | 1.6477411 | 1 | 1.5363262 | 2.4025694 | 2.5324614 |
| 1112 | 1.6821022 | 1 | 2.1605468 | 1.3623691 | 1.7327251 | 0.8060086 | 1 | 4.4145997 |
| 1113 | 1.4428063 | 1 | 4.2912063 | 3.1511551 | 4.2221313 | 1.4357218 | 2.7138989 | 4.2456654 |
| 1114 | 0.4388724 | 0.4824622 | 1 | 1 | 0.7072351 | 0.6785896 | 0.7532279 | 0.7227456 |
| 1115 | 1 | 1 | 2.6619011 | 0.310525 | 1.3817564 | 0.4629615 | 1 | 1.7846454 |
| 1116 | 2.1813156 | 0.7370879 | 2.8884776 | 3.4505688 | 3.011502 | 0.8617458 | 1 | 3.2161625 |
| 1117 | 1 | 0.875436 | 0.589302 | 0.7448387 | 0.3928157 | 1.1062276 | 1 | 0.7341068 |
| 1118 | 0.1743017 | 0.135776 | 0.4073626 | 0.4865684 | 1 | 0.2110364 | 0.2666208 | 0.4418504 |
| 1119 | 0.2238811 | 1 | 0.5671449 | 0.3491234 | 0.7618748 | 0.2175522 | 0.0864666 | 0.1823218 |
| 1120 | 1 | 1 | 3.4292773 | 1.8516223 | 3.1813618 | 1 | 1 | 3.3035332 |
| 1121 | 1.7856231 | 1.5682644 | 2.3018301 | 2.1083845 | 2.6373322 | 1.6598511 | 1.7472784 | 2.1500941 |
| 1122 | 1 | 1 | 2.007994 | 3.4211646 | 1.86136 | 0.8018385 | 1.7206357 | 2.2965967 |
| 1123 | 5.4954414 | 5.5088343 | 2.2364472 | 1.6315143 | 0.7158768 | 1.3298663 | 2.3337826 | 0.8021494 |
| 1124 | 1.6265674 | 1 | 4.0294441 | 2.7022355 | 2.9543628 | 1 | 1 | 2.2481609 |
| 1125 | 1 | 1.1565145 | 1.561063 | 1.7934674 | 1 | 1.2456511 | 1.5304818 | 1.3904591 |
| 1126 | 2.4410716 | 1.9133481 | 4.2494554 | 3.4142034 | 2.425151 | 2.6778236 | 3.7072263 | 3.8700073 |
| 1127 | 2.0396217 | 1.6544389 | 3.9457728 | 2.9354523 | 2.1816021 | 2.455603 | 2.0774874 | 2.8744602 |

Table 4

| SEQ ID NO | Patient ID | | | | | | | |
|--------------|------------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|
| | 392 | 393 | 413 | 452 | 505 | 517 | 534 | 546 |
| 1128 | 1.4458766 | 1.313708 | 3.5398992 | 3.1453995 | 3.4589919 | 1.8286342 | 1.9078724 | 2.202303 |
| 1129 | 0.599104 | 0.5587045 | 1 | 2.5114187 | 3.124942 | 1.2248311 | 1.2862294 | 2.4036944 |
| 1130 | 10.346323 | 6.8500833 | 2.6333953 | 5.7676747 | 1.3846427 | 3.1948205 | 1 | 3.3264818 |
| 1131 | 1 | 1.9597543 | 1.6155297 | 1.8086352 | 2.1993186 | 1.5434937 | 2.2144835 | 3.2750858 |
| 1132 | 1 | 1 | 0.4925961 | 0.5896083 | 0.3374553 | 1 | 0.8205513 | 0.7011634 |
| 1133 | 1.9669369 | 1 | 2.550167 | 2.4491948 | 1.9874881 | 1.2823544 | 1 | 2.1409791 |
| 1134 | 1 | 0.5613854 | 1 | 1 | 3.560014 | 1 | 1 | 1.9738509 |
| 1135 | 1.4439513 | 0.9180137 | 2.14723 | 2.5031571 | 2.5047443 | 1.4539814 | 2.5023876 | 2.8389643 |
| 1136 | 1.3873002 | 1.1312488 | 2.372625 | 2.4729815 | 2.6441452 | 1.4497576 | 2.5693184 | 2.786746 |
| 1137 | 1.9517744 | 1 | 2.3277078 | 2.1671039 | 2.660824 | 1.648 | 1 | 3.0565084 |
| 1138 | 1 | 1.207036 | 1.7848473 | 2.7443924 | 3.3297533 | 3.3026231 | 1 | 2.114092 |
| 1139 | 1.4742505 | 1.1519738 | 1.7415096 | 2.0100143 | 2.5560718 | 1.2462107 | 1 | 1.9624505 |
| 1140 | 1.4402706 | 1.9393063 | 3.8341049 | 1.3058495 | 1 | 1.7983624 | 0.1588615 | 2.8246476 |
| 1141 | 1 | 0.604715 | 3.1209606 | 2.6143597 | 3.867628 | 1.3264321 | 1 | 3.0066903 |
| 1142 | 1.3343291 | 0.6969833 | 1.7292631 | 1.7231492 | 2.2371379 | 1.3429133 | 1 | 2.5076555 |
| 1143 | 1 | 1 | 1 | 0.3739367 | 0.8095496 | 0.438094 | 1 | 0.7235151 |
| 1144 | 1 | 1 | 1.1365955 | 0.4216878 | 0.7480368 | 0.4822483 | 1 | 0.6406508 |
| 1145 | 1.3796161 | 1 | 1.8186046 | 1 | 2.5215315 | 1.3511232 | 1 | 3.1260873 |
| 1146 | 1.1872229 | 1.3657035 | 1.7629476 | 2.0307857 | 1 | 1.6642435 | 1 | 2.4602594 |
| 1147 | 1.2577289 | 0.4594718 | 3.9360428 | 1.7154251 | 3.1532567 | 1.3593409 | 2.2652582 | 2.691155 |
| 1148 | 0.8157247 | 1 | 2.1312787 | 2.5495787 | 2.5416971 | 1.1379712 | 2.3788922 | 2.9567663 |
| 1149 | 2.5418124 | 1.5658704 | 2.7477152 | 2.4373361 | 1 | 2.0511077 | 0.6717496 | 1.8592509 |
| 1150 | 0.282405 | 0.266754 | 0.6930622 | 0.1639004 | 0.2568589 | 0.185433 | 0.1737567 | 0.4436129 |
| 1151 | 0.8989645 | 0.6696797 | 2.1762934 | 2.4136927 | 2.7244621 | 1.4833103 | 1 | 2.4557487 |
| 1152 | 11.901713 | 8.2268467 | 2.0214953 | 4.4040674 | 4.5131523 | 3.7153973 | 1 | 1 |
| 1153 | 1 | 0.7158782 | 1.9813465 | 2.0309747 | 2.0238386 | 1.4067608 | 1 | 2.8254248 |
| 1154 | 1.7261062 | 0.7491965 | 1.9876718 | 1.7693191 | 2.4912071 | 1.3311311 | 1 | 1.9280201 |
| 1155 | 2.835163 | 3.5951697 | 3.2063367 | 2.7673716 | 1.6024735 | 0.766331 | 1 | 3.205565 |
| 1156 | 0.90842 | 1 | 0.5162023 | 0.7992676 | 0.4174348 | 1 | 0.7992505 | 0.7279487 |
| 1157 | 3.3336474 | 1.8910304 | 1.7273237 | 5.4015714 | 2.0746322 | 1.8156945 | 3.6668767 | 1.9827861 |
| 1158 | 1 | 0.7714647 | 0.6526324 | 0.4260169 | 0.5226658 | 0.6614414 | 1 | 0.6839769 |
| 1159 | 1 | 0.7974328 | 0.7241984 | 0.3677481 | 0.5887882 | 0.5053834 | 1 | 0.6022589 |
| 1160 | 0.4094694 | 1 | 0.5062978 | 2.2674996 | 1 | 1 | 1 | 0.5598273 |
| 1161 | 0.7810932 | 0.7045116 | 1 | 0.35804 | 1 | 0.2394454 | 1 | 0.6297203 |
| 1162 | 1.2475706 | 0.8037344 | 0.7308301 | 0.2518736 | 0.4718544 | 0.6262559 | 1 | 0.7134779 |
| 1163 | 1 | 1 | 1 | 0.4110813 | 0.5558986 | 0.6458188 | 1 | 0.5235707 |
| 1164 | 1 | 1 | 2.296291 | 2.1300709 | 3.5906848 | 1.2168358 | 2.6908971 | 3.5525522 |
| 1165 | 2.1364295 | 1 | 1.9124169 | 1.4823213 | 2.6046641 | 1.2323741 | 1 | 1.7288919 |
| 1166 | 2.0614764 | 0.81796 | 2.2702224 | 1 | 2.6614345 | 2.0330627 | 2.0681291 | 3.4814904 |
| 1167 | 2.148616 | 1 | 9.5113217 | 1 | 4.1218663 | 1.6197596 | 2.4587673 | 7.331983 |
| 1168 | 2.0846544 | 1 | 4.2605921 | 1.9512788 | 2.020138 | 1.4173011 | 1.7529687 | 3.2408614 |
| 1169 | 0.0139254 | 0.1430371 | 0.0640895 | 0.3335272 | 0.0663447 | 1 | 0.0262222 | 0.0274931 |
| 1170 | 0.4807244 | 1.3029943 | 0.6017101 | 0.8281872 | 0.4518925 | 1.8775566 | 1 | 0.4297189 |
| 1171 | 1 | 1 | 0.4840381 | 0.6716069 | 0.3821967 | 1 | 1 | 0.7162814 |
| 1172 | 0.0596476 | 0.001 | 0.0819305 | 0.2567091 | 0.5319777 | 0.0774158 | 1 | 0.2193428 |
| 1173 | 0.718973 | 0.494274 | 2.162516 | 1.5857716 | 3.1291568 | 1 | 1 | 2.5793928 |
| 1174 | 2.0104018 | 1.9998985 | 3.1126613 | 2.992639 | 5.2163557 | 1.8661347 | 1.6600089 | 3.8726019 |
| 1175 | 0.0318324 | 0.092753 | 0.264722 | 0.1470949 | 0.039078 | 0.0688225 | 0.1301146 | 0.0923217 |
| 1176 | 0.7867892 | 1 | 1 | 0.2895436 | 0.7217711 | 0.2646195 | 1 | 0.6194844 |

Table 4

| SEQ ID NO | Patient ID | | | | | | | |
|--------------|------------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|
| | 392 | 393 | 413 | 452 | 505 | 517 | 534 | 546 |
| 1177 | 0.7278841 | 1 | 1 | 0.3515598 | 0.7436491 | 0.2702998 | 1 | 0.579419 |
| 1178 | 0.7510753 | 1 | 2.1592715 | 0.4734552 | 0.6723775 | 0.3011005 | 0.5084794 | 0.7072048 |
| 1179 | 2.1097268 | 1.2145643 | 2.4825241 | 1.3499193 | 2.9203975 | 1 | 3.0303609 | 3.6210338 |
| 1180 | 1.4837866 | 1 | 2.7864375 | 2.2380314 | 2.2744211 | 1.2544053 | 1.8171818 | 3.3475676 |
| 1181 | 1.2766646 | 1.867021 | 2.1623029 | 1.903544 | 2.7444436 | 1.7261516 | 2.594586 | 2.6086611 |
| 1182 | 1.6797598 | 1.1198228 | 2.0877904 | 2.147758 | 2.0833259 | 1.2744281 | 2.5722821 | 3.2321342 |
| 1183 | 1.4234648 | 1 | 1.4606509 | 1.7407043 | 2.4302316 | 1 | 1 | 2.5909629 |
| 1184 | 1.9740621 | 1.7033677 | 3.6109534 | 3.3456052 | 4.1145563 | 1 | 1 | 3.7634746 |
| 1185 | 1.3493903 | 1.2011994 | 2.2250538 | 2.0995232 | 2.1773708 | 1.3773859 | 1 | 2.3322393 |
| 1186 | 1.4389578 | 1.2923696 | 2.3605039 | 2.3221332 | 2.7916667 | 1.4026137 | 1 | 2.1875508 |
| 1187 | 1.6802067 | 1.3979138 | 2.7423935 | 2.6982244 | 2.3764625 | 1.4492517 | 2.6809608 | 3.8708178 |
| 1188 | 0.7749417 | 1.1654574 | 2.271985 | 1.8684341 | 1.7952498 | 1.4213026 | 1.9650329 | 1.905599 |
| 1189 | 0.7884476 | 1 | 0.4904332 | 0.846638 | 0.4710338 | 1 | 1 | 1 |
| 1190 | 0.1887361 | 0.804051 | 0.429915 | 1.9527927 | 1.6598344 | 1.0736484 | 0.3112641 | 0.6364463 |
| 1191 | 2.1012615 | 1.6494134 | 2.0227529 | 2.7944332 | 1 | 1 | 0.6232531 | 1 |
| 1192 | 0.0959609 | 0.0975213 | 0.1463922 | 0.3805649 | 0.2518074 | 0.1895188 | 0.3760378 | 0.1104952 |
| 1193 | 1 | 1 | 0.42319 | 0.592491 | 0.3694051 | 1 | 1 | 0.7101556 |
| 1194 | 0.4373883 | 1 | 0.6874021 | 0.6178776 | 0.3232784 | 0.3889339 | 0.2609041 | 1 |
| 1195 | 1 | 1 | 2.4070383 | 2.6750618 | 3.3606216 | 1.43356 | 2.8229358 | 3.1484515 |
| 1196 | 0.6207052 | 0.5203806 | 0.4984868 | 0.5132995 | 0.6020503 | 0.57104 | 1 | 0.6635862 |
| 1197 | 0.5674342 | 0.2021059 | 1 | 0.4247864 | 1 | 0.5860187 | 0.2602415 | 0.3792291 |
| 1198 | 0.5877132 | 0.5549255 | 0.6032855 | 0.5263838 | 0.5732698 | 0.4969818 | 0.585858 | 0.5711898 |
| 1199 | 0.0876581 | 1 | 0.4727643 | 0.5397517 | 1 | 0.0234417 | 0.034294 | 0.0948713 |
| 1200 | 0.8628727 | 0.8593605 | 0.5675593 | 0.5683963 | 0.4997116 | 0.7364962 | 1 | 0.6440887 |
| 1201 | 1 | 1 | 2.7023795 | 3.1344016 | 3.0291959 | 1 | 1.4147085 | 2.8699079 |
| 1202 | 1.8899922 | 0.5797659 | 2.2232507 | 1.8346474 | 2.424053 | 1 | 1 | 1.9149171 |
| 1203 | 0.12243 | 0.3823887 | 0.4460985 | 1 | 0.3202956 | 0.3995356 | 1 | 0.1593019 |
| 1204 | 1.9786101 | 1.437692 | 5.064584 | 4.0800572 | 2.9162372 | 4.0319058 | 2.5079493 | 2.9197752 |
| 1205 | 1.343749 | 1.1459789 | 2.0662673 | 1.4340193 | 1.8397123 | 1.5050579 | 2.0285762 | 1.8023606 |
| 1206 | 1.0907021 | 1.274553 | 2.3009855 | 2.8570197 | 2.6510945 | 3.198615 | 1.8315381 | 2.2184264 |
| 1207 | 1.1610297 | 1 | 2.1934214 | 3.5283354 | 3.1981728 | 1.4172551 | 2.7335424 | 3.1535007 |
| 1208 | 2.7841346 | 2.0246497 | 1 | 2.1139694 | 2.244786 | 0.1164035 | 3.5075786 | 1 |
| 1209 | 1 | 1.5936488 | 2.6644864 | 1 | 2.1006801 | 1.3510389 | 1.4554454 | 2.3580049 |
| 1210 | 1.2543196 | 1.3666927 | 1.516986 | 2.5439293 | 3.5132923 | 2.5819872 | 2.4163299 | 1 |
| 1211 | 1.2310752 | 0.565293 | 4.0609446 | 3.583203 | 5.3709263 | 1.5733668 | 3.2926477 | 3.3594927 |
| 1212 | 1 | 0.8728144 | 0.5903919 | 0.5205676 | 0.3764296 | 1 | 1 | 0.6609334 |
| 1213 | 1 | 1.2746124 | 2.6316586 | 1.1869701 | 3.6783551 | 1.303619 | 2.4560593 | 3.2613327 |
| 1214 | 1.1531973 | 1 | 2.708048 | 2.8544027 | 3.1036223 | 0.8504006 | 1 | 3.3036513 |
| 1215 | 1 | 1 | 0.4955072 | 0.6005767 | 0.3868767 | 1 | 1 | 0.63895 |
| 1216 | 0.7084493 | 1.2293142 | 2.2889865 | 1.270705 | 3.3667989 | 1 | 2.5013852 | 3.0330362 |
| 1217 | 2.5562779 | 2.7784562 | 2.273397 | 1.8473883 | 1 | 1 | 1 | 2.2894851 |
| 1218 | 1.2498509 | 1 | 2.0397662 | 1.3300821 | 2.749865 | 2.0894438 | 1 | 1.6163215 |
| 1219 | 0.046059 | 0.1421072 | 0.0788984 | 0.3702595 | 0.2836295 | 0.2105534 | 0.0552329 | 0.0984366 |
| 1220 | 2.0457628 | 1 | 1 | 1.8154591 | 3.3788938 | 0.8310447 | 1.8784469 | 3.2135904 |
| 1221 | 1 | 1 | 0.3492997 | 2.9044444 | 2.028794 | 1 | 1 | 2.8865804 |
| 1222 | 0.0572153 | 0.0460402 | 0.4286429 | 0.0582527 | 0.0344236 | 0.0418853 | 0.1953626 | 0.1357031 |
| 1223 | 0.6357353 | 5.4245988 | 2.278353 | 2.0464081 | 1.2797513 | 3.4676423 | 0.5002129 | 2.7295444 |
| 1224 | 1 | 0.6040819 | 2.7306221 | 1.9036548 | 3.6429307 | 1.2335699 | 1 | 3.5822956 |
| 1225 | 1 | 2.4064548 | 2.9946955 | 1.5610323 | 2.5309758 | 1.5219224 | 1.2957853 | 3.5161941 |

Table 4

| SEQ ID NO | Patient ID | | | | | | | |
|--------------|------------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|
| | 392 | 393 | 413 | 452 | 505 | 517 | 534 | 546 |
| 1226 | 0.0263608 | 0.001 | 0.0761612 | 0.2416822 | 0.316853 | 0.1963872 | 0.0396495 | 0.0288324 |
| 1227 | 0.2890009 | 0.4578297 | 0.768479 | 0.3399836 | 0.4743628 | 0.2772219 | 0.5518626 | 0.1829592 |
| 1228 | 1.5828706 | 1 | 2.2193725 | 2.7786522 | 2.653419 | 1.689709 | 3.3404439 | 3.1528552 |
| 1229 | 1.6913513 | 1 | 2.7627612 | 1 | 1 | 1 | 1.6487293 | 3.4559736 |
| 1230 | 1.4988683 | 1.3374502 | 3.6381889 | 2.3493103 | 3.5556493 | 2.2120028 | 1.4232864 | 2.6673876 |
| 1231 | 1.2579352 | 2.5457723 | 1.9694342 | 1.6953377 | 1.4234668 | 1.1124751 | 1.8460867 | 1.8411388 |
| 1232 | 0.2353159 | 1 | 0.5742943 | 0.5472765 | 0.4479315 | 0.3604482 | 0.4512356 | 0.4570931 |
| 1233 | 1 | 1.3595008 | 2.9425004 | 1.6969644 | 1.978449 | 1.2110788 | 2.0291915 | 2.486538 |
| 1234 | 5.2601033 | 6.6909905 | 2.3440537 | 1.8022594 | 0.7434584 | 3.1187922 | 4.0967267 | 1 |
| 1235 | 2.0735412 | 1 | 3.1391511 | 3.6446693 | 1.7318628 | 1.7366306 | 0.5604788 | 1.7632289 |
| 1236 | 0.2607343 | 0.3904412 | 0.6243786 | 0.629861 | 1 | 0.2887741 | 0.2454817 | 0.6132975 |
| 1237 | 1 | 1 | 1 | 2.5996122 | 2.0909615 | 0.941078 | 1 | 2.2721486 |
| 1238 | 0.7413861 | 0.2592258 | 0.5863187 | 0.6831329 | 0.4174499 | 0.5099368 | 0.5138355 | 0.6086847 |
| 1239 | 1 | 0.7540933 | 2.5667943 | 2.5173118 | 3.1535424 | 1.4851424 | 1 | 2.9018979 |
| 1240 | 1.3241252 | 1 | 2.0523074 | 2.2626387 | 2.4309956 | 1.3954539 | 1 | 2.448981 |
| 1241 | 0.7863281 | 0.6201969 | 2.2529191 | 2.7206601 | 3.2764597 | 1.3246613 | 1 | 3.163323 |
| 1242 | 1.7969209 | 1.3136387 | 2.1780752 | 1 | 2.1972357 | 1.2732245 | 1 | 2.1463989 |
| 1243 | 1.6365104 | 1.2596449 | 1.9972585 | 1.9949406 | 2.1607424 | 1.33235 | 1 | 2.2705856 |
| 1244 | 1.963591 | 1.3201184 | 2.8450432 | 1.9905109 | 2.2037055 | 1.2646543 | 1 | 2.1583793 |
| 1245 | 1.3066707 | 1 | 2.5255897 | 1 | 3.0182929 | 1.6165323 | 1 | 2.7307542 |
| 1246 | 1.5626412 | 1.3534465 | 3.5023338 | 2.6505746 | 3.2718392 | 1.5839531 | 1 | 3.8144226 |
| 1247 | 1.161105 | 1.3861911 | 2.0914213 | 1.5827034 | 1 | 1.1405315 | 1 | 2.1225402 |
| 1248 | 1.5760155 | 1.2560934 | 2.6099087 | 2.2150026 | 2.0826402 | 1.4373546 | 1 | 2.3735078 |
| 1249 | 1 | 0.6040918 | 2.0468524 | 2.296464 | 3.3299127 | 1.4323565 | 1 | 1 |
| 1250 | 0.9120939 | 1 | 0.5282478 | 0.6999384 | 0.3604128 | 1 | 1 | 0.5639092 |
| 1251 | 0.767331 | 1 | 1 | 0.303652 | 0.8077926 | 0.2710817 | 1 | 0.5069841 |
| 1252 | 0.4560702 | 0.5292542 | 0.5254937 | 0.4015046 | 1 | 0.5340377 | 0.368391 | 0.3617448 |
| 1253 | 2.0055943 | 2.0258369 | 3.1469154 | 1.4741071 | 2.0835753 | 1 | 1 | 2.6918605 |
| 1254 | 2.3040682 | 1.4167988 | 1.9487558 | 1 | 2.1580626 | 1 | 1 | 3.0647183 |
| 1255 | 0.6926655 | 1.3234819 | 1.8392554 | 2.2946119 | 2.7138392 | 1.0833378 | 1 | 2.29062 |
| 1256 | 1 | 0.4877251 | 2.1239566 | 2.7087229 | 2.0550307 | 0.8806111 | 3.3782775 | 2.3279508 |
| 1257 | 0.2341436 | 0.6465113 | 0.463208 | 0.70183 | 0.7412178 | 0.558292 | 1 | 0.4154364 |
| 1258 | 2.6045283 | 2.0779115 | 2.222519 | 3.2798736 | 1.4412406 | 1.5888285 | 1 | 1 |
| 1259 | 0.6996764 | 0.5234968 | 0.5168862 | 0.4880598 | 0.5158404 | 0.4931719 | 0.4614557 | 0.6390914 |
| 1260 | 1 | 1 | 0.501013 | 0.6033453 | 0.4306671 | 1 | 1 | 0.6502839 |
| 1261 | 0.9090893 | 1 | 0.5086033 | 0.5965309 | 0.3617822 | 1.0995584 | 1 | 0.6749704 |
| 1262 | 1.5382133 | 1 | 1.6757239 | 2.0119919 | 1.7902167 | 1.8549658 | 2.2809255 | 2.3701599 |
| 1263 | 1.3929885 | 0.6303072 | 1.8130085 | 1.8924244 | 2.0578256 | 1.8533484 | 1 | 2.7824671 |
| 1264 | 1.385617 | 1 | 0.8062885 | 0.25652 | 0.4736011 | 0.565375 | 1 | 0.7050737 |
| 1265 | 0.6373394 | 1 | 0.5454424 | 0.7284632 | 0.6408478 | 0.6333544 | 1 | 0.6838403 |
| 1266 | 1.1981278 | 0.7957412 | 0.686687 | 0.2737779 | 0.456636 | 0.5603157 | 1 | 0.6252344 |
| 1267 | 0.7309519 | 0.3596752 | 1 | 2.1368873 | 2.6374321 | 0.7756602 | 1 | 1 |
| 1268 | 2.9041132 | 0.6701249 | 2.893428 | 2.988266 | 1.5222499 | 1.9579083 | 1 | 2.4796664 |
| 1269 | 3.4794013 | 1.6322992 | 3.8595577 | 3.6838571 | 5.448711 | 4.5611065 | 5.0805188 | 4.448599 |
| 1270 | 0.7693933 | 1 | 1.8279958 | 3.7561725 | 3.3690805 | 1.8029388 | 2.638292 | 2.9031741 |
| 1271 | 16.600193 | 9.7496843 | 4.5057226 | 7.8701187 | 1 | 4.3842054 | 4.8000904 | 4.467091 |
| 1272 | 0.7802473 | 0.8352226 | 0.7561607 | 0.3880412 | 0.5987152 | 0.5579853 | 1 | 0.6277997 |
| 1273 | 1.7752881 | 1.5142706 | 2.2529769 | 2.6881382 | 2.3788993 | 1.9181234 | 2.1930169 | 2.5005992 |
| 1274 | 0.1326285 | 1 | 0.2415722 | 0.1296852 | 0.3231448 | 0.4160168 | 0.3405944 | 0.0907015 |

Table 4

| SEQ ID | Patient ID | | | | | | | |
|--------|------------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|
| NO | 392 | 393 | 413 | 452 | 505 | 517 | 534 | 546 |
| 1275 | 0.6941165 | 1 | 0.3319965 | 2.1264025 | 1 | 0.6240942 | 0.4364959 | 0.2949378 |
| 1276 | 0.5690947 | 1.2909451 | 1 | 0.4379281 | 0.4924426 | 1.4866373 | 0.7090089 | 0.5804962 |
| 1277 | 0.7025427 | 1.3378954 | 2.1218006 | 2.8958331 | 3.3815204 | 1.1438431 | 2.5973922 | 2.7129585 |
| 1278 | 2.0350979 | 1 | 3.2254207 | 2.3272534 | 2.3455494 | 1.3614183 | 1 | 2.8558076 |
| 1279 | 1.60793 | 1.4941589 | 3.0778494 | 1 | 3.5742738 | 1.5243448 | 1 | 4.0485213 |
| 1280 | 0.3760625 | 1 | 0.3662046 | 1 | 1 | 0.8619528 | 0.4224485 | 0.2240264 |
| 1281 | 1.8604483 | 2.0948872 | 2.9893928 | 0.6716138 | 2.1863993 | 1 | 1 | 1.9945969 |
| 1282 | 2.0319393 | 1.7879198 | 3.3579215 | 4.1449225 | 2.471656 | 2.9824657 | 3.7246228 | 3.7693073 |
| 1283 | 1 | 0.8500417 | 0.5017804 | 0.6914336 | 0.4005677 | 1 | 0.8135238 | 0.7272499 |
| 1284 | 1 | 1 | 2.330241 | 3.0513866 | 2.7390435 | 1.5574989 | 2.8216601 | 2.8558958 |
| 1285 | 1.1401294 | 1.3073965 | 1.8459072 | 1.6645903 | 1.8669519 | 1.3681181 | 1 | 1 |
| 1286 | 1.3161544 | 1 | 2.3185479 | 1 | 2.1375172 | 1.2918982 | 1 | 1 |
| 1287 | 3.0445378 | 1 | 1 | 2.9871747 | 2.399815 | 1.2116614 | 1 | 3.4546817 |
| 1288 | 0.7054095 | 1.6799123 | 2.3831881 | 2.4088948 | 1.4168601 | 0.6314993 | 1 | 2.2304191 |
| 1289 | 1.9568976 | 1 | 1 | 4.4821943 | 2.3407377 | 2.1659397 | 1 | 3.652806 |
| 1290 | 1.5647822 | 1.252077 | 3.4875854 | 3.1428315 | 2.7940201 | 1.3796626 | 1 | 3.4705086 |
| 1291 | 1.1925246 | 1 | 2.8149389 | 2.9989477 | 2.9437419 | 1 | 1 | 4.0550939 |
| 1292 | 0.0455355 | 0.0809512 | 0.1543351 | 0.2716921 | 0.0447633 | 0.0920572 | 0.2501091 | 0.1071634 |
| 1293 | 1 | 1 | 0.5138908 | 0.6727462 | 0.40535 | 1 | 1 | 0.6487638 |
| 1294 | 1.6152606 | 0.7485139 | 3.2425759 | 0.9460481 | 2.6244046 | 1 | 1.6489905 | 1.3606131 |
| 1295 | 1 | 1 | 0.4983424 | 0.6785148 | 0.4003396 | 1 | 0.8742508 | 0.6699794 |
| 1296 | 0.1764069 | 1 | 0.3302505 | 0.5137508 | 1.3589331 | 0.2769306 | 0.2754833 | 0.4257322 |
| 1297 | 0.5145712 | 0.1790363 | 0.7412588 | 1 | 1.2410912 | 0.4242114 | 0.1262775 | 0.4563663 |
| 1298 | 1 | 1.9243882 | 2.4868138 | 1.4690441 | 2.714395 | 0.7545565 | 1.6682584 | 1.6455318 |
| 1299 | 1 | 2.7512317 | 0.3031761 | 1 | 0.6447079 | 2.7821996 | 1 | 1 |
| 1300 | 0.6427696 | 0.844947 | 1 | 0.4650934 | 0.6199714 | 1 | 1 | 0.7368754 |
| 1301 | 1 | 1.1957684 | 2.8163838 | 1 | 3.462211 | 1.139466 | 1 | 1.7521973 |
| 1302 | 1 | 7.4440352 | 1 | 2.5429407 | 0.1884052 | 1 | 1 | 1 |
| 1303 | 0.2018878 | 1 | 0.363932 | 0.3563224 | 0.2938868 | 0.3504522 | 0.3658755 | 0.5794517 |

Table 4

| SEQ ID NO | Patient ID | | | | | | | |
|--------------|------------|-----|-----------|-----------|-----|-----|-----|-----------|
| | 577 | 695 | 784 | 786 | 787 | 789 | 790 | 791 |
| 1 | 3.0227714 | | 2.1325895 | 2.4193425 | | | | 1 |
| 2 | 1.1420539 | | 0.4234378 | 0.6369584 | | | | 0.6101431 |
| 3 | 3.3396938 | | 1 | 1.7731123 | | | | 1 |
| 4 | 0.7037364 | | 0.3062226 | 0.1378194 | | | | 0.3583218 |
| 5 | 0.5675847 | | 0.8255816 | 0.5523191 | | | | 0.380477 |
| 6 | 0.6217617 | | 1 | 0.6081652 | | | | 0.4779032 |
| 7 | 2.0221867 | | 1 | 1 | | | | 2.9054189 |
| 8 | 2.2439893 | | 5.668234 | 4.2907423 | | | | 1 |
| 9 | 0.5089518 | | 1 | 0.7079489 | | | | 0.5356492 |
| 10 | 0.289236 | | 0.4625569 | 1 | | | | 0.1376797 |
| 11 | 0.3943149 | | 0.174106 | 0.5714198 | | | | 1 |
| 12 | 1.274314 | | 1 | 1.7664955 | | | | 1 |
| 13 | 0.323844 | | 0.179401 | 1 | | | | 0.6267236 |
| 14 | 2.9293078 | | 1 | 1 | | | | 1 |
| 15 | 0.3356003 | | 0.1954688 | 1 | | | | 0.2402416 |
| 16 | 2.5876474 | | 1.7496184 | 2.8249407 | | | | 3.0280874 |
| 17 | 1.7005707 | | 1 | 1 | | | | 1 |
| 18 | 1.4851995 | | 3.12969 | 2.1237625 | | | | 1 |
| 19 | 0.3467773 | | 0.1824525 | 1 | | | | 1 |
| 20 | 5.2618963 | | 1 | 1 | | | | 1 |
| 21 | 0.3696512 | | 2.2453032 | 1 | | | | 1 |
| 22 | 2.3899812 | | 2.3942221 | 1 | | | | 1.7921614 |
| 23 | 2.7148872 | | 2.4261572 | 1 | | | | 1 |
| 24 | 2.3188716 | | 1.2859785 | 1 | | | | 2.597565 |
| 25 | 0.6083493 | | 0.6017115 | 0.506961 | | | | 0.4305362 |
| 26 | 2.9646286 | | 1.4292156 | 3.7626717 | | | | 1 |
| 27 | 0.6228831 | | 0.8514508 | 0.5773087 | | | | 0.41871 |
| 28 | 1.4147138 | | 0.3618134 | 0.6768505 | | | | 1 |
| 29 | 1.8397376 | | 2.0064229 | 2.3606947 | | | | 4.4422274 |
| 30 | 6.0024463 | | 3.1467064 | 1 | | | | 5.0531366 |
| 31 | 3.1453027 | | 2.470817 | 6.7701719 | | | | 3.1328726 |
| 32 | 0.6358499 | | 0.6386399 | 1 | | | | 1.29421 |
| 33 | 1.4362954 | | 3.0922288 | 1 | | | | 1.3250643 |
| 34 | 2.0827431 | | 1.2679762 | 1 | | | | 1.6447695 |
| 35 | 2.6943824 | | 1 | 1 | | | | 1.9494872 |
| 36 | 1.8746203 | | 1 | 1 | | | | 1.5647616 |
| 37 | 2.3991011 | | 1.3002555 | 1 | | | | 1.8569642 |
| 38 | 2.6218543 | | 1.662885 | 1 | | | | 2.6150981 |
| 39 | 0.3338104 | | 0.2518389 | 1 | | | | 0.136367 |
| 40 | 2.8165721 | | 1.4508996 | 2.023825 | | | | 2.2143928 |
| 41 | 1 | | 0.4316427 | 2.9332133 | | | | 0.2325446 |
| 42 | 3.8487867 | | 3.0567018 | 1 | | | | 1 |
| 43 | 0.5786429 | | 1 | 0.5752042 | | | | 0.4834042 |
| 44 | 0.650666 | | 1 | 1 | | | | 1 |
| 45 | 1.8729196 | | 0.8094977 | 2.4554112 | | | | 2.0355442 |
| 46 | 1.7464893 | | 1.8383967 | 1 | | | | 1 |
| 47 | 2.144265 | | 1 | 3.7950345 | | | | 2.3679103 |
| 48 | 0.5499985 | | 1 | 0.6984646 | | | | 0.5455243 |
| 49 | 1.4624667 | | 1 | 1 | | | | 1 |

Table 4

| SEQ ID NO | Patient ID | | | | | | | |
|--------------|------------|-----|-----------|-----------|-----|-----|-----|-----------|
| | 577 | 695 | 784 | 786 | 787 | 789 | 790 | 791 |
| 50 | 0.1732253 | | 0.8935786 | 1 | | | | 1 |
| 51 | 3.1714889 | | 1 | 4.0245186 | | | | 1 |
| 52 | 0.5591035 | | 1 | 0.659709 | | | | 0.4830261 |
| 53 | 1000 | | 1000 | 1 | | | | 1 |
| 54 | 3.406949 | | 1.8471599 | 1 | | | | 1 |
| 55 | 0.4901922 | | 0.0393104 | 1 | | | | 1 |
| 56 | 2.0522644 | | 1 | 1.7254737 | | | | 2.0233503 |
| 57 | 0.3853956 | | 1.3418544 | 0.8502073 | | | | 0.666336 |
| 58 | 0.6217468 | | 1 | 1 | | | | 0.4598705 |
| 59 | 1.9706759 | | 2.2379739 | 1.6575719 | | | | 2.4834598 |
| 60 | 3.8685785 | | 1 | 1 | | | | 1 |
| 61 | 2.5293041 | | 2.8556378 | 2.2839812 | | | | 2.6106926 |
| 62 | 1.9122509 | | 1 | 1 | | | | 1.6343957 |
| 63 | 2.1381084 | | 1.2365741 | 1.9174193 | | | | 1.9712211 |
| 64 | 1.9335429 | | 1 | 1.9026692 | | | | 2.2156344 |
| 65 | 3.6687661 | | 2.5039279 | 2.1100952 | | | | 2.2394273 |
| 66 | 0.6043612 | | 0.8867595 | 0.6712444 | | | | 0.3954237 |
| 67 | 2.4947779 | | 1.3056842 | 2.272436 | | | | 2.17162 |
| 68 | 2.7754139 | | 6.6562593 | 2.4720552 | | | | 1 |
| 69 | 2.3939767 | | 1.1721109 | 1.7857369 | | | | 1.8669653 |
| 70 | 3.1568957 | | 1 | 1 | | | | 1 |
| 71 | 3.7703247 | | 1 | 0.5487404 | | | | 1 |
| 72 | 0.2868595 | | 0.1942216 | 0.7774494 | | | | 1 |
| 73 | 4.3107875 | | 1.4367494 | 1 | | | | 1 |
| 74 | 2.3713925 | | 1.8591429 | 1 | | | | 2.5302891 |
| 75 | 1 | | 1.8662279 | 1 | | | | 1 |
| 76 | 1.9024997 | | 1 | 1.9025172 | | | | 1 |
| 77 | 0.6232916 | | 1.1263261 | 0.6491584 | | | | 0.6519571 |
| 78 | 0.5889584 | | 0.8221698 | 0.5870763 | | | | 0.3961988 |
| 79 | 0.5715431 | | 0.8007197 | 0.5822843 | | | | 0.4690542 |
| 80 | 3.904189 | | 1.3711261 | 2.5555765 | | | | 2.4015104 |
| 81 | 6.6156229 | | 3.320566 | 3.848362 | | | | 4.7776165 |
| 82 | 0.8994048 | | 0.4414844 | 2.1553333 | | | | 1 |
| 83 | 2.287925 | | 1 | 1 | | | | 2.709314 |
| 84 | 2.8537199 | | 2.0383605 | 2.3193314 | | | | 1 |
| 85 | 0.2396933 | | 0.0692054 | 0.5435536 | | | | 0.4566766 |
| 86 | 2.4067653 | | 1 | 2.5486513 | | | | 1.9736823 |
| 87 | 4.3638654 | | 1.8553116 | 1 | | | | 3.9319491 |
| 88 | 2.3319795 | | 1.5638565 | 1.9430635 | | | | 1.9418714 |
| 89 | 1.7550596 | | 1.2950034 | 1.8482566 | | | | 2.3162801 |
| 90 | 2.4621677 | | 1 | 1.9793829 | | | | 1.6753102 |
| 91 | 1.9291166 | | 1.6333855 | 1 | | | | 1 |
| 92 | 4.4696126 | | 2.5328174 | 2.8741245 | | | | 3.2717684 |
| 93 | 0.6311712 | | 1 | 0.5860318 | | | | 0.4339877 |
| 94 | 1.9151992 | | 1 | 1 | | | | 1 |
| 95 | 2.7916039 | | 4.0021245 | 1 | | | | 1 |
| 96 | 2.0312323 | | 1.4906227 | 1.8570439 | | | | 1.7905779 |
| 97 | 1 | | 4.6163211 | 1.8917922 | | | | 1 |
| 98 | 2.2565105 | | 3.1322197 | 2.6934763 | | | | 1 |

Table 4

| SEQ ID | Patient ID | | | | | | | |
|--------|------------|-----|-----------|-----------|-----|-----|-----|-----------|
| NO | 577 | 695 | 784 | 786 | 787 | 789 | 790 | 791 |
| 99 | 0.5859061 | | 1 | 1 | | | | 0.5446822 |
| 100 | 0.7169186 | | 0.8008276 | 0.6204439 | | | | 0.5413803 |
| 101 | 4.5326941 | | 2.1245069 | 2.5984977 | | | | 1 |
| 102 | 1.817391 | | 2.1129229 | 1.9272419 | | | | 1 |
| 103 | 0.282463 | | 0.3904623 | 0.4616613 | | | | 0.5081924 |
| 104 | 0.5832028 | | 1 | 0.6324946 | | | | 0.4402709 |
| 105 | 3.2264457 | | 1 | 2.1821796 | | | | 1 |
| 106 | 2.6624332 | | 1 | 1.8952532 | | | | 1.9537279 |
| 107 | 0.2864734 | | 0.6535554 | 2.193362 | | | | 1 |
| 108 | 1.8570416 | | 1 | 1 | | | | 2.1813896 |
| 109 | 2.4840613 | | 1.4953996 | 1.7804881 | | | | 1 |
| 110 | 1.8653296 | | 1.5794314 | 1.2661319 | | | | 3.8722311 |
| 111 | 2.4203411 | | 1 | 1 | | | | 2.0127871 |
| 112 | 0.4879197 | | 0.2083159 | 1.504641 | | | | 4.0469078 |
| 113 | 0.6197268 | | 0.9032044 | 0.5704439 | | | | 0.6104683 |
| 114 | 0.6041607 | | 0.775074 | 0.5323404 | | | | 0.4613577 |
| 115 | 2.1698273 | | 1.1317323 | 2.158653 | | | | 5.2895268 |
| 116 | 0.5780785 | | 1 | 0.5779996 | | | | 0.4602856 |
| 117 | 0.5808115 | | 1 | 0.6987104 | | | | 1 |
| 118 | 0.4474076 | | 0.3493052 | 0.7336947 | | | | 1 |
| 119 | 0.5225276 | | 0.7209606 | 0.6504343 | | | | 0.3104849 |
| 120 | 0.5555759 | | 0.6392629 | 0.6877722 | | | | 0.3019031 |
| 121 | 2.2477397 | | 2.9573068 | 1.2510847 | | | | 1 |
| 122 | 0.2985119 | | 0.4310144 | 0.4282131 | | | | 1 |
| 123 | 1 | | 3.1488187 | 2.2910823 | | | | 2.6749284 |
| 124 | 3.0320695 | | 4.2457751 | 6.4740037 | | | | 1 |
| 125 | 2.2865585 | | 2.116033 | 2.5574967 | | | | 1.5908399 |
| 126 | 0.2194261 | | 0.485213 | 2.0928581 | | | | 0.4864299 |
| 127 | 0.578888 | | 0.798503 | 0.5682264 | | | | 0.490685 |
| 128 | 0.6117655 | | 1 | 0.6642025 | | | | 0.4320282 |
| 129 | 3.2824125 | | 3.0561778 | 1 | | | | 1 |
| 130 | 1 | | 0.5088802 | 1 | | | | 1 |
| 131 | 2.9332216 | | 1.8409029 | 1 | | | | 1 |
| 132 | 6.2918829 | | 1.6360239 | 1.7661027 | | | | 1 |
| 133 | 2.0240656 | | 1.2802153 | 2.3133265 | | | | 1.8713415 |
| 134 | 0.6211973 | | 0.6777175 | 0.5239394 | | | | 0.44088 |
| 135 | 0.5474438 | | 1 | 0.7358019 | | | | 0.4998394 |
| 136 | 0.2554822 | | 0.1429803 | 0.5828826 | | | | 0.4378198 |
| 137 | 4.0370953 | | 1 | 1 | | | | 1 |
| 138 | 0.7339552 | | 0.0299838 | 0.3544202 | | | | 1.0969011 |
| 139 | 1.4362212 | | 2.0907671 | 2.2231735 | | | | 3.4283035 |
| 140 | 1.5781805 | | 2.3449002 | 1 | | | | 1 |
| 141 | 2.960544 | | 1.215809 | 1.8993324 | | | | 2.1939848 |
| 142 | 2.4305156 | | 1.1933923 | 1.9565728 | | | | 1.7956223 |
| 143 | 2.2728416 | | 1.4200614 | 1 | | | | 1.2895854 |
| 144 | 2.4194499 | | 1 | 1.5108746 | | | | 1 |
| 145 | 3.1014042 | | 2.0796442 | 2.2317111 | | | | 1 |
| 146 | 1.8492436 | | 1.3105801 | 1.9519245 | | | | 1.9988394 |
| 147 | 2.1017626 | | 1.5603794 | 1.3697847 | | | | 1.9405841 |

Table 4

| SEQ ID NO | Patient ID | | | | | | | |
|--------------|------------|-----|-----------|-----------|-----|-----|-----|-----------|
| | 577 | 695 | 784 | 786 | 787 | 789 | 790 | 791 |
| 148 | 2.4984837 | | 1.3731752 | 1.7167297 | | | | 2.5972235 |
| 149 | 0.5308825 | | 0.8298014 | 0.5063146 | | | | 0.4143831 |
| 150 | 0.6715793 | | 0.4445829 | 0.7433544 | | | | 0.5712187 |
| 151 | 1.7850111 | | 2.2905428 | 1.7560367 | | | | 2.7633071 |
| 152 | 2.0711131 | | 1 | 1.7571159 | | | | 2.0885265 |
| 153 | 1.4737774 | | 8.0650902 | 1 | | | | 1 |
| 154 | 1.7000137 | | 1 | 3.0020779 | | | | 2.4802645 |
| 155 | 2.400371 | | 1.4068143 | 2.6269561 | | | | 1 |
| 156 | 2.4374966 | | 1.6240103 | 1 | | | | 2.1592795 |
| 157 | 3.315899 | | 1 | 1.6885048 | | | | 2.1813896 |
| 158 | 2.700487 | | 6.3666913 | 2.6258945 | | | | 1.5940163 |
| 159 | 0.7386414 | | 0.7733591 | 0.6119242 | | | | 0.4891121 |
| 160 | 0.5884312 | | 0.8395723 | 0.6593257 | | | | 0.4382155 |
| 161 | 0.5945284 | | 1 | 0.7607761 | | | | 0.5253628 |
| 162 | 0.7492986 | | 1 | 0.8674273 | | | | 0.2664136 |
| 163 | 1.5336135 | | 1.6062448 | 1 | | | | 1 |
| 164 | 2.5527795 | | 1 | 2.3030407 | | | | 2.4494409 |
| 165 | 0.216344 | | 0.7418806 | 1 | | | | 0.2428451 |
| 166 | 3.4916047 | | 1 | 3.8146801 | | | | 1.9625573 |
| 167 | 0.434827 | | 0.209014 | 0.6108313 | | | | 0.3157908 |
| 168 | 0.4335941 | | 0.0653526 | 0.6776205 | | | | 3.3172211 |
| 169 | 1.6148307 | | 1.1871928 | 1.4568323 | | | | 1.4479456 |
| 170 | 3.4314048 | | 1 | 1 | | | | 2.3077584 |
| 171 | 3.0122108 | | 1.831634 | 2.5554852 | | | | 1 |
| 172 | 2.5958686 | | 0.6688879 | 2.4541466 | | | | 1.567959 |
| 173 | 2.3662755 | | 1.6625748 | 1.526752 | | | | 1.9576477 |
| 174 | 0.8397619 | | 0.7119534 | 1.7109358 | | | | 1.2751462 |
| 175 | 2.3434016 | | 1.5500941 | 1.536334 | | | | 2.2511638 |
| 176 | 1.9341073 | | 1.5812528 | 1 | | | | 1 |
| 177 | 0.2371162 | | 0.3185519 | 0.3446156 | | | | 0.2709686 |
| 178 | 1.7079008 | | 2.2033401 | 1 | | | | 1 |
| 179 | 2.90581 | | 1.3394748 | 2.1154658 | | | | 2.2990316 |
| 180 | 1.7124904 | | 1 | 1.4397252 | | | | 1.6140359 |
| 181 | 1.3557838 | | 1.9891381 | 2.5870241 | | | | 1 |
| 182 | 1.8056198 | | 1.3396157 | 1 | | | | 1.8867987 |
| 183 | 2.4329515 | | 2.5569416 | 2.8586073 | | | | 2.5360536 |
| 184 | 2.5301953 | | 1.2857188 | 1.4861216 | | | | 3.6497857 |
| 185 | 1.488289 | | 1.5074132 | 2.4207354 | | | | 1 |
| 186 | 1.7952523 | | 1.672496 | 1.345952 | | | | 1.9579386 |
| 187 | 1.7613277 | | 1 | 1.6971645 | | | | 1.907242 |
| 188 | 2.9758428 | | 1.8324248 | 1.9780683 | | | | 2.1966678 |
| 189 | 3.0400605 | | 2.4930019 | 2.3530788 | | | | 2.6179566 |
| 190 | 0.5258398 | | 1 | 0.527929 | | | | 0.6447559 |
| 191 | 1.6693048 | | 1.6401787 | 1.9502735 | | | | 1 |
| 192 | 0.5636932 | | 0.9271636 | 0.563994 | | | | 0.4582042 |
| 193 | 3.0722102 | | 1.3675286 | 1.3918156 | | | | 2.9108761 |
| 194 | 0.3031163 | | 0.2460286 | 1 | | | | 0.341633 |
| 195 | 0.6246506 | | 1 | 0.6251977 | | | | 0.4527915 |
| 196 | 2.2090917 | | 2.4121712 | 1.8793079 | | | | 1.6280999 |

Table 4

| SEQ ID | Patient ID | | | | | | | |
|--------|------------|-----|-----------|-----------|-----|-----|-----|-----------|
| | 577 | 695 | 784 | 786 | 787 | 789 | 790 | 791 |
| 197 | 0.6336368 | | 1.0471891 | 0.6008799 | | | | 0.5253209 |
| 198 | 3.1632677 | | 3.7426435 | 1.4067994 | | | | 1 |
| 199 | 2.4770432 | | 1 | 1 | | | | 1.8674947 |
| 200 | 2.6557047 | | 8.5354637 | 1 | | | | 1 |
| 201 | 1.9132089 | | 1 | 3.680904 | | | | 2.2383492 |
| 202 | 1.9965872 | | 1 | 1 | | | | 1 |
| 203 | 3.4948353 | | 2.5027326 | 1 | | | | 1 |
| 204 | 4.120689 | | 1 | 1 | | | | 1 |
| 205 | 0.746469 | | 2.393772 | 1.8322433 | | | | 1 |
| 206 | 2.2871304 | | 1 | 2.127682 | | | | 1 |
| 207 | 2.3090908 | | 1.2908396 | 1.945655 | | | | 1.9928419 |
| 208 | 1 | | 28.30337 | 1 | | | | 1 |
| 209 | 0.3463762 | | 1.3638456 | 0.531691 | | | | 0.6957649 |
| 210 | 0.5912681 | | 1 | 0.6590582 | | | | 0.4711851 |
| 211 | 3.8259053 | | 1.8804024 | 3.9059822 | | | | 1 |
| 212 | 2.0442585 | | 0.5784783 | 1.4714675 | | | | 1 |
| 213 | 0.5192227 | | 0.8398254 | 0.5391341 | | | | 0.4013615 |
| 214 | 2.7334834 | | 1.6678951 | 1.5845945 | | | | 2.635767 |
| 215 | 1.8098233 | | 2.2610815 | 2.2543752 | | | | 1 |
| 216 | 0.5290333 | | 1 | 0.5000593 | | | | 0.5252581 |
| 217 | 3.7944092 | | 0.9307363 | 1 | | | | 2.9350902 |
| 218 | 1.8879956 | | 2.3583021 | 1 | | | | 1 |
| 219 | 1.7878703 | | 2.4480817 | 1 | | | | 1 |
| 220 | 2.6300607 | | 1.4870166 | 1 | | | | 1 |
| 221 | 0.5730433 | | 0.861225 | 0.5275861 | | | | 0.4113379 |
| 222 | 0.5686913 | | 0.8669888 | 0.5966119 | | | | 0.3882579 |
| 223 | 0.5205224 | | 0.7642738 | 0.5316198 | | | | 0.3389736 |
| 224 | 0.5135711 | | 0.7744679 | 0.5571624 | | | | 1 |
| 225 | 0.6240491 | | 1 | 0.5346938 | | | | 0.5319002 |
| 226 | 1 | | 2.1385764 | 1 | | | | 1 |
| 227 | 1.89817 | | 1.3853412 | 1 | | | | 1 |
| 228 | 1.5380769 | | 1.5646252 | 1.5514396 | | | | 1 |
| 229 | 4.9083311 | | 1.2250503 | 0.5958361 | | | | 1 |
| 230 | 1.6281317 | | 1.398624 | 2.3335665 | | | | 1 |
| 231 | 0.5499837 | | 1 | 0.5871004 | | | | 0.507732 |
| 232 | 1 | | 1 | 1 | | | | 1 |
| 233 | 1 | | 1 | 1 | | | | 1 |
| 234 | 1000 | | 1 | 1 | | | | 1 |
| 235 | 0.1573546 | | 0.2184552 | 0.4839668 | | | | 0.6340083 |
| 236 | 2.5399538 | | 1.3785701 | 1.9021628 | | | | 2.4019483 |
| 237 | 1.7511904 | | 1 | 1.374711 | | | | 1 |
| 238 | 0.1840755 | | 0.220024 | 0.4900486 | | | | 0.0904023 |
| 239 | 0.5521151 | | 0.8246573 | 0.5827258 | | | | 0.4447452 |
| 240 | 0.4460634 | | 0.406573 | 0.3519943 | | | | 0.5981919 |
| 241 | 0.5598462 | | 0.4848091 | 0.4672105 | | | | 0.6941151 |
| 242 | 2.2350625 | | 2.578393 | 2.1307263 | | | | 5.4063964 |
| 243 | 2.0915214 | | 1.1608142 | 1.8753142 | | | | 2.4195962 |
| 244 | 3.1960115 | | 1.2494366 | 1.6309833 | | | | 1.8895955 |
| 245 | 1.6753649 | | 0.8168799 | 2.5425773 | | | | 1.4913318 |

Table 4

| SEQ ID | Patient ID | | | | | | | |
|--------|------------|-----|-----------|-----------|-----|-----|-----|-----------|
| | 577 | 695 | 784 | 786 | 787 | 789 | 790 | 791 |
| 246 | 1 | | 1 | 1 | | | | 1 |
| 247 | 3.4774571 | | 1 | 1.7643154 | | | | 1.6144315 |
| 248 | 2.1907926 | | 1.6632885 | 1.9757719 | | | | 1 |
| 249 | 0.4807604 | | 0.5929961 | 0.5982948 | | | | 0.723211 |
| 250 | 2.1910451 | | 1 | 1 | | | | 2.4518725 |
| 251 | 1.5397404 | | 2.4629649 | 1.2948007 | | | | 1 |
| 252 | 10.025424 | | 1 | 1 | | | | 1 |
| 253 | 2.9242131 | | 0.5743627 | 1.6360603 | | | | 1 |
| 254 | 0.6648434 | | 0.8202479 | 0.5481723 | | | | 0.4133623 |
| 255 | 1 | | 1 | 1 | | | | 1 |
| 256 | 1 | | 9.3847859 | 1 | | | | 1 |
| 257 | 0.5469685 | | 0.8582725 | 0.5686785 | | | | 0.3854912 |
| 258 | 2.1833066 | | 1.3015086 | 1.8764465 | | | | 1 |
| 259 | 2.4775185 | | 1.4753002 | 1.9625357 | | | | 2.2628295 |
| 260 | 0.1726534 | | 0.2175099 | 0.3212561 | | | | 1 |
| 261 | 1.9860043 | | 1.6009936 | 1.9941268 | | | | 2.3159407 |
| 262 | 1 | | 6.6742034 | 2.2207561 | | | | 1 |
| 263 | 5.2409978 | | 0.6110721 | 2.9439652 | | | | 1 |
| 264 | 3.5870216 | | 1 | 2.9880225 | | | | 1 |
| 265 | 0.6823033 | | 0.8796529 | 0.5416096 | | | | 1 |
| 266 | 0.0458072 | | 0.014865 | 0.026302 | | | | 1 |
| 267 | 2.8336161 | | 1 | 1.7749615 | | | | 2.0002052 |
| 268 | 2.566036 | | 1.4866445 | 2.7078636 | | | | 2.5562311 |
| 269 | 4.151799 | | 1.4502386 | 2.0961108 | | | | 1 |
| 270 | 2.3092765 | | 1.2038212 | 1.7362029 | | | | 2.0798976 |
| 271 | 0.5321673 | | 0.8544383 | 0.5061641 | | | | 0.4226259 |
| 272 | 0.6262177 | | 1 | 0.6191969 | | | | 1 |
| 273 | 1.2848598 | | 0.7885977 | 2.2334544 | | | | 3.2664948 |
| 274 | 1 | | 0.2856205 | 0.5424975 | | | | 1 |
| 275 | 0.5971797 | | 1 | 0.577374 | | | | 0.48467 |
| 276 | 1 | | 1 | 8.369962 | | | | 1 |
| 277 | 6.8532292 | | 1 | 1 | | | | 1 |
| 278 | 2.6629679 | | 2.3337255 | 2.060521 | | | | 1 |
| 279 | 2.0722939 | | 1.6520967 | 2.3919779 | | | | 2.3188625 |
| 280 | 1.5680357 | | 0.1105969 | 1 | | | | 1 |
| 281 | 1 | | 0.8727362 | 0.6018564 | | | | 0.4197217 |
| 282 | 1.3196163 | | 1.3379667 | 1.7558642 | | | | 2.1068992 |
| 283 | 1 | | 1 | 2.6871983 | | | | 0.588719 |
| 284 | 2.148164 | | 1.5349047 | 2.6314046 | | | | 2.1853705 |
| 285 | 0.2319028 | | 0.197934 | 0.789715 | | | | 0.1024021 |
| 286 | 1.0811558 | | 1.614245 | 1.800672 | | | | 2.0524595 |
| 287 | 2.3035505 | | 0.645275 | 3.6113512 | | | | 1 |
| 288 | 2.9440198 | | 1.3775686 | 2.9487016 | | | | 1 |
| 289 | 2.2314309 | | 1 | 2.1167187 | | | | 1.8256094 |
| 290 | 2.0264273 | | 1 | 1.9349632 | | | | 1.8201858 |
| 291 | 1.8926595 | | 1 | 1.7117552 | | | | 1.7577642 |
| 292 | 2.0323983 | | 1 | 1 | | | | 1 |
| 293 | 1 | | 0.7096237 | 1 | | | | 0.6267136 |
| 294 | 2.8462042 | | 0.4712938 | 1 | | | | 1 |

Table 4

| SEQ ID | Patient ID | | | | | | | |
|--------|------------|-----|-----------|-----------|-----------|-----------|-----------|-----------|
| | 577 | 695 | 784 | 786 | 787 | 789 | 790 | 791 |
| 295 | 3.6559998 | | 1 | 1 | | | | 2.9810323 |
| 296 | 0.6288467 | | 1 | 0.6239806 | | | | 0.4536856 |
| 297 | 0.580559 | | 1 | 1 | 1 | 0.53067 | 0.8063207 | 0.3992892 |
| 298 | 1.5880578 | | 1 | 1 | 2.3301342 | 2.8295486 | 1.4369235 | 1.8269176 |
| 299 | 0.5283203 | | 1 | 0.623056 | 1 | 0.59282 | 0.7276859 | 0.3433874 |
| 300 | 1.1869625 | | 1 | 1 | 0.8040121 | 2.0466557 | 1.8417565 | 1.6467228 |
| 301 | 1 | | 1 | 1 | 1.4271644 | 5.3504393 | 6.3638147 | 1 |
| 302 | 2.2156048 | | 1 | 1 | 1.4909722 | 4.1373737 | 1.6715152 | 1 |
| 303 | 0.2742715 | | 1 | 1 | 1 | 0.3805516 | 0.3855942 | 1 |
| 304 | 0.690116 | | 0.5201083 | 1 | 1 | 4.1512592 | 2.4541085 | 1.9668063 |
| 305 | 1 | | 1 | 1 | 0.6698285 | 8.4573392 | 2.5575293 | 1 |
| 306 | 0.6295373 | | 0.346112 | 0.4149342 | 0.1606429 | 0.424532 | 0.0777455 | 0.0927229 |
| 307 | 1.8443347 | | 1 | 1 | 2.6915221 | 2.9723364 | 1.8364633 | 1 |
| 308 | 1 | | 1 | 1 | 0.2119874 | 0.091272 | 0.5131799 | 0.3876828 |
| 309 | 0.4104157 | | 0.222128 | 0.3518314 | 0.2226691 | 0.0506181 | 0.8440078 | 0.2423595 |
| 310 | 1 | | 0.0981741 | 1 | 1 | 2.6583891 | 0.7778225 | 1 |
| 311 | 1 | | 1 | 1 | 1 | 1 | 0.259787 | 0.7261345 |
| 312 | 1.8354599 | | 0.7948782 | 2.4091498 | 0.8500952 | 1 | 4.0567706 | 2.8116723 |
| 313 | 1.3717584 | | 1 | 1 | 1 | 1 | 2.7811113 | 1 |
| 314 | 1 | | 0.261599 | 1 | 0.3438118 | 1 | 0.5200821 | 1 |
| 315 | 0.1722821 | | 0.1683992 | 0.4592882 | 0.0751915 | 0.4314378 | 0.5260246 | 0.0488609 |
| 316 | 1.4067525 | | 1 | 2.9238547 | 1.1846143 | 1 | 1.3441737 | 1.4214361 |
| 317 | 1.3582791 | | 1.4890537 | 1 | 2.7260178 | 2.6968539 | 1.8858377 | 1.7000303 |
| 318 | 13.402971 | | 1 | 1 | 1 | 1 | 1 | 1 |
| 319 | 1.6197545 | | 1 | 1.7328778 | 0.863139 | 1 | 2.9766185 | 2.0243868 |
| 320 | 0.5906071 | | 0.2266141 | 1 | 0.0104955 | 0.0218735 | 1 | 0.1408256 |
| 321 | 0.5917657 | | 1 | 1 | 0.5633027 | 0.5461429 | 0.4965665 | 0.4859574 |
| 322 | 2.5138122 | | 1.2802889 | 1 | 1 | 3.7598561 | 1.2899014 | 1.8325514 |
| 323 | 0.5425645 | | 1 | 1 | 1.6229955 | 0.4924703 | 0.6957718 | 0.5158241 |
| 324 | 0.8282135 | | 0.2486131 | 1 | 0.3573488 | 0.5064004 | 1 | 0.174468 |
| 325 | 1 | | 1 | 1 | 1 | 0.5167396 | 0.6898859 | 1 |
| 326 | 0.6220662 | | 1 | 1 | 1.6262058 | 0.6602372 | 0.670506 | 0.4454269 |
| 327 | 1 | | 1 | 1 | 3.9686365 | 2.7710006 | 6.02552 | 1 |
| 328 | 0.4273187 | | 1 | 0.6461129 | 1 | 1 | 1 | 1 |
| 329 | 0.5919439 | | 0.6350632 | 0.6751755 | 0.538854 | 0.1758757 | 0.7752818 | 0.4565052 |
| 330 | 1.4261507 | | 1 | 0.8196812 | 0.4331919 | 1.2123035 | 2.2017884 | 1.6445642 |
| 331 | 3.0104953 | | 2.7606415 | 1 | 1 | 1 | 1 | 1 |
| 332 | 2.9263074 | | 1 | 1 | 3.0131541 | 3.6463974 | 2.0521691 | 1 |
| 333 | 2.3198891 | | 1 | 1 | 1 | 1000 | 4.013748 | 1 |
| 334 | 0.573823 | | 1 | 1 | 1.664414 | 0.4778889 | 0.7686195 | 0.4067422 |
| 335 | 0.6983596 | | 1.2147319 | 0.6154702 | 1.3494567 | 0.3584494 | 1.0830457 | 0.5737774 |
| 336 | 0.5592224 | | 1 | 1 | 1 | 1000 | 0.8146203 | 3.9431306 |
| 337 | 0.4782651 | | 1 | 1 | 1 | 0.7769536 | 0.6938522 | 1 |
| 338 | 1 | | 0.1403281 | 1 | 1 | 2.5656523 | 0.8267593 | 1 |
| 339 | 2.3893425 | | 1 | 1 | 1.6416295 | 1.6328446 | 1.6137565 | 1.8782792 |
| 340 | 1 | | 1 | 1 | 1 | 5.566716 | 1 | 1 |
| 341 | 1.6008539 | | 1 | 1 | 1.5573131 | 1.9629753 | 1.2687994 | 6.5890879 |
| 342 | 2.1195642 | | 2.2370752 | 1 | 1 | 2.0683724 | 1.7111784 | 1.8875647 |
| 343 | 2.2872863 | | 1 | 1 | 0.5826844 | 1 | 1.6995758 | 1 |

Table 4

| SEQ ID | Patient ID | | | | | | | | |
|--------|------------|-----------|-----|-----------|-----------|-----------|-----------|-----------|-----------|
| | NO | 577 | 695 | 784 | 786 | 787 | 789 | 790 | 791 |
| 344 | | 0.783951 | | 0.4814336 | 0.6834517 | 0.128028 | 0.2954009 | 1 | 0.5788071 |
| 345 | | 0.4518561 | | 0.4828576 | 1 | 1 | 0.4666902 | 1 | 1 |
| 346 | | 0.4765495 | | 1 | 0.5692718 | 1 | 1 | 0.7672221 | 0.2968849 |
| 347 | | 0.496891 | | 1 | 0.6077463 | 1.9844564 | 0.431312 | 0.7111008 | 0.3916945 |
| 348 | | 1.993327 | | 0.9075084 | 2.2804108 | 0.7270463 | 1.6952191 | 2.7875336 | 1.4471237 |
| 349 | | 2.5205036 | | 1 | 3.5779095 | 1 | 1 | 2.5922099 | 2.028908 |
| 350 | | 1 | | 1 | 1 | 0.3838128 | 0.2249965 | 0.6268058 | 0.7289607 |
| 351 | | 2.2927077 | | 2.255474 | 1.5630079 | 1 | 2.5793682 | 1 | 2.1939239 |
| 352 | | 2.1415023 | | 1 | 1 | 1 | 1 | 1 | 1 |
| 353 | | 4.3473635 | | 3.8224176 | 1 | 1 | 2.5020536 | 1.7143966 | 1.2733383 |
| 354 | | 1.6190119 | | 1 | 1 | 0.356299 | 0.0884272 | 1 | 1 |
| 355 | | 1 | | 0.2318928 | 1 | 0.194685 | 0.5333493 | 0.3174186 | 0.4724017 |
| 356 | | 1 | | 1 | 1 | 1000 | 1000 | 1 | 1 |
| 357 | | 0.3850614 | | 0.4794111 | 1 | 0.3091116 | 1 | 0.5300191 | 0.2266827 |
| 358 | | 2.2115722 | | 1 | 1 | 2.5169784 | 0.8931682 | 0.3910567 | 6.4661793 |
| 359 | | 0.5361182 | | 1 | 0.628137 | 1.859678 | 0.5158071 | 0.7109878 | 0.4376913 |
| 360 | | 0.4854466 | | 0.5406702 | 0.784394 | 0.265383 | 0.1763741 | 0.4905535 | 0.2682828 |
| 361 | | 1.5880801 | | 0.5175502 | 0.6693085 | 0.1672364 | 0.2323688 | 0.4732344 | 1 |
| 362 | | 3.6297468 | | 1 | 1 | 1 | 1 | 1 | 1 |
| 363 | | 1.8845571 | | 1 | 1 | 1.7754578 | 1 | 1 | 1 |
| 364 | | 1.8906246 | | 1.6391531 | 2.6612858 | 2.0380968 | 2.8848629 | 3.0437213 | 2.3215188 |
| 365 | | 1 | | 1 | 1 | 1 | 1000 | 1 | 1 |
| 366 | | 2.4904333 | | 1 | 1 | 2.6882219 | 3.6648622 | 1.3644711 | 2.0657634 |
| 367 | | 1.3246886 | | 0.4466549 | 1 | 0.3928991 | 0.4081842 | 0.5056425 | 1 |
| 368 | | 1.2334307 | | 1 | 1 | 2.7060884 | 5.480612 | 2.7178336 | 1 |
| 369 | | 1.9664575 | | 2.4875746 | 1.5392122 | 1.388417 | 2.5364765 | 0.4583148 | 3.5317087 |
| 370 | | 0.6015539 | | 1 | 1 | 0.7233191 | 0.4690294 | 1.610623 | 0.6170502 |
| 371 | | 1 | | 0.5691254 | 1 | 2.5950492 | 1.9692256 | 2.2441334 | 1 |
| 372 | | 0.1216699 | | 0.1455793 | 1 | 0.1686159 | 0.234922 | 0.060624 | 0.0602449 |
| 373 | | 2.3832082 | | 1.761862 | 2.935261 | 1.919805 | 1.6422256 | 2.353666 | 2.4136111 |
| 374 | | 1.6312509 | | 0.6616236 | 1.6775675 | 1.5857912 | 1 | 2.0899692 | 2.9998144 |
| 375 | | 1 | | 0.7558735 | 1 | 0.6995073 | 1.3457595 | 1.6078282 | 1 |
| 376 | | 1.7154313 | | 0.8524443 | 2.9891471 | 0.6109587 | 1 | 2.2888075 | 1.9319036 |
| 377 | | 1 | | 0.5742406 | 1 | 0.2424553 | 0.6255767 | 1.0901879 | 0.2685243 |
| 378 | | 0.7073309 | | 0.2821753 | 1 | 0.5970385 | 1 | 0.7021236 | 0.5249615 |
| 379 | | 0.4586218 | | 1 | 0.5162501 | 1.4245014 | 0.5940987 | 0.8155943 | 0.4940467 |
| 380 | | 1 | | 1 | 1 | 1 | 0.5894198 | 2.6859619 | 1 |
| 381 | | 0.5523082 | | 1 | 0.7495043 | 1.7959687 | 0.5519788 | 0.7288151 | 0.3877303 |
| 382 | | 0.7152848 | | 1 | 1 | 1 | 1 | 1.6692285 | 1 |
| 383 | | 1 | | 1 | 1 | 0.6733946 | 1 | 1 | 0.4990599 |
| 384 | | 2.1490032 | | 1.7330166 | 1 | 1 | 3.0179592 | 2.9538227 | 1.6478902 |
| 385 | | 4.9147105 | | 2.9868402 | 1 | 2.1528924 | 4.3348309 | 1.6078282 | 3.3423313 |
| 386 | | 0.4831221 | | 1 | 0.6158467 | 1 | 0.6399228 | 0.6645071 | 0.5310317 |
| 387 | | 0.5192227 | | 0.8617163 | 0.4204452 | 1.9005596 | 0.5053508 | 0.7458096 | 0.3985201 |
| 388 | | 1 | | 0.5218135 | 1 | 0.6435667 | 0.372486 | 0.9136937 | 0.4557339 |
| 389 | | 1.4696111 | | 2.8972243 | 1 | 0.5921103 | 2.1692123 | 2.5499072 | 1.6682732 |
| 390 | | 0.3514783 | | 0.2798662 | 0.5136496 | 0.2263024 | 0.5585592 | 0.3194936 | 0.4313774 |
| 391 | | 0.6573054 | | 1 | 1 | 0.4484976 | 0.3355885 | 1 | 1 |
| 392 | | 2.3997398 | | 1.190857 | 2.0267516 | 1 | 1.6906692 | 2.3061407 | 2.0414855 |

Table 4

| SEQ ID NO | Patient ID | | | | | | | |
|--------------|------------|-----|-----------|-----------|-----------|-----------|-----------|-----------|
| | 577 | 695 | 784 | 786 | 787 | 789 | 790 | 791 |
| 393 | 0.4799361 | | 0.460202 | 1 | 0.6948234 | 0.324052 | 0.5755683 | 0.7352196 |
| 394 | 0.5142841 | | 1 | 0.4985213 | 1 | 0.4991221 | 0.6834918 | 0.4165188 |
| 395 | 1.9797734 | | 1 | 2.2846382 | 2.052973 | 2.6609887 | 1.7137332 | 1.2072111 |
| 396 | 1 | | 0.3370315 | 1 | 1 | 1 | 1 | 0.2110269 |
| 397 | 1.8404134 | | 1 | 1 | 3.0269143 | 4.2228949 | 2.4909064 | 3.4008653 |
| 398 | 1.7916504 | | 1.4994248 | 1.3660674 | 1.7567085 | 1.8441039 | 1.6418454 | 1.4139598 |
| 399 | 0.5018148 | | 1 | 1 | 0.6696134 | 0.2369248 | 0.5403513 | 0.8020225 |
| 400 | 1 | | 1 | 1 | 1 | 0.3194431 | 1 | 0.3204916 |
| 401 | 0.7966059 | | 0.1456205 | 0.4723761 | 0.1480509 | 0.521353 | 1 | 0.2478165 |
| 402 | 1 | | 1 | 1 | 1 | 0.001 | 1 | 1 |
| 403 | 1 | | 0.3657315 | 1 | 1 | 0.001 | 0.438582 | 1 |
| 404 | 0.345537 | | 0.3845855 | 1 | 0.5163676 | 1 | 0.6947697 | 0.3844767 |
| 405 | 0.4289897 | | 0.1954881 | 0.5979044 | 0.1936387 | 0.225627 | 0.5527867 | 0.1163103 |
| 406 | 3.7228614 | | 2.6049192 | 1.4046154 | 3.3598285 | 5.2347519 | 5.3538707 | 3.4158574 |
| 407 | 0.3468515 | | 0.1881621 | 1 | 0.298414 | 0.5376062 | 1 | 0.5405361 |
| 408 | 2.113868 | | 1 | 1.7761523 | 1.2920543 | 1 | 1.6854608 | 1.7273764 |
| 409 | 1 | | 1 | 1 | 0.202697 | 0.001 | 0.3634195 | 0.1861943 |
| 410 | 5.0742931 | | 3.1637965 | 3.2055014 | 2.4227665 | 5.5854545 | 3.7850847 | 3.4909942 |
| 411 | 0.4868651 | | 0.1627744 | 0.4503211 | 0.2561987 | 0.1480898 | 0.6137071 | 0.2186501 |
| 412 | 0.6643012 | | 0.8666937 | 0.4751456 | 1.5805733 | 0.4693109 | 0.9174906 | 0.5103417 |
| 413 | 1 | | 1 | 1 | 2.8436022 | 1.1951169 | 1 | 1.8715631 |
| 414 | 1 | | 0.0490545 | 0.0984559 | 0.0273167 | 0.1197429 | 0.0252094 | 0.078508 |
| 415 | 0.0269065 | | 0.0107262 | 1 | 0.0216033 | 0.1119969 | 0.0100076 | 0.016254 |
| 416 | 2.4612617 | | 1.9364137 | 1.9768101 | 1.2434092 | 1.8095233 | 2.2726317 | 1.9125958 |
| 417 | 1.5367995 | | 1 | 1 | 3.061816 | 2.4730392 | 2.2883276 | 1.8119236 |
| 418 | 1 | | 1 | 1 | 1000 | 1000 | 1 | 1 |
| 419 | 2.4819002 | | 2.0196993 | 1 | 1 | 1.5819285 | 1.5129611 | 1.9962646 |
| 420 | 2.8169731 | | 1 | 1 | 0.4122834 | 0.2109693 | 0.2207872 | 0.6053531 |
| 421 | 1 | | 1 | 1 | 1 | 1 | 1 | 1 |
| 422 | 1 | | 1 | 1 | 1 | 1 | 0.3535531 | 1 |
| 423 | 2.0759478 | | 1.7084016 | 1 | 1.433457 | 1.6441306 | 2.0489932 | 1.5223551 |
| 424 | 0.7425032 | | 0.3701162 | 1 | 0.4976213 | 0.413177 | 0.6153444 | 0.4278304 |
| 425 | 1 | | 1 | 1 | 1.4097287 | 1 | 2.0411453 | 1 |
| 426 | 1 | | 1 | 1 | 1 | 0.1256524 | 0.8548482 | 0.3396437 |
| 427 | 1.6990334 | | 1.7910357 | 2.9764512 | 1.9755614 | 1 | 3.6124861 | 3.7803659 |
| 428 | 0.4796984 | | 1 | 0.6651729 | 1.4740591 | 0.4651681 | 0.7584425 | 0.4149705 |
| 429 | 1 | | 1.659881 | 1.5542395 | 1 | 1.4374332 | 1.5471195 | 1 |
| 430 | 1.982046 | | 1 | 1 | 1 | 3.0862785 | 1.2379581 | 2.6677955 |
| 431 | 1 | | 1 | 1 | 0.1446572 | 0.2541708 | 0.6371522 | 0.4135245 |
| 432 | 1 | | 0.0437379 | 1 | 0.1619188 | 0.2446431 | 0.2201238 | 0.0204494 |
| 433 | 1.6441954 | | 1.1549327 | 1.8648441 | 1.7586597 | 1.3039472 | 2.4570303 | 2.0373807 |
| 434 | 0.514388 | | 0.8558331 | 0.5710409 | 1.9360627 | 0.5193749 | 0.7450615 | 0.4778801 |
| 435 | 1 | | 1 | 1 | 1 | 1 | 1 | 1 |
| 436 | 0.2254193 | | 1 | 1 | 1 | 1 | 1 | 1.5286857 |
| 437 | 0.4887143 | | 0.7125397 | 0.6494179 | 0.5501002 | 0.4334969 | 0.6132272 | 0.3866208 |
| 438 | 1.4005958 | | 1 | 1 | 1.4017784 | 3.8084777 | 2.6418666 | 3.0227601 |
| 439 | 2.501744 | | 1.6499863 | 1 | 0.6876651 | 1.4179294 | 1.2823781 | 2.4868981 |
| 440 | 1.786994 | | 1 | 1.9214913 | 1.2537467 | 1.3130578 | 1.7773496 | 2.0733502 |
| 441 | 1.8671566 | | 1 | 2.4208174 | 2.5135009 | 4.2921663 | 1.8992752 | 1.584811 |

Table 4

| SEQ ID | Patient ID | | | | | | | |
|--------|------------|-----|-----------|-----------|-----------|-----------|-----------|-----------|
| | 577 | 695 | 784 | 786 | 787 | 789 | 790 | 791 |
| 442 | 1 | | 1 | 1 | 1.4038267 | 0.4727154 | 1.1939757 | 1 |
| 443 | 0.4773219 | | 1 | 0.6375493 | 1.9671983 | 0.4289947 | 0.7581179 | 0.4054007 |
| 444 | 0.5050528 | | 1 | 0.5703574 | 1.483728 | 0.698612 | 0.7183982 | 0.4672877 |
| 445 | 1.8750956 | | 2.1029024 | 1 | 0.4799539 | 2.6000702 | 1.2912988 | 1.1321927 |
| 446 | 0.4464421 | | 0.3630544 | 1 | 0.5515017 | 0.3496489 | 1 | 0.2779868 |
| 447 | 1 | | 1 | 1 | 2.2314971 | 3.6171223 | 1.6640907 | 2.2109239 |
| 448 | 2.2678286 | | 2.1677566 | 2.2471463 | 1.9777091 | 1.9251468 | 2.6553041 | 1.8389044 |
| 449 | 2.5888951 | | 1.2374153 | 2.3934997 | 1 | 1.3804959 | 1.6380061 | 2.4101518 |
| 450 | 1 | | 1 | 1 | 0.3877868 | 0.4213375 | 1.4257444 | 0.177184 |
| 451 | 1.5339997 | | 1 | 1 | 1.6479893 | 1 | 1.4840253 | 1.5417168 |
| 452 | 1.754109 | | 1 | 1 | 2.0899048 | 1 | 6.063447 | 1 |
| 453 | 1 | | 0.635199 | 0.6910703 | 0.6377584 | 0.339005 | 0.4960301 | 0.4805036 |
| 454 | 1.6235867 | | 1 | 1 | 1.5612942 | 3.425348 | 3.0474759 | 1 |
| 455 | 0.5195941 | | 1 | 0.5987157 | 1.777377 | 0.5176676 | 0.7311864 | 0.4146113 |
| 456 | 0.4725466 | | 1 | 1 | 1 | 0.001 | 1 | 0.5413284 |
| 457 | 0.3790235 | | 1 | 1 | 1 | 1 | 0.517612 | 1 |
| 458 | 1.894687 | | 1 | 1 | 0.6313633 | 6.1622134 | 1 | 5.5970618 |
| 459 | 1.3745433 | | 1 | 2.6555513 | 2.5071626 | 1 | 2.4685623 | 1.4244077 |
| 460 | 1 | | 1 | 1 | 1 | 1 | 1 | 1 |
| 461 | 0.528558 | | 1 | 0.6746465 | 1.8833955 | 0.6062436 | 0.6967176 | 0.4613712 |
| 462 | 2.6590095 | | 1 | 1 | 1 | 2.4793482 | 2.728928 | 2.7454533 |
| 463 | 2.5903655 | | 1 | 1 | 0.622157 | 2.4528876 | 1.8418976 | 2.3185224 |
| 464 | 1.819062 | | 1 | 2.076805 | 0.6671682 | 1 | 1.4765161 | 1.8691288 |
| 465 | 1 | | 1 | 1 | 1.2767168 | 1.8395164 | 2.1456953 | 1.732982 |
| 466 | 1 | | 0.6581207 | 1 | 0.6184847 | 2.5696255 | 1 | 0.766552 |
| 467 | 1.3660844 | | 2.4390376 | 1.6353865 | 2.5315098 | 3.4056286 | 1.5276407 | 1.7021172 |
| 468 | 1.7370798 | | 1 | 3.2755694 | 1.8481017 | 1.2160307 | 2.6597785 | 2.5544135 |
| 469 | 1 | | 1 | 1 | 1.844832 | 6.2299301 | 1 | 1.2043781 |
| 470 | 0.4848153 | | 1 | 0.6066528 | 1 | 1 | 0.699103 | 0.4110299 |
| 471 | 1 | | 1 | 1 | 0.2818045 | 0.1487556 | 1 | 0.2779644 |
| 472 | 0.4973886 | | 1 | 0.6416931 | 1.7416796 | 0.5588575 | 0.7486185 | 0.4473556 |
| 473 | 2.6858047 | | 1.6091738 | 1.4880087 | 1.2879477 | 1.3404827 | 1.8364492 | 3.413497 |
| 474 | 1 | | 0.4248386 | 1 | 0.4132458 | 0.2915661 | 1 | 0.4407079 |
| 475 | 4.2149548 | | 2.0529152 | 1 | 1 | 1 | 1 | 1 |
| 476 | 2.0878675 | | 1 | 1 | 0.7813462 | 1.6234539 | 1.8195112 | 3.1424639 |
| 477 | 1.6424428 | | 1 | 1 | 1.5214554 | 2.3275116 | 1 | 1.601737 |
| 478 | 1 | | 1 | 1 | 0.1800662 | 0.6042244 | 1 | 0.6221405 |
| 479 | 1 | | 1 | 1 | 2.0361069 | 2.0637919 | 1.5883777 | 1 |
| 480 | 1 | | 0.1138087 | 1 | 0.1942065 | 1 | 1 | 0.6142926 |
| 481 | 1 | | 1 | 1 | 1 | 0.4598698 | 0.658 | 0.5478157 |
| 482 | 1 | | 2.1089731 | 3.1538773 | 1 | 4.4224687 | 1 | 1 |
| 483 | 0.4982129 | | 1 | 1 | 1.5523088 | 0.5460202 | 0.7537846 | 0.4270675 |
| 484 | 1 | | 0.4945061 | 1 | 0.3244932 | 0.0893566 | 1 | 0.4335045 |
| 485 | 2.1405963 | | 2.9888435 | 1 | 1.5856441 | 3.1297252 | 2.9629269 | 1 |
| 486 | 0.1695639 | | 0.1476916 | 1 | 0.0773445 | 0.013028 | 0.1501697 | 0.0727991 |
| 487 | 1.552633 | | 1.7676625 | 3.0486853 | 1.7893164 | 9.0023602 | 1.2556019 | 1.8241768 |
| 488 | 0.559163 | | 1 | 0.6123436 | 1 | 0.6782194 | 0.7768768 | 0.42247 |
| 489 | 2.3998586 | | 1 | 1.8863006 | 1.40468 | 6.1689188 | 2.2823287 | 2.1971564 |
| 490 | 1 | | 0.6668411 | 1 | 1.826195 | 2.7636836 | 1.5983852 | 1 |

Table 4

| SEQ ID | Patient ID | | | | | | | |
|--------|------------|-----|-----------|-----------|-----------|-----------|-----------|-----------|
| NO | 577 | 695 | 784 | 786 | 787 | 789 | 790 | 791 |
| 491 | 0.5790439 | | 0.4945583 | 1 | 0.7508278 | 0.4020189 | 0.7775684 | 0.425786 |
| 492 | 2.0916847 | | 1.3696301 | 2.7019269 | 0.4231104 | 2.0101299 | 1.918881 | 2.0421712 |
| 493 | 0.4000259 | | 0.3652384 | 1 | 1 | 0.8483706 | 1.2670633 | 0.8846963 |
| 494 | 1.6632966 | | 1 | 1.5432665 | 1.2003464 | 2.9818469 | 1.3451053 | 2.0726434 |
| 495 | 1 | | 0.2109422 | 1 | 0.0399715 | 0.0588685 | 0.3910426 | 0.1679347 |
| 496 | 0.5819552 | | 0.6301422 | 1 | 0.472569 | 0.4919824 | 1 | 0.4814373 |
| 497 | 1 | | 0.2792699 | 1 | 1 | 0.001 | 1 | 0.5581764 |
| 498 | 3.9073379 | | 1 | 1 | 1 | 1.6987324 | 1 | 3.773147 |
| 499 | 1.760184 | | 1 | 2.400251 | 2.8455895 | 3.3540816 | 3.2118453 | 2.5310994 |
| 500 | 1 | | 1 | 1 | 0.3608323 | 1 | 1 | 0.4167428 |
| 501 | 1.5525216 | | 1 | 1.5196113 | 0.6445418 | 1.625704 | 2.0684014 | 1.6855643 |
| 502 | 0.372956 | | 0.3175667 | 0.6315334 | 1 | 0.3446798 | 1 | 0.2477792 |
| 503 | 2.1191706 | | 1 | 1.9319299 | 1 | 4.3342786 | 1.851143 | 2.2903706 |
| 504 | 2.1626904 | | 1 | 1.7838651 | 1 | 2.1269606 | 1.8758725 | 1.8875196 |
| 505 | 0.5668792 | | 0.6079874 | 1 | 0.2670607 | 0.4033847 | 0.7077837 | 0.3822583 |
| 506 | 2.0984281 | | 1 | 1.8229909 | 1.4142288 | 1 | 1.8514111 | 2.2969604 |
| 507 | 2.3406167 | | 1 | 2.0697691 | 1 | 3.4023924 | 1.2919622 | 1.8424194 |
| 508 | 1 | | 1 | 1 | 1 | 3.3981437 | 1 | 2.1389437 |
| 509 | 1 | | 1 | 1 | 1 | 4.466017 | 1 | 1 |
| 510 | 1 | | 0.4936024 | 1 | 0.5355397 | 1 | 1 | 0.3250802 |
| 511 | 7.8017981 | | 2.5481691 | 10.63841 | 3.83961 | 14.502417 | 8.1048746 | 13.06814 |
| 512 | 0.1756463 | | 0.4757288 | 1 | 1 | 0.2212702 | 1 | 0.3370942 |
| 513 | 0.4702072 | | 1 | 0.6400497 | 1 | 0.3875518 | 0.5971502 | 0.3874357 |
| 514 | 3.1156187 | | 2.1566364 | 2.3101117 | 1.6103106 | 4.965392 | 5.589888 | 2.7825697 |
| 515 | 2.1449705 | | 1.547376 | 1.5410373 | 1.4421122 | 2.557358 | 1 | 1.6590283 |
| 516 | 2.7131271 | | 1 | 1 | 1 | 1 | 1 | 1 |
| 517 | 0.1975102 | | 0.0184638 | 0.3516081 | 0.1843508 | 0.0206263 | 0.4508197 | 0.4044299 |
| 518 | 3.4435695 | | 1 | 1 | 1 | 1 | 1 | 1 |
| 519 | 0.8067135 | | 1 | 1 | 0.4871345 | 1 | 1.2214577 | 1.9593463 |
| 520 | 0.1464227 | | 0.2075678 | 1 | 0.4169354 | 0.1210304 | 1 | 0.2158248 |
| 521 | 1.7436821 | | 2.1999682 | 1 | 1.2780526 | 2.2604611 | 1.5426309 | 1.6584713 |
| 522 | 1.5386264 | | 0.8060131 | 2.1529314 | 1 | 1 | 2.2564559 | 2.0006609 |
| 523 | 1.9794838 | | 1 | 1 | 1000 | 1 | 1 | 2.523664 |
| 524 | 0.5919439 | | 1 | 0.5543322 | 1.6680832 | 0.6074453 | 0.7118912 | 0.5339773 |
| 525 | 5.3436185 | | 2.9718019 | 1 | 1.6944625 | 2.556493 | 1.733706 | 5.9470361 |
| 526 | 2.0357774 | | 1 | 1 | 1.7897659 | 1 | 1.6854326 | 1.1560226 |
| 527 | 1.5905606 | | 1 | 1.8664023 | 1 | 2.926561 | 1.486312 | 2.9686039 |
| 528 | 2.5888505 | | 1 | 1 | 1 | 4.2816311 | 1 | 1 |
| 529 | 0.2921993 | | 1 | 1 | 1 | 1 | 1 | 1 |
| 530 | 0.4031822 | | 1 | 1 | 1 | 1 | 1 | 1 |
| 531 | 1.5389755 | | 1 | 1 | 1.8032029 | 3.311631 | 1 | 1 |
| 532 | 2.5850332 | | 1 | 1 | 0.8389352 | 2.1709429 | 3.2102503 | 1 |
| 533 | 0.1621745 | | 0.0147924 | 0.2401275 | 0.1131522 | 0.195451 | 0.2943829 | 0.0925217 |
| 534 | 2.1741793 | | 1.6486129 | 2.4519578 | 0.809347 | 2.0551881 | 1 | 1.4958761 |
| 535 | 3.0500121 | | 1 | 1 | 1 | 1.973739 | 1 | 1 |
| 536 | 0.4986585 | | 1 | 0.5489806 | 1.674322 | 0.620691 | 0.6680217 | 0.4208817 |
| 537 | 1.8245948 | | 1 | 1 | 1.1549481 | 1.7306242 | 2.5062212 | 1.7194846 |
| 538 | 2.5796861 | | 1 | 3.8242724 | 1 | 4.1939977 | 4.4319056 | 1 |
| 539 | 4.1133813 | | 1 | 1 | 1.9584121 | 3.0661094 | 1.706591 | 3.5233644 |

Table 4

| SEQ ID | Patient ID | | | | | | | | |
|--------|------------|-----------|-----|-----------|-----------|-----------|-----------|-----------|-----------|
| | NO | 577 | 695 | 784 | 786 | 787 | 789 | 790 | 791 |
| 540 | | 2.7060198 | | 1 | 1 | 2.1127817 | 4.1908973 | 1.7058288 | 1 |
| 541 | | 1.9870812 | | 2.9575031 | 1.6774888 | 1.3968091 | 2.5403598 | 1.8573395 | 1 |
| 542 | | 3.2406156 | | 2.6334745 | 1.6896623 | 2.0353799 | 3.0487961 | 1.9639643 | 2.3793873 |
| 543 | | 0.5241837 | | 1 | 0.5547237 | 1.4773191 | 0.620708 | 0.7027447 | 0.428531 |
| 544 | | 0.1876328 | | 0.3430322 | 0.7116847 | 0.3850365 | 0.2589619 | 0.5864651 | 0.2038521 |
| 545 | | 2.7711956 | | 1.7832952 | 1 | 2.5500827 | 1 | 1.7889522 | 2.4652561 |
| 546 | | 2.6934392 | | 1 | 1 | 1 | 1 | 1 | |
| 547 | | 1.7611123 | | 1 | 1.5835063 | 2.0638749 | 2.5195673 | 1.7074097 | 1.4505498 |
| 548 | | 2.8033453 | | 2.0184644 | 1.1842585 | 1 | 1 | 1.5434637 | 2.1225155 |
| 549 | | 1.9287082 | | 1 | 1.367034 | 1.4154931 | 2.1889648 | 1 | 1.4136057 |
| 550 | | 1.6834524 | | 1 | 1 | 1.4894399 | 2.6728023 | 1.5370272 | 1.568737 |
| 551 | | 0.2756751 | | 0.5637365 | 0.0819887 | 0.0440206 | 0.219779 | 0.1008377 | 0.1580836 |
| 552 | | 1 | | 1 | 1 | 1 | 1 | 1 | 1 |
| 553 | | 0.6901532 | | 0.5317922 | 0.4510685 | 0.3414312 | 0.5821717 | 0.4358437 | 0.479754 |
| 554 | | 0.4344705 | | 0.842238 | 0.4679232 | 1.5481211 | 0.4930128 | 1 | 0.4034698 |
| 555 | | 0.3592465 | | 0.0234481 | 0.0153429 | 0.0366223 | 0.2117303 | 0.0130987 | 0.3333774 |
| 556 | | 2.4045596 | | 1 | 1 | 0.6088183 | 1 | 1 | 2.5679417 |
| 557 | | 0.5418961 | | 0.4889797 | 1 | 0.32682 | 0.4074386 | 0.5270267 | 0.4732928 |
| 558 | | 1 | | 0.8265693 | 2.8396423 | 1 | 5.0092656 | 1.2367442 | 1 |
| 559 | | 1.4577954 | | 1 | 1 | 2.4367829 | 3.5167142 | 1.6782198 | 1 |
| 560 | | 3.1579205 | | 1 | 1 | 1 | 1000 | 1 | 1 |
| 561 | | 2.2406919 | | 1 | 1 | 1 | 2.1076534 | 0.776411 | 2.7366126 |
| 562 | | 2.6543679 | | 1 | 1 | 0.8965344 | 1.2594338 | 2.3568984 | 4.4492293 |
| 563 | | 0.5596605 | | 1 | 0.4422961 | 1.7866991 | 0.4908394 | 0.7076426 | 0.4143722 |
| 564 | | 1.3444136 | | 1 | 1 | 1.9330426 | 1.660828 | 2.181985 | 2.0601634 |
| 565 | | 0.5672134 | | 1 | 0.3695615 | 1.6553593 | 0.4846606 | 0.6530174 | 0.4631122 |
| 566 | | 2.2636326 | | 1 | 1 | 0.4897825 | 1.5233399 | 1.4133514 | 1.8508327 |
| 567 | | 7.5899546 | | 12.470591 | 12.195781 | 1 | 1 | 2.0214831 | 1 |
| 568 | | 0.6225489 | | 1 | 1 | 1.74012 | 0.5116986 | 0.7193157 | 0.43994 |
| 569 | | 1 | | 0.5983144 | 0.3487246 | 1 | 1 | 1 | 1 |
| 570 | | 0.415191 | | 0.2606382 | 0.4083981 | 0.2856398 | 0.1501791 | 0.2806914 | 0.3209158 |
| 571 | | 0.6881703 | | 0.5802446 | 0.5930775 | 1 | 1 | 1 | 1 |
| 572 | | 1.6796723 | | 1 | 1 | 0.7355459 | 2.20865 | 1 | 1 |
| 573 | | 2.6702979 | | 1 | 1 | 1 | 1 | 1 | 2.2410148 |
| 574 | | 0.3325925 | | 1 | 1 | 1.7548337 | 0.4039068 | 0.632466 | 0.6785555 |
| 575 | | 0.7439737 | | 0.8195615 | 0.7208935 | 1 | 1 | 1 | 0.4657896 |
| 576 | | 0.8011436 | | 0.5740187 | 1 | 1 | 0.6468839 | 1 | 0.4837474 |
| 577 | | 0.7370001 | | 0.4747987 | 0.2340696 | 1 | 0.7032919 | 1 | 0.6109355 |
| 578 | | 1.3741794 | | 1 | 2.4153367 | 2.1069507 | 1.8314445 | 1.7917046 | 1.9171888 |
| 579 | | 0.575442 | | 1 | 0.5441909 | 1 | 0.3925815 | 0.5074915 | 0.4495107 |
| 580 | | 0.4310542 | | 0.8492764 | 1 | 0.6252186 | 0.5024434 | 0.6872746 | 0.4520198 |
| 581 | | 2.1476812 | | 2.9012797 | 1 | 1.2888991 | 1.8970174 | 2.2571757 | 2.0684666 |
| 582 | | 1.7968342 | | 1 | 1 | 1 | 1.3898026 | 2.135603 | 1.9475657 |
| 583 | | 1.9344786 | | 1 | 1.6660717 | 1.1134674 | 0.8708059 | 1.7438829 | 1.6922046 |
| 584 | | 1.9231605 | | 1 | 1 | 2.2806613 | 2.186643 | 1.79409 | 1.4954798 |
| 585 | | 1 | | 0.4584502 | 2.4808064 | 1.1174984 | 1.6661565 | 1.2290515 | 1 |
| 586 | | 2.5342131 | | 1 | 1 | 1.4530917 | 3.0550941 | 1.1205917 | 2.3422965 |
| 587 | | 0.273254 | | 0.2648476 | 0.4527857 | 1 | 0.4828855 | 0.7223645 | 0.3270212 |
| 588 | | 1.4619989 | | 0.1613561 | 0.4082932 | 0.3042445 | 0.7190204 | 0.2823428 | |

Table 4

| SEQ ID | Patient ID | | | | | | | |
|--------|------------|-----|-----------|-----------|-----------|-----------|-----------|-----------|
| | 577 | 695 | 784 | 786 | 787 | 789 | 790 | 791 |
| 589 | 0.5347443 | | 0.1184378 | 0.3539604 | 0.2142819 | 0.4371965 | 0.1003437 | 1 |
| 590 | 0.6376992 | | 0.6735078 | 0.6225513 | 1 | 1 | 0.7703697 | 0.5083787 |
| 591 | 0.6366669 | | 0.6693601 | 0.5502061 | 0.7134572 | 0.5718655 | 1 | 1 |
| 592 | 0.5752267 | | 0.7005102 | 0.5335524 | 2.1073662 | 0.8039854 | 0.7697487 | 0.4799667 |
| 593 | 0.3788602 | | 0.701177 | 1 | 1.3759498 | 2.187346 | 1.4719287 | 0.6919517 |
| 594 | 0.4155475 | | 0.596808 | 0.6988129 | 0.4760844 | 0.5481142 | 0.6862442 | 0.367923 |
| 595 | 1.5686373 | | 1 | 1 | 1 | 1.602611 | 1.4312916 | 1 |
| 596 | 0.559059 | | 1 | 0.7087351 | 1.6624076 | 0.5560483 | 0.6927795 | 0.5166231 |
| 597 | 1 | | 7.9027586 | 5.2523679 | 1000 | 7.2127689 | 1.3803646 | 1 |
| 598 | 1.9949237 | | 1.9362454 | 1 | 1.5898898 | 2.6754301 | 1.1888802 | 1.9100536 |
| 599 | 1 | | 2.0605089 | 2.3207622 | 3.2000103 | 2.5600525 | 1.693097 | 1 |
| 600 | 7.5080987 | | 10.691856 | 1 | 4.9885808 | 1 | 0.659101 | 1 |
| 601 | 0.6416427 | | 0.6765652 | 0.6202554 | 0.7097322 | 0.5765765 | 1.616396 | 0.5188446 |
| 602 | 2.8908529 | | 1 | 1 | 2.4841451 | 3.7550829 | 1.3658826 | 2.038379 |
| 603 | 1.4346987 | | 1 | 1 | 1 | 1.8951677 | 1.4371493 | 2.3654299 |
| 604 | 2.9311867 | | 1.6310539 | 1 | 4.7339317 | 3.9140922 | 4.0734264 | 2.1893053 |
| 605 | 1 | | 1 | 1 | 1.6138363 | 0.4822796 | 0.6848327 | 0.4331434 |
| 606 | 2.63266 | | 1 | 2.0575554 | 1.1775664 | 1.7863364 | 1.8037729 | 2.8258468 |
| 607 | 2.498714 | | 1.5994421 | 1.9763182 | 1.6305474 | 2.2269415 | 1.8828171 | 2.5672744 |
| 608 | 1 | | 0.4441951 | 1 | 2.5645384 | 0.475142 | 1 | 0.4533967 |
| 609 | 1.8396485 | | 1 | 1 | 0.257391 | 1.3608617 | 0.5149302 | 1.8698805 |
| 610 | 1 | | 0.1356607 | 1 | 0.5846806 | 0.6414796 | 0.8220025 | 0.5388336 |
| 611 | 0.4020905 | | 0.297768 | 1 | 0.7552914 | 0.7913047 | 1 | 1 |
| 612 | 0.6118992 | | 1 | 0.5611955 | 1.5228645 | 0.5690433 | 0.6841128 | 0.5418145 |
| 613 | 0.5478894 | | 1 | 0.476568 | 1.5917841 | 0.6464106 | 0.7363949 | 0.4895119 |
| 614 | 0.460263 | | 0.6788273 | 0.473917 | 2.2062203 | 0.3747925 | 1 | 0.3529895 |
| 615 | 0.5712534 | | 0.8777643 | 1 | 1.3313239 | 0.4443498 | 1 | 0.6419333 |
| 616 | 1.6569395 | | 1 | 1 | 1 | 1.4116624 | 1.410232 | 1.830175 |
| 617 | 0.2090437 | | 0.8467992 | 1 | 0.1093827 | 0.3140416 | 0.1908069 | 0.1407641 |
| 618 | 0.1671949 | | 0.8340256 | 1 | 0.1096706 | 0.3159977 | 0.1573543 | 0.1186989 |
| 619 | 0.392837 | | 0.2273621 | 1 | 0.813157 | 0.7523954 | 0.5206185 | 0.4834131 |
| 620 | 1.0959347 | | 0.3855788 | 1 | 0.1998188 | 1 | 0.3535531 | 0.6479697 |
| 621 | 1 | | 1 | 0.7027082 | 0.4548922 | 0.1425237 | 0.6715646 | 0.4478144 |
| 622 | 4.8985503 | | 1.9889606 | 1 | 1.7979325 | 2.6788012 | 2.1682652 | 1 |
| 623 | 5.0440966 | | 1.6952736 | 1 | 1.3416223 | 1.747966 | 2.3461851 | 2.7007042 |
| 624 | 1 | | 1 | 1 | 1000 | 1.1524985 | 1 | 1 |
| 625 | 1.5883623 | | 2.3057124 | 2.256439 | 1 | 1 | 1.6336446 | 1 |
| 626 | 0.9263262 | | 0.4907946 | 0.4870733 | 0.505028 | 0.814965 | 0.4952821 | 0.5424988 |
| 627 | 1 | | 0.5197716 | 0.5422794 | 0.682936 | 0.4494994 | 1.208613 | 0.4948788 |
| 628 | 1 | | 0.7741181 | 0.4029782 | 0.6906981 | 0.494385 | 1 | 0.5016032 |
| 629 | 2.2814564 | | 1 | 1.9610281 | 1 | 1 | 1.5289534 | 2.5098796 |
| 630 | 6.0168613 | | 6.7038219 | 1.7568136 | 5.6896643 | 4.1813667 | 2.1985701 | 3.66842 |
| 631 | 1 | | 0.3832098 | 0.5698891 | 1 | 0.2841675 | 1 | 0.2539427 |
| 632 | 0.2324598 | | 0.4061673 | 0.674252 | 1 | 0.3990055 | 0.8213956 | 0.3818926 |
| 633 | 2.0312174 | | 1 | 1 | 0.5824542 | 1 | 1.4943999 | 1 |
| 634 | 1 | | 0.6158944 | 1.8498829 | 1 | 1.5397514 | 1.2243936 | 1.2103539 |
| 635 | 0.5880895 | | 0.4981656 | 0.5687192 | 0.7745584 | 0.5024063 | 1.2319734 | 0.4610724 |
| 636 | 1.9960525 | | 1 | 1 | 0.8355004 | 1.6919727 | 1 | 1.9664637 |
| 637 | 2.0739872 | | 1.4802497 | 1 | 1.2115721 | 2.0740476 | 1.5265115 | 2.6162234 |

Table 4

| SEQ ID NO | Patient ID | | | | | | | |
|--------------|------------|-----|-----------|-----------|-----------|-----------|-----------|-----------|
| | 577 | 695 | 784 | 786 | 787 | 789 | 790 | 791 |
| 638 | 0.7618495 | | 0.2311303 | 0.424755 | 0.4961544 | 1 | 0.6949532 | 1 |
| 639 | 1.9505127 | | 1.3321871 | 2.4027522 | 3.2816839 | 2.1470314 | 1.6522199 | 2.3623191 |
| 640 | 2.2579216 | | 1.9013827 | 4.2984831 | 1.9666553 | 3.3043927 | 1.3426069 | 3.0920586 |
| 641 | 0.4065316 | | 0.6158902 | 0.3677571 | 0.3957615 | 0.7024713 | 0.4172401 | 0.4168022 |
| 642 | 0.5792964 | | 0.8012668 | 0.5516456 | 1 | 0.6734926 | 1 | 0.5098512 |
| 643 | 0.5505704 | | 1 | 0.4791781 | 1.7104618 | 0.4579166 | 0.6489382 | 0.425566 |
| 644 | 5.0587121 | | 1 | 1 | 1 | 4.7220682 | 1.6496934 | 2.7681462 |
| 645 | 4.6133023 | | 2.3072643 | 1 | 1.6745843 | 2.5630425 | 2.1573402 | 1 |
| 646 | 0.5624158 | | 0.866382 | 0.5760386 | 1.7592748 | 0.4852725 | 0.7571863 | 0.4537038 |
| 647 | 0.5731844 | | 0.8706305 | 0.4769527 | 2.0510524 | 0.8263591 | 1 | 0.4991166 |
| 648 | 2.1398388 | | 1 | 3.166732 | 1 | 1 | 1.5682638 | 1 |
| 649 | 5.1419865 | | 2.267582 | 1 | 1.8578193 | 3.772993 | 1.5303932 | 4.2141354 |
| 650 | 2.3283182 | | 2.0650443 | 1 | 1 | 3.1000609 | 1 | 2.3101868 |
| 651 | 2.6934986 | | 2.1797914 | 1 | 3.3600925 | 4.7855118 | 1.7270437 | 1 |
| 652 | 1.9908316 | | 1.2933872 | 2.2322687 | 5.2286598 | 2.7373289 | 2.1009648 | 1 |
| 653 | 0.5030625 | | 0.7050263 | 1 | 1 | 1 | 0.2697946 | 1.742265 |
| 654 | 0.3013488 | | 0.9264408 | 0.4030896 | 0.7620023 | 0.2786299 | 0.464469 | 0.4166352 |
| 655 | 2.424604 | | 0.001 | 2.4480111 | 1 | 0.7245802 | 3.4225544 | 2.4568265 |
| 656 | 0.48662 | | 0.2128896 | 1 | 0.2387394 | 1.9433495 | 1 | 0.3592632 |
| 657 | 1.6851011 | | 0.5624452 | 1 | 1 | 1 | 1 | 1 |
| 658 | 1.8605469 | | 1 | 1 | 0.8277277 | 2.1416243 | 1 | 1.9680796 |
| 659 | 0.4458629 | | 0.2297972 | 0.2833743 | 0.314642 | 0.4297508 | 0.4930095 | 0.6159922 |
| 660 | 1 | | 1 | 2.4316882 | 1 | 1 | 1.6849386 | 1 |
| 661 | 1 | | 0.6185402 | 0.767639 | 1 | 0.4288108 | 1 | 0.354484 |
| 662 | 1 | | 1 | 0.6588031 | 1 | 1 | 1 | 1 |
| 663 | 1 | | 1 | 0.3034475 | 1 | 0.4352859 | 1 | 0.2956179 |
| 664 | 2.0815549 | | 1.1905707 | 1 | 1 | 1.7011537 | 1.9416626 | 1 |
| 665 | 1 | | 1 | 3.3069385 | 1.9549643 | 7.7378112 | 1.5893799 | 1 |
| 666 | 2.3846489 | | 1.8666969 | 1.2226028 | 1.1636559 | 1.5374548 | 1 | 1.7120724 |
| 667 | 9.2925305 | | 1 | 8.6317444 | 1 | 5.5905034 | 2.9831396 | 9.7551357 |
| 668 | 4.7048499 | | 2.4158981 | 1.2426027 | 1.5046417 | 2.3474289 | 1 | 5.3934836 |
| 669 | 2.7792089 | | 2.3758413 | 1.8965607 | 1 | 8.7781724 | 2.1872499 | 1 |
| 670 | 4.0329958 | | 1 | 2.1066127 | 1 | 1 | 1 | 1 |
| 671 | 1 | | 0.5558922 | 0.4649102 | 2.0053538 | 1 | 1.6102983 | 0.479059 |
| 672 | 3.4706246 | | 1 | 1.9968007 | 2.4978608 | 3.9454176 | 2.1206552 | 3.3982333 |
| 673 | 1.581515 | | 1.2787643 | 1 | 1.8588694 | 2.9299641 | 1.3853048 | 2.1981341 |
| 674 | 1 | | 17.469093 | 1 | 1 | 2.9478653 | 1 | 1.5023591 |
| 675 | 3.1811435 | | 2.9413984 | 1.8749698 | 2.5693934 | 16.444485 | 1 | 1 |
| 676 | 1.8090064 | | 0.6909683 | 1.3660413 | 1.160702 | 1.203404 | 0.7092093 | 3.0561892 |
| 677 | 1.7562033 | | 1 | 1.7384832 | 1.6196139 | 1.5516921 | 2.2073215 | 2.2340468 |
| 678 | 0.5811457 | | 0.8349476 | 0.5398752 | 2.1467305 | 0.5513481 | 0.6754039 | 0.4295698 |
| 679 | 1.5514893 | | 1 | 1 | 1 | 1.9357739 | 1 | 1.6642334 |
| 680 | 7.352519 | | 1 | 1.5520122 | 3.0947293 | 5.2586254 | 1 | 1 |
| 681 | 1 | | 1 | 1 | 1 | 3.2103646 | 1.3764406 | 1 |
| 682 | 0.5459882 | | 0.2039541 | 0.1126829 | 0.1590085 | 0.4247017 | 0.03461 | 0.6399685 |
| 683 | 3.4942486 | | 1.3802353 | 2.125594 | 3.4214027 | 2.1791485 | 1.6239617 | 2.8348676 |
| 684 | 0.7299374 | | 0.2125774 | 0.5965671 | 0.7768949 | 0.3599591 | 0.4349827 | 0.4423902 |
| 685 | 0.5712534 | | 0.4627346 | 0.5885749 | 0.2135439 | 1.177167 | 0.3638147 | 0.5073572 |
| 686 | 1 | | 0.391316 | 0.6089631 | 1 | 0.4167484 | 1 | 0.542216 |

Table 4

| SEQ ID NO | Patient ID | | | | | | | |
|--------------|------------|-----|-----------|-----------|-----------|-----------|-----------|-----------|
| | 577 | 695 | 784 | 786 | 787 | 789 | 790 | 791 |
| 687 | 1 | | 1 | 1 | 1 | 1 | 1 | 1 |
| 688 | 0.5010647 | | 0.8185378 | 0.6467736 | 1.4107288 | 0.434613 | 1 | 0.3857659 |
| 689 | 0.4283658 | | 0.5228911 | 0.5907004 | 0.8523323 | 0.6423457 | 1 | 0.3821955 |
| 690 | 2.541053 | | 1 | 1.9527777 | 1 | 2.4162968 | 1 | 1 |
| 691 | 1 | | 1 | 2.0470081 | 1 | 1 | 1 | 1 |
| 692 | 2.7715001 | | 1 | 1.1750888 | 2.5195001 | 2.4321918 | 1 | 2.3772403 |
| 693 | 0.5746994 | | 1 | 0.6494002 | 1.3528729 | 0.5904378 | 0.7412222 | 0.4946651 |
| 694 | 1.915266 | | 1.3005021 | 1.8255517 | 2.2422058 | 1.5025473 | 1 | 1 |
| 695 | 2.2801865 | | 2.2821558 | 1 | 0.9025913 | 2.3422564 | 1 | 2.3297306 |
| 696 | 1 | | 0.0246724 | 0.0653719 | 0.070743 | 0.0217265 | 0.6300382 | 0.0122661 |
| 697 | 1.9148056 | | 10.689291 | 5.0316398 | 3.0634615 | 4.7888805 | 1 | 3.6994996 |
| 698 | 1.8170791 | | 1.2902603 | 1.7936683 | 1.767311 | 1.5285767 | 1 | 1.5921218 |
| 699 | 0.520968 | | 1 | 0.5433925 | 1.7323286 | 0.5672356 | 1 | 0.4209714 |
| 700 | 1 | | 1 | 1 | 1 | 1 | 1.9353673 | 1 |
| 701 | 0.4599882 | | 0.7712577 | 0.5951415 | 1.8844748 | 0.5769236 | 0.6688827 | 0.4342739 |
| 702 | 2.036728 | | 2.269083 | 1.282212 | 1.7083771 | 1.0584339 | 1 | 1 |
| 703 | 0.5124571 | | 0.8184702 | 0.6456344 | 1 | 0.5250589 | 0.575653 | 0.4688678 |
| 704 | 2.0507197 | | 1 | 2.1610024 | 1 | 1.5439798 | 1.6400951 | 1.700945 |
| 705 | 1 | | 0.7346102 | 0.60362 | 0.750874 | 0.6035169 | 1 | 0.5478157 |
| 706 | 0.5844951 | | 0.7968753 | 0.53727 | 1.616124 | 0.4808581 | 1 | 0.4332336 |
| 707 | 0.4734601 | | 0.8125974 | 0.5562648 | 2.4200236 | 0.443527 | 1 | 0.4055942 |
| 708 | 1 | | 1 | 0.5290778 | 1 | 1.9576656 | 1 | 1 |
| 709 | 2.5353345 | | 1 | 1.8984244 | 1 | 1 | 1.6048076 | 3.3951677 |
| 710 | 2.6196337 | | 1.531555 | 3.0285347 | 4.578297 | 2.6642192 | 2.4679695 | 2.7418341 |
| 711 | 2.9823485 | | 1 | 2.1091613 | 1.957874 | 2.233375 | 1 | 2.2356899 |
| 712 | 2.8713061 | | 1 | 1 | 1.9580534 | 2.4435486 | 1 | 1 |
| 713 | 1.5687636 | | 1 | 1 | 1 | 1 | 6.6394952 | 1 |
| 714 | 1 | | 1 | 1 | 1 | 1 | 1 | 1 |
| 715 | 0.5631288 | | 1 | 0.4656067 | 1.4661981 | 0.5532582 | 1 | 0.4826515 |
| 716 | 1 | | 1 | 1 | 1 | 1 | 1 | 1 |
| 717 | 0.5380714 | | 1 | 0.6512936 | 1.4511956 | 0.3753073 | 0.7682384 | 0.3946084 |
| 718 | 1.5385373 | | 1 | 1 | 1 | 1 | 2.3332557 | 1 |
| 719 | 5.6360851 | | 2.1415568 | 7.0002424 | 3.3298015 | 8.1581528 | 1 | 14.443733 |
| 720 | 4.9338711 | | 2.0696958 | 1 | 3.7566559 | 8.6785095 | 8.4552801 | 1 |
| 721 | 3.1039218 | | 1.48548 | 1 | 1 | 1.7535528 | 2.199657 | 3.374583 |
| 722 | 2.6904983 | | 1 | 1.9414274 | 0.6569635 | 1.4675735 | 1.4098509 | 2.4632584 |
| 723 | 1.6305899 | | 0.5418798 | 1 | 2.2300028 | 1.9256917 | 1.3509489 | 2.8949895 |
| 724 | 2.2070494 | | 1.1906025 | 0.8257891 | 1.2559723 | 2.630431 | 1.392193 | 1.9564362 |
| 725 | 0.4059004 | | 0.4296617 | 0.3245335 | 0.7584144 | 0.2156553 | 1 | 0.4259375 |
| 726 | 1.3004705 | | 0.7036848 | 1.3927377 | 1 | 4.9916235 | 1.5206256 | 1.8076552 |
| 727 | 2.2518318 | | 1.3404821 | 1.8345004 | 1 | 2.1655526 | 1 | 1 |
| 728 | 0.3965206 | | 0.5217097 | 1 | 1.8311424 | 1 | 0.7190193 | 0.3832332 |
| 729 | 0.3089908 | | 0.4586319 | 0.5510332 | 1.8172394 | 1 | 1 | 0.3831385 |
| 730 | 0.1517698 | | 0.4276825 | 1 | 0.5439354 | 0.2358161 | 1 | 0.3409286 |
| 731 | 1 | | 1.6510255 | 1.214295 | 1 | 1 | 1.2731892 | 0.4586643 |
| 732 | 2.2349511 | | 1 | 1 | 1 | 1.5025805 | 1.7153141 | 1.6983499 |
| 733 | 0.5819923 | | 0.8488073 | 1 | 0.1928036 | 1 | 0.302739 | 1 |
| 734 | 1.9899033 | | 1 | 1 | 0.6832476 | 1 | 2.0580833 | 1.7413821 |
| 735 | 0.5502733 | | 0.5047418 | 0.7229789 | 1 | 0.3356266 | 1 | 1 |

Table 4

| SEQ ID | Patient ID | | | | | | | |
|--------|------------|-----|-----------|-----------|-----------|-----------|-----------|-----------|
| | 577 | 695 | 784 | 786 | 787 | 789 | 790 | 791 |
| 736 | 2.3038625 | | 0.7325813 | 1.2385548 | 1 | 1 | 1.6088162 | 1 |
| 737 | 0.6669822 | | 0.4763721 | 0.5657976 | 0.389395 | 0.3902686 | 0.7552808 | 18.764508 |
| 738 | 5.8887823 | | 1 | 1 | 1.3555249 | 4.6216601 | 1.8631548 | 5.4294229 |
| 739 | 0.7627704 | | 0.4452781 | 0.5437976 | 1 | 0.3999132 | 0.4591899 | 0.4486813 |
| 740 | 2.0268877 | | 1.3379868 | 1 | 1.8564261 | 1 | 3.9297778 | 1 |
| 741 | 2.4094835 | | 1 | 3.4608054 | 1.6450338 | 2.4244774 | 2.2365819 | 2.0397994 |
| 742 | 1.8019363 | | 0.8774187 | 1.3958381 | 1 | 1 | 2.0568271 | 2.0798429 |
| 743 | 1 | | 0.2308459 | 0.2345951 | 0.001 | 1 | 1 | 1 |
| 744 | 3.8465884 | | 1.2389118 | 1.1790623 | 1.3283175 | 1.6642815 | 1.5370978 | 2.7547353 |
| 745 | 1.8836956 | | 1 | 1.6454002 | 1.3264706 | 1.4830257 | 1.7287798 | 2.2536672 |
| 746 | 0.2807326 | | 0.0199671 | 0.0579936 | 0.0267714 | 0.1745728 | 0.0109956 | 0.4480861 |
| 747 | 2.3746527 | | 1.504487 | 3.1080735 | 2.3024164 | 1.965925 | 2.3521416 | 2.6655462 |
| 748 | 0.2596485 | | 0.498369 | 0.612029 | 1.4564542 | 1 | 0.6228395 | 0.1481112 |
| 749 | 0.0557737 | | 0.0446167 | 0.0326055 | 1 | 1 | 0.10455 | 0.0238081 |
| 750 | 0.2518803 | | 0.1801072 | 0.288743 | 1 | 1 | 1 | 0.1916501 |
| 751 | 2.6891838 | | 1 | 1 | 2.1961687 | 3.7013513 | 2.0717184 | 2.3457724 |
| 752 | 0.5734443 | | 0.4050873 | 0.2689028 | 1 | 1 | 0.3206228 | 2.4502762 |
| 753 | 4.6904869 | | 2.5129645 | 2.8926177 | 2.182223 | 5.7385775 | 2.4247211 | 4.2533693 |
| 754 | 0.5864334 | | 1 | 0.6662268 | 1.5212493 | 0.6213032 | 0.5985334 | 0.4718461 |
| 755 | 0.2731798 | | 0.0254652 | 0.0802274 | 0.0456507 | 0.139384 | 0.0642234 | 0.4540583 |
| 756 | 0.4554357 | | 0.4319732 | 0.1273302 | 1 | 1.4643514 | 0.001 | 1 |
| 757 | 2.2845236 | | 1.3061435 | 1 | 1.5812904 | 3.7732022 | 1 | 1.7781702 |
| 758 | 2.8200329 | | 1.7128668 | 1.5271434 | 2.2608271 | 4.3995885 | 1.6063743 | 3.4057013 |
| 759 | 2.3790864 | | 1 | 1 | 1 | 1 | 1 | 1.8648949 |
| 760 | 2.3986778 | | 1 | 1.3960017 | 0.5764784 | 1 | 1 | 1.6801537 |
| 761 | 1.8971526 | | 1.0878736 | 1.6709401 | 0.4402444 | 1.1977471 | 1.5954775 | 1.7523082 |
| 762 | 3.6534079 | | 4.05419 | 7.4419027 | 2.7425753 | 2.2274519 | 1.7391967 | 1 |
| 763 | 0.458904 | | 1 | 0.4185716 | 1 | 1 | 1 | 0.4310669 |
| 764 | 1 | | 0.4840377 | 3.0190689 | 2.0096412 | 7.8268334 | 1.280529 | 1 |
| 765 | 2.6072982 | | 0.4523035 | 1 | 1.4346164 | 1 | 2.5370484 | 1 |
| 766 | 2.1131327 | | 1 | 1 | 0.8462016 | 1 | 1.3388947 | 2.1151312 |
| 767 | 1.8202057 | | 1.2212232 | 1.3518066 | 1 | 1.7152217 | 2.8668459 | 3.2321641 |
| 768 | 2.1052977 | | 1 | 1 | 0.5052191 | 1 | 1.4425272 | 2.0283352 |
| 769 | 2.1081718 | | 1 | 2.0134496 | 0.8428242 | 2.2360911 | 1.4465641 | 2.1202379 |
| 770 | 0.5873914 | | 0.7986247 | 0.5540572 | 0.6950728 | 0.6252949 | 1 | 0.4995772 |
| 771 | 1.6738498 | | 2.9080955 | 1 | 2.0276826 | 1 | 1.1848997 | 1 |
| 772 | 2.5131735 | | 1 | 1.7108129 | 1 | 1 | 3.6798148 | 1 |
| 773 | 0.8023987 | | 0.4347801 | 0.3938697 | 1 | 0.4632328 | 1 | 0.5714748 |
| 774 | 1 | | 0.8399679 | 0.3261892 | 1 | 0.4468305 | 1.8229411 | 0.63078 |
| 775 | 9.017093 | | 0.7557389 | 1.9927925 | 1.8020881 | 1 | 3.8718215 | 1 |
| 776 | 2.2727748 | | 1.2028627 | 1.9380585 | 0.4990457 | 1.7077299 | 1.6261918 | 1.964118 |
| 777 | 0.6230613 | | 0.7560017 | 0.714409 | 1.6874611 | 0.5448962 | 0.6072142 | 0.4400821 |
| 778 | 7.8114453 | | 4.6439825 | 2.2540198 | 3.6521355 | 7.2043669 | 2.5430896 | 1 |
| 779 | 1.342156 | | 0.7147339 | 1.4286752 | 0.7661611 | 1 | 1.7307136 | 1.3438316 |
| 780 | 0.1552752 | | 0.3376111 | 0.4880478 | 0.3871976 | 0.0880257 | 0.3629819 | 1 |
| 781 | 2.6524741 | | 1 | 4.5493556 | 2.0826875 | 2.0479496 | 4.0245743 | 4.448478 |
| 782 | 0.4013999 | | 0.0481831 | 0.0524001 | 0.0422135 | 1 | 0.0225982 | 0.4069495 |
| 783 | 5.6405633 | | 1 | 1.7606649 | 3.1942088 | 4.8255665 | 3.3028308 | 4.2116652 |
| 784 | 0.6316168 | | 0.3582129 | 1 | 1 | 0.6515802 | 1 | 1.4061113 |

Table 4

| SEQ ID | Patient ID | | | | | | | |
|--------|------------|-----|-----------|-----------|-----------|-----------|-----------|-----------|
| | 577 | 695 | 784 | 786 | 787 | 789 | 790 | 791 |
| 785 | 0.0283547 | | 0.0526896 | 0.118833 | 0.2446534 | 0.2375636 | 0.2576839 | 0.001 |
| 786 | 2.1390218 | | 1.4367262 | 2.023825 | 1.7360189 | 2.1678298 | 2.6899847 | 1.8033246 |
| 787 | 2.4050424 | | 1 | 1 | 1.4151043 | 2.5476851 | 1 | 2.1605191 |
| 788 | 1.2841394 | | 1.1072816 | 2.2264975 | 2.8874708 | 2.2353564 | 4.1656963 | 3.7699074 |
| 789 | 0.0683841 | | 0.0875485 | 0.0926809 | 1 | 1 | 1 | 1 |
| 790 | 1.9676978 | | 1 | 1.6280486 | 1.8549896 | 3.2100616 | 1.8794577 | 3.9311668 |
| 791 | 1.6571697 | | 0.6253276 | 1.9274498 | 1.6148679 | 2.4160394 | 1.4702208 | 1.7259807 |
| 792 | 0.6763694 | | 0.790416 | 0.3909058 | 1 | 0.447922 | 1.7054477 | 0.7175186 |
| 793 | 0.2302318 | | 0.2582786 | 0.3732707 | 0.3302346 | 0.4394615 | 0.5297086 | 0.1393257 |
| 794 | 2.2142532 | | 1 | 1 | 1 | 2.042784 | 1.6063038 | 2.1725751 |
| 795 | 0.2724222 | | 0.4383318 | 0.4226079 | 1.5131606 | 1 | 1 | 0.3409845 |
| 796 | 1 | | 1 | 1 | 0.575307 | 0.485612 | 0.7552526 | 0.406441 |
| 797 | 1.842983 | | 0.7405922 | 1.58277 | 1 | 1 | 2.6753333 | 1.2879462 |
| 798 | 4.7055109 | | 3.6220308 | 1.6887043 | 1 | 4.314761 | 1.795685 | 1 |
| 799 | 2.8535491 | | 1 | 2.7784916 | 1.9304728 | 1.5301583 | 1.9210264 | 2.6511509 |
| 800 | 2.5087101 | | 1 | 1.8587823 | 1 | 1 | 1.3017157 | 2.3629547 |
| 801 | 0.5823785 | | 0.4504451 | 0.5689727 | 0.8302465 | 0.4424712 | 1.2492501 | 0.479274 |
| 802 | 2.8631517 | | 1 | 2.2364593 | 1 | 2.3606245 | 2.3410613 | 2.1636538 |
| 803 | 0.6255121 | | 1 | 0.4446485 | 0.6765013 | 0.5491805 | 0.879366 | 0.4378392 |
| 804 | 1 | | 0.2458013 | 0.6513352 | 0.1551048 | 1.775752 | 0.2104409 | 0.4720687 |
| 805 | 2.2632539 | | 1.1321923 | 1.2582864 | 0.6557152 | 1.5201063 | 1.7462401 | 2.2201154 |
| 806 | 1.7608895 | | 1 | 3.7944301 | 1.3955153 | 1.5592674 | 2.7657824 | 2.6591787 |
| 807 | 1.7556389 | | 1 | 0.7881911 | 0.5100672 | 1 | 2.1718222 | 1.692567 |
| 808 | 2.6146728 | | 1.5238564 | 1.6677821 | 1.0595091 | 1.4937715 | 1.9804366 | 3.4035014 |
| 809 | 2.9440941 | | 1 | 1 | 1 | 1.5882438 | 2.223342 | 4.3979806 |
| 810 | 2.6474092 | | 1 | 1.4503881 | 1 | 1.212952 | 2.6022457 | 2.4748281 |
| 811 | 2.833475 | | 1 | 1 | 1 | 1 | 2.1715822 | 2.3521251 |
| 812 | 2.7327259 | | 1 | 1 | 0.6400508 | 1 | 1.4399018 | 2.7846284 |
| 813 | 5.0674161 | | 1 | 1 | 1 | 1 | 1.2976929 | 2.70616 |
| 814 | 2.9993628 | | 1 | 1.4123587 | 0.6183071 | 1 | 1 | 2.2130907 |
| 815 | 2.3429041 | | 1.1646518 | 1 | 0.4697348 | 1.1821171 | 1.6158455 | 2.0613993 |
| 816 | 0.5649186 | | 0.7940992 | 0.5586036 | 1.4817207 | 0.5290071 | 1 | 0.4322763 |
| 817 | 0.5617103 | | 1 | 0.5721562 | 1.6308658 | 1 | 0.7120324 | 0.3848268 |
| 818 | 0.5697236 | | 1 | 0.6025667 | 1.5318091 | 0.603908 | 0.813844 | 0.4801066 |
| 819 | 0.5014732 | | 0.5492058 | 0.5068388 | 0.7498383 | 0.5321311 | 1 | 0.4719532 |
| 820 | 0.6812264 | | 0.7075112 | 1 | 1.4962564 | 0.5040703 | 0.5608887 | 0.4134596 |
| 821 | 2.3159901 | | 1 | 1 | 1 | 0.7021306 | 1.8940385 | 2.3647929 |
| 822 | 1.9809691 | | 1 | 1 | 1 | 1 | 2.5464349 | 1 |
| 823 | 2.6206215 | | 1 | 1.7344756 | 0.7859895 | 0.7270271 | 1.616029 | 2.198501 |
| 824 | 0.2250183 | | 0.6567193 | 0.5626843 | 0.4981308 | 0.2009702 | 0.7586825 | 0.2030957 |
| 825 | 0.2054195 | | 0.3568518 | 0.5377753 | 0.2895602 | 0.2614077 | 0.5285512 | 0.2252761 |
| 826 | 2.4400513 | | 1 | 3.426136 | 2.1208395 | 1.3049977 | 2.9714806 | 2.6326941 |
| 827 | 0.5929242 | | 0.7772166 | 0.5515136 | 1.4907072 | 0.6422184 | 0.6076941 | 0.4478702 |
| 828 | 0.2582152 | | 0.6035614 | 0.3017539 | 0.6617176 | 1 | 1 | 1 |
| 829 | 2.0418226 | | 1 | 1 | 0.813975 | 1.7839942 | 0.7703274 | 2.2403795 |
| 830 | 0.0712656 | | 0.0622026 | 0.1176388 | 0.0661119 | 0.0597742 | 0.0237556 | 0.0129291 |
| 831 | 0.1270987 | | 0.4499016 | 0.2178688 | 0.2899621 | 0.1142477 | 0.4387655 | 1 |
| 832 | 2.5368198 | | 1 | 1 | 2.3060075 | 3.8210984 | 1.2496171 | 1 |
| 833 | 0.0516074 | | 0.055384 | 0.0582388 | 0.0630509 | 0.0570901 | 0.0196622 | 1 |

Table 4

| SEQ ID NO | Patient ID | | | | | | | |
|--------------|------------|-----|-----------|-----------|-----------|-----------|-----------|-----------|
| | 577 | 695 | 784 | 786 | 787 | 789 | 790 | 791 |
| 834 | 0.6140232 | | 1 | 0.5660934 | 1.4437482 | 1 | 0.6073412 | 0.4345724 |
| 835 | 0.2193815 | | 0.672791 | 0.5024072 | 0.5211058 | 0.3875628 | 0.5139562 | 0.0731556 |
| 836 | 0.5711495 | | 0.8425485 | 0.6204062 | 1.4127016 | 0.5812614 | 0.8944267 | 0.398225 |
| 837 | 0.5528578 | | 0.7444212 | 0.5778314 | 1.4858676 | 0.6296878 | 0.8888371 | 0.4325271 |
| 838 | 3.4418688 | | 2.191745 | 1.4380741 | 2.4494238 | 3.0795725 | 2.4290261 | 3.6984609 |
| 839 | 3.4845792 | | 1.8689281 | 2.0180541 | 2.2714296 | 3.338609 | 3.2937548 | 3.8955153 |
| 840 | 1.894479 | | 1 | 2.6718303 | 1.7228342 | 2.5847582 | 1.0930674 | 2.0808833 |
| 841 | 2.6408664 | | 1 | 1.8050373 | 1.8407531 | 2.9745458 | 3.7889945 | 3.93763 |
| 842 | 2.7760972 | | 1 | 1 | 1.4362153 | 2.5473036 | 1.4626834 | 2.999359 |
| 843 | 0.1565823 | | 0.2335009 | 0.5369512 | 0.296127 | 0.2329847 | 0.6050828 | 0.246561 |
| 844 | 2.1468643 | | 1 | 1 | 1.4100595 | 1.3497378 | 2.495155 | 3.0852992 |
| 845 | 1.9238883 | | 1 | 3.475107 | 1.7555823 | 1.7805857 | 4.1607419 | 3.0996984 |
| 846 | 0.3432422 | | 0.1576021 | 0.2533646 | 0.2849002 | 1 | 0.3869351 | 0.1322461 |
| 847 | 1.7962326 | | 1.5237261 | 1 | 1.9875212 | 1.4163648 | 3.2034187 | 5.1888202 |
| 848 | 0.189586 | | 0.194698 | 1 | 0.7845701 | 0.4214732 | 2.3642099 | 0.8019248 |
| 849 | 0.560975 | | 0.8286442 | 0.6484281 | 1.6500016 | 0.6100873 | 0.7005004 | 0.4260201 |
| 850 | 2.0485957 | | 1.3532844 | 1.5535977 | 1 | 0.8522925 | 1.4829244 | 2.0020292 |
| 851 | 0.2345838 | | 0.2244382 | 0.279979 | 0.3087217 | 0.2595081 | 0.2123746 | 1 |
| 852 | 1.3682307 | | 0.5172708 | 1 | 1.2198895 | 1.9252012 | 1.5893516 | 1 |
| 853 | 2.2441527 | | 1.3525041 | 2.1546836 | 1.7763855 | 1 | 1.6425935 | 2.621169 |
| 854 | 3.1902633 | | 1 | 1.9268263 | 1.7694853 | 2.5332652 | 1.727453 | 5.2487787 |
| 855 | 0.5111352 | | 0.5156279 | 0.4206259 | 0.7501632 | 1 | 1 | 1 |
| 856 | 1.3844281 | | 1.2976619 | 1 | 1.7066482 | 2.0944165 | 1.5672334 | 2.3883751 |
| 857 | 0.3375312 | | 0.5804109 | 0.4678589 | 2.7771959 | 0.5661782 | 1.3431292 | 0.2394221 |
| 858 | 0.1060072 | | 0.1428906 | 0.2076063 | 0.2297329 | 0.1884636 | 0.3925388 | 0.1544126 |
| 859 | 0.4494054 | | 0.4082117 | 0.649713 | 0.3548855 | 0.7309485 | 0.3152449 | 0.4906089 |
| 860 | 0.1536488 | | 0.3581352 | 0.4497743 | 1 | 1 | 0.475394 | 0.0988562 |
| 861 | 2.6590021 | | 1.8783812 | 2.5433915 | 1.7691689 | 4.4748297 | 1.724136 | 1 |
| 862 | 2.6590021 | | 1.8783812 | 2.5433915 | 1.7691689 | 4.4748297 | 1.724136 | 1 |
| 863 | 0.5618588 | | 0.7384997 | 0.704148 | 1.4541541 | 0.5982048 | 1 | 0.4423704 |
| 864 | 0.477463 | | 0.1766986 | 0.6571013 | 0.5799498 | 0.4495053 | 0.1521458 | 0.3350138 |
| 865 | 0.4913953 | | 0.3190354 | 0.4303789 | 0.2146927 | 0.3520773 | 0.1429711 | 0.3350848 |
| 866 | 2.7156076 | | 1 | 1 | 1 | 2.1781717 | 1.8126936 | 2.8366991 |
| 867 | 2.7711659 | | 1 | 1 | 0.5446451 | 1 | 1.5610087 | 1.9260188 |
| 868 | 0.6267004 | | 1.1424235 | 0.6397748 | 1.6726945 | 1 | 0.5099334 | 0.4930974 |
| 869 | 2.6081151 | | 1.5820948 | 2.9880225 | 1.8898924 | 3.6662447 | 1.3474625 | 2.7522412 |
| 870 | 2.6333878 | | 1 | 1 | 1.3070867 | 1 | 1.4148335 | 2.9129145 |
| 871 | 2.4493791 | | 1.3691252 | 2.1462085 | 1 | 1.8041965 | 2.5616085 | 2.4029707 |
| 872 | 2.0229591 | | 1 | 1.6083767 | 1 | 1.391679 | 1.5388763 | 2.1856727 |
| 873 | 2.6404356 | | 1 | 1 | 0.5365564 | 1.6185101 | 1.719351 | 1.8780114 |
| 874 | 2.1824377 | | 1 | 1 | 1 | 1 | 1.3113421 | 1.9199366 |
| 875 | 1.6940279 | | 1.5858952 | 2.1686076 | 1.3598258 | 2.250069 | 1.798748 | 2.0132998 |
| 876 | 1.3081496 | | 1 | 1 | 0.6404954 | 1.3313015 | 2.3515064 | 1.8602422 |
| 877 | 0.350342 | | 0.372888 | 0.1346543 | 0.0347147 | 0.3072507 | 0.0993839 | 0.114405 |
| 878 | 0.5977664 | | 0.8755655 | 0.2164818 | 1 | 0.5183144 | 1.8184243 | 0.7516797 |
| 879 | 2.4151351 | | 1.5278793 | 1.3339954 | 0.6734744 | 1 | 1 | 3.1653694 |
| 880 | 0.5655498 | | 1 | 0.628391 | 1.3495653 | 1 | 1 | 0.3860637 |
| 881 | 0.1028806 | | 0.1896362 | 0.2068511 | 0.3310726 | 0.1024189 | 0.3765606 | 1 |
| 882 | 0.3808282 | | 0.2961276 | 0.4448035 | 0.475438 | 0.2658555 | 0.6982984 | 0.3015863 |

Table 4

| SEQ ID NO | Patient ID | | | | | | | |
|--------------|------------|-----|-----------|-----------|-----------|-----------|-----------|-----------|
| | 577 | 695 | 784 | 786 | 787 | 789 | 790 | 791 |
| 883 | 0.0663195 | | 0.1255569 | 0.1772176 | 0.2131194 | 0.0443638 | 0.3342155 | 0.0631841 |
| 884 | 3.0286458 | | 1.4208764 | 2.3541638 | 0.9071234 | 1.6130607 | 1.7754159 | 2.4530901 |
| 885 | 2.479078 | | 1 | 1 | 1 | 0.6876942 | 1.3726154 | 2.6513287 |
| 886 | 1.7754233 | | 0.7929406 | 1.7583262 | 1 | 1 | 2.6655939 | 3.0075767 |
| 887 | 2.1775733 | | 1 | 1 | 0.6734744 | 1.5075417 | 0.7929538 | 2.2959595 |
| 888 | 2.1245994 | | 1.2841812 | 1.6568419 | 1.7600713 | 2.095126 | 2.4865307 | 2.5622807 |
| 889 | 0.4336313 | | 0.5902627 | 0.6737245 | 0.6246002 | 1 | 1 | 0.7672589 |
| 890 | 2.3027411 | | 1 | 1 | 0.8913393 | 1.3182738 | 1.7176854 | 2.878122 |
| 891 | 0.5669757 | | 1 | 0.5951465 | 1.4865089 | 0.6453498 | 0.5494414 | 0.466155 |
| 892 | 0.6097975 | | 0.9275689 | 0.564279 | 1.5182139 | 0.7310663 | 0.6556993 | 0.4346727 |
| 893 | 1 | | 1.046648 | 1.424859 | 1.5451135 | 1 | 1.6887496 | 1 |
| 894 | 2.2930791 | | 1.3012616 | 2.0344237 | 1.3187068 | 1.7828722 | 1.3727848 | 1 |
| 895 | 3.0565475 | | 3.2949099 | 6.8095146 | 2.054454 | 1.5985816 | 0.6497286 | 1.98718 |
| 896 | 2.128179 | | 0.8005831 | 1 | 0.6499693 | 2.1586811 | 1.8595979 | 1.4988832 |
| 897 | 0.7061575 | | 0.5321351 | 1.4210631 | 1 | 0.6315115 | 1.2206813 | 1.2481028 |
| 898 | 1.8966476 | | 1.5420751 | 1.5529226 | 1.1970256 | 1.529264 | 1.4161885 | 1.7661306 |
| 899 | 2.0374261 | | 1 | 1.8188624 | 0.8149327 | 1.5268271 | 1.8385947 | 1.7521917 |
| 900 | 0.7418497 | | 0.5281869 | 1.5966645 | 1 | 0.6618687 | 1.2606833 | 1.7274142 |
| 901 | 2.7636428 | | 1.3250373 | 1.1205085 | 1 | 1 | 2.5540006 | 2.8014075 |
| 902 | 0.6770972 | | 0.4291404 | 1 | 1.1176777 | 0.7857388 | 1 | 1.5124791 |
| 903 | 0.5541203 | | 0.6665419 | 0.6297529 | 1.5845652 | 0.5631039 | 0.6015964 | 0.3600258 |
| 904 | 2.2106439 | | 1 | 1 | 1 | 1 | 1.6494393 | 1.935357 |
| 905 | 0.5669237 | | 0.5221284 | 0.4942572 | 0.7187831 | 0.5136574 | 1 | 0.4889094 |
| 906 | 2.3684367 | | 1 | 1 | 0.5126665 | 1.288829 | 1.4451102 | 2.0834065 |
| 907 | 0.0652575 | | 0.3732581 | 0.5474879 | 1 | 0.0367633 | 0.6393823 | 0.045138 |
| 908 | 0.7271079 | | 0.5930592 | 0.6238608 | 0.5256974 | 0.4842535 | 1 | 0.4572341 |
| 909 | 0.3521467 | | 0.4259736 | 0.4537688 | 0.5960588 | 0.3971212 | 1.1080999 | 0.3689173 |
| 910 | 0.1931359 | | 0.2315368 | 0.2766812 | 0.2705099 | 0.1898044 | 0.5129541 | 0.1201294 |
| 911 | 0.1696234 | | 0.1634014 | 0.2554198 | 0.3024457 | 0.1934359 | 0.6135095 | 0.0542864 |
| 912 | 0.6407515 | | 0.650346 | 0.6069722 | 0.7757974 | 0.4806135 | 1.5859358 | 0.5208413 |
| 913 | 0.6612563 | | 0.7319076 | 1 | 1.5242676 | 0.6125703 | 0.5521233 | 0.4196682 |
| 914 | 0.5988135 | | 0.8603936 | 0.6071733 | 1.4982572 | 0.5970445 | 0.6573225 | 0.3975699 |
| 915 | 0.3338921 | | 0.0526741 | 0.0424741 | 0.0416064 | 0.2438058 | 0.0112214 | 0.343374 |
| 916 | 0.7131385 | | 0.8587853 | 0.4317097 | 0.7329683 | 0.5729443 | 1 | 0.5000545 |
| 917 | 2.2355155 | | 1 | 1.1772564 | 0.760723 | 1.5779291 | 0.8602966 | 2.4188557 |
| 918 | 0.535539 | | 0.8064142 | 0.5829919 | 1.5022246 | 0.5847739 | 0.6431793 | 0.4088822 |
| 919 | 2.5574063 | | 1 | 1 | 1 | 1.5535701 | 1.3351259 | 2.801904 |
| 920 | 7.11518 | | 2.3998953 | 2.1904047 | 3.185667 | 6.9746603 | 3.1842081 | 4.6639979 |
| 921 | 0.308055 | | 0.3191519 | 0.4145107 | 0.3661464 | 0.6775237 | 0.3279626 | 0.4406096 |
| 922 | 2.1139422 | | 1.4722054 | 2.3292321 | 1.7310939 | 2.2623403 | 2.2742267 | 1.8168803 |
| 923 | 2.5899422 | | 1 | 1.8842122 | 1.2543477 | 3.2404895 | 1 | 1 |
| 924 | 0.3228488 | | 0.0341647 | 0.0157791 | 0.0353218 | 0.2319038 | 0.0103887 | 0.3843832 |
| 925 | 1.5431715 | | 1 | 1.6062803 | 1.9784663 | 1.6920989 | 1.3838792 | 1.647478 |
| 926 | 0.5645695 | | 0.7335823 | 0.6628044 | 1.3781408 | 0.6418851 | 0.59516 | 0.4115328 |
| 927 | 2.5668232 | | 1.6502002 | 0.857963 | 1 | 1.7841814 | 1.2065945 | 2.0841207 |
| 928 | 0.5195347 | | 1.1817777 | 0.2914972 | 3.461384 | 0.6359211 | 1 | 0.1789795 |
| 929 | 0.4913656 | | 0.5128242 | 0.367015 | 0.1975833 | 0.4629901 | 0.127868 | 0.3336124 |
| 930 | 0.1780377 | | 0.3967403 | 0.1898243 | 1 | 1 | 1 | 0.0798495 |
| 931 | 2.9371057 | | 1.4821451 | 1.3988156 | 1.3469916 | 1 | 1.5597524 | 2.9974253 |

Table 4

| SEQ ID NO | Patient ID | | | | | | | |
|--------------|------------|-----|-----------|-----------|-----------|-----------|-----------|-----------|
| | 577 | 695 | 784 | 786 | 787 | 789 | 790 | 791 |
| 932 | 4.6550546 | | 7.6926732 | 4.0983588 | 5.494385 | 8.6006114 | 3.7285681 | 8.5778282 |
| 933 | 1.8997296 | | 1 | 1 | 1 | 2.2888281 | 1.3950442 | 2.7156442 |
| 934 | 2.4232746 | | 1.2356654 | 1 | 1.3418699 | 2.7809687 | 1.4653229 | 2.6779193 |
| 935 | 1.3852525 | | 1.73204 | 1 | 1 | 1 | 2.0645621 | 1 |
| 936 | 0.5549075 | | 0.3798713 | 0.4290691 | 0.6820932 | 1 | 0.4649489 | 0.5710083 |
| 937 | 0.2909813 | | 0.2011894 | 0.3967203 | 0.5141971 | 1 | 0.8934104 | 0.3087541 |
| 938 | 3.0425261 | | 1 | 2.1735533 | 0.7229985 | 1.9082448 | 1 | 2.3217916 |
| 939 | 2.5511011 | | 1.2895696 | 1 | 1.0904275 | 1 | 1.3958629 | 2.9720644 |
| 940 | 0.5911641 | | 0.6699287 | 0.6372367 | 1.3078563 | 0.5212372 | 0.5073927 | 0.3939239 |
| 941 | 3.0413527 | | 1 | 4.6127694 | 0.1512314 | 1 | 1 | 2.1193283 |
| 942 | 0.0468395 | | 0.0892287 | 0.1091788 | 1 | 1 | 0.3478365 | 0.0700862 |
| 943 | 0.1823377 | | 0.4467266 | 0.5219309 | 1 | 1 | 1 | 0.1310456 |
| 944 | 2.0998688 | | 1 | 1 | 1 | 2.5378012 | 1.3502572 | 2.1558634 |
| 945 | 2.3076575 | | 1.4061706 | 1.762836 | 1 | 1.7433076 | 1.6847974 | 2.1481874 |
| 946 | 0.3113524 | | 0.0406387 | 0.0281824 | 0.0387078 | 0.1954892 | 1 | 0.3577768 |
| 947 | 2.74925 | | 1 | 1.9894093 | 0.669336 | 3.20764 | 1.103202 | 2.2265574 |
| 948 | 2.9506741 | | 1.4938456 | 2.0063851 | 1.3055562 | 4.0391163 | 2.7037609 | 1 |
| 949 | 2.6420546 | | 1.7009678 | 3.5206361 | 2.2927544 | 3.771947 | 2.1433239 | 2.8451747 |
| 950 | 5.7276476 | | 1.8351414 | 2.3223456 | 1.8315443 | 4.1614165 | 2.2690747 | 1 |
| 951 | 0.5380492 | | 0.8301028 | 0.5358482 | 1.5482686 | 1 | 0.5595195 | 0.4884199 |
| 952 | 2.5987576 | | 1 | 1 | 1.2668399 | 4.7613967 | 2.5250365 | 2.3512155 |
| 953 | 1.6047231 | | 1.2106728 | 1.3420351 | 1.626317 | 3.0719243 | 2.47761 | 2.8070787 |
| 954 | 0.2849583 | | 0.208604 | 0.6487813 | 0.3434108 | 1.3592846 | 0.453671 | 0.526374 |
| 955 | 0.4535197 | | 0.3301146 | 0.5474921 | 1 | 0.3791899 | 0.3373067 | 1 |
| 956 | 1.3061444 | | 4.5629095 | 1.7580667 | 1 | 5.2818972 | 0.8199982 | 1 |
| 957 | 2.307858 | | 1.7360547 | 1.5622222 | 0.5528963 | 1 | 2.0151031 | 1 |
| 958 | 1.9252697 | | 1.1859133 | 1.2460903 | 1 | 2.4145816 | 2.2888357 | 1.8072419 |
| 959 | 1.6768947 | | 1 | 1 | 0.8349663 | 1.1976838 | 1.906121 | 1.9080247 |
| 960 | 1 | | 1 | 1 | 1.2440359 | 1 | 1.6898506 | 1.7497478 |
| 961 | 2.0006793 | | 1 | 1.4568917 | 1 | 1.2271074 | 2.0137339 | 2.7729049 |
| 962 | 2.0576487 | | 1 | 1.6881061 | 1.2218219 | 1 | 1.1636143 | 2.6142331 |
| 963 | 1.9934235 | | 0.8728217 | 1.5095663 | 0.7080523 | 2.1535561 | 1.8374937 | 1.7482384 |
| 964 | 5.6158476 | | 1 | 1 | 1 | 1 | 1 | 4.4342521 |
| 965 | 2.0753314 | | 1.3425012 | 1.5579999 | 0.6038397 | 0.7149851 | 2.8098918 | 1 |
| 966 | 2.2405953 | | 1 | 1 | 0.5527253 | 1.8100047 | 1.2868243 | 1 |
| 967 | 0.5508823 | | 0.397698 | 0.8198504 | 1 | 0.3349491 | 1 | 0.5479372 |
| 968 | 2.003947 | | 1 | 1 | 1 | 1 | 1.967112 | 2.3003699 |
| 969 | 0.5833885 | | 0.8059839 | 0.4977229 | 1.547653 | 0.5722503 | 0.6126908 | 0.3997234 |
| 970 | 3.1463945 | | 1.4886807 | 2.3005206 | 0.7903588 | 1 | 1.4355826 | 2.6997817 |
| 971 | 2.1249707 | | 1.7781719 | 1.656458 | 1 | 1 | 1.7658741 | 2.0712311 |
| 972 | 0.1543543 | | 0.4879037 | 0.2916268 | 1 | 0.2743455 | 0.3556845 | 1 |
| 973 | 0.7381512 | | 0.4836437 | 0.469543 | 0.7878449 | 0.5186028 | 1 | 0.4991702 |
| 974 | 0.6275619 | | 0.794701 | 0.6991889 | 1.3000839 | 0.7056482 | 0.607073 | 0.4541157 |
| 975 | 1 | | 0.4852949 | 1 | 0.7274875 | 0.5758883 | 1 | 0.4004647 |
| 976 | 0.5113803 | | 0.7579369 | 0.4278543 | 0.8166428 | 0.5229682 | 1.2949546 | 0.48562 |
| 977 | 2.0403224 | | 0.7597912 | 1 | 1.4631748 | 1.7063592 | 1 | 1.6725095 |
| 978 | 2.3032758 | | 1.1420575 | 1.95038 | 1 | 1 | 1.8342049 | 1.5319154 |
| 979 | 3.6093236 | | 1 | 1 | 1.8026182 | 1 | 3.653702 | 1 |
| 980 | 1.6648117 | | 1.6307257 | 1 | 1.693985 | 2.044073 | 1.1157502 | 3.5266659 |

Table 4

| SEQ ID | Patient ID | | | | | | | |
|--------|------------|-----|-----------|-----------|-----------|-----------|-----------|-----------|
| | 577 | 695 | 784 | 786 | 787 | 789 | 790 | 791 |
| 981 | 1 | | 0.5994734 | 0.7375862 | 1 | 0.4245373 | 0.6131707 | 0.4594455 |
| 982 | 1 | | 2.6458265 | 1.5139145 | 1.4137619 | 2.6798565 | 1.5607122 | 1 |
| 983 | 2.2694773 | | 0.717409 | 1 | 1 | 0.7331699 | 1 | 1 |
| 984 | 2.8961183 | | 1.6648419 | 1 | 1.1476469 | 2.2285464 | 1.8764371 | 3.1108005 |
| 985 | 0.4052097 | | 0.0669818 | 0.0756065 | 1 | 1 | 0.0198598 | 0.342994 |
| 986 | 2.3987298 | | 1 | 1 | 0.6253783 | 1.5140843 | 1.3177362 | 1.8960324 |
| 987 | 0.3583553 | | 0.1528451 | 0.1947102 | 0.322847 | 0.464536 | 0.4103096 | 0.0456478 |
| 988 | 0.6215092 | | 0.7698388 | 0.6189985 | 1.5797513 | 0.7466398 | 0.5732958 | 0.3988258 |
| 989 | 0.5522934 | | 0.8896273 | 0.4073229 | 0.6572372 | 0.5474746 | 0.7370583 | 0.4676859 |
| 990 | 1.9027003 | | 1 | 1 | 1.8653784 | 2.1456094 | 1.4232319 | 3.0108994 |
| 991 | 0.292474 | | 0.5493886 | 0.5434544 | 1 | 1 | 0.3814303 | 0.5379827 |
| 992 | 0.6330798 | | 0.8124197 | 0.5870184 | 1.4720501 | 2.507587 | 0.4674896 | 1 |
| 993 | 0.2450553 | | 1 | 0.6080927 | 1 | 1 | 1 | 0.2890416 |
| 994 | 2.1824971 | | 1 | 1 | 1.9167493 | 1 | 3.2812207 | 1 |
| 995 | 0.6295893 | | 0.7095954 | 0.4733865 | 1.4666548 | 0.5253752 | 0.5596889 | 0.4117558 |
| 996 | 2.1969864 | | 1 | 0.8586742 | 0.5343077 | 1 | 2.0326198 | 2.0036025 |
| 997 | 5.1772628 | | 1 | 1 | 1 | 1 | 0.2243865 | 1 |
| 998 | 4.4504743 | | 2.4055955 | 1.1163261 | 1 | 1 | 1.590749 | 3.313883 |
| 999 | 0.292125 | | 1.6063896 | 0.494541 | 0.6590926 | 1 | 1 | 1 |
| 1000 | 1 | | 0.8231189 | 0.4163869 | 0.6879674 | 0.5819874 | 0.8007312 | 0.5083623 |
| 1001 | 0.0655471 | | 0.0825352 | 0.1066791 | 0.1208517 | 0.0628581 | 0.5539441 | 0.028058 |
| 1002 | 0.2929419 | | 0.2885182 | 0.379919 | 0.5753839 | 0.3758838 | 0.8925494 | 0.2237709 |
| 1003 | 2.3009215 | | 1.2366427 | 1.909378 | 1 | 1 | 2.9014842 | 1 |
| 1004 | 2.1590959 | | 1.4446674 | 2.0841928 | 0.8609083 | 1.9011524 | 1 | 1.5822095 |
| 1005 | 0.5479859 | | 0.7824294 | 0.6149407 | 1.4551801 | 0.6283733 | 0.6620652 | 0.4559968 |
| 1006 | 0.6569934 | | 1 | 1 | 1 | 0.2562647 | 2.0465796 | 1 |
| 1007 | 0.1450636 | | 0.20271 | 0.0861857 | 0.1483157 | 0.1495555 | 0.3674282 | 1 |
| 1008 | 0.6190881 | | 0.8126271 | 0.6079634 | 1.4033731 | 0.7283737 | 0.6401869 | 0.4608815 |
| 1009 | 0.6102133 | | 1 | 0.6208049 | 1.3861525 | 0.7463368 | 0.597376 | 0.4365334 |
| 1010 | 2.1118479 | | 1.8106843 | 1.8060862 | 1.4971969 | 2.6606765 | 1.971163 | 3.5142779 |
| 1011 | 0.571142 | | 1 | 0.5739525 | 1.3155602 | 0.6401517 | 0.6630815 | 0.2878845 |
| 1012 | 2.4106717 | | 1.6284017 | 2.0295138 | 1.5335961 | 3.220852 | 1.8247338 | 1 |
| 1013 | 2.5442464 | | 1.24112 | 2.9834081 | 1.8878916 | 1 | 1.7110372 | 2.9708356 |
| 1014 | 0.5807521 | | 1 | 0.58155 | 1 | 0.6079556 | 1 | 0.4796521 |
| 1015 | 2.5636966 | | 1 | 1.5528889 | 1 | 0.8289872 | 1.3343073 | 2.2649695 |
| 1016 | 0.5548778 | | 0.8663904 | 0.6252688 | 1.4486134 | 1 | 0.4816469 | 0.4161723 |
| 1017 | 1.9559044 | | 1 | 1.5784709 | 1 | 1 | 2.9906629 | 1 |
| 1018 | 0.6016728 | | 1 | 0.2031573 | 1 | 0.5389392 | 1.7958262 | 0.5981331 |
| 1019 | 1.5849387 | | 0.4488368 | 3.0701604 | 1.2755613 | 2.5784883 | 2.0553732 | 0.567462 |
| 1020 | 2.7527777 | | 3.1978512 | 2.3631922 | 1 | 2.8584385 | 2.5337314 | 3.7335778 |
| 1021 | 2.7123027 | | 1 | 1.9484129 | 1 | 1 | 1.6477596 | 2.6155308 |
| 1022 | 3.0505691 | | 2.5438781 | 3.7335845 | 1 | 1 | 1.3571877 | 1 |
| 1023 | 0.5476517 | | 1 | 0.5783457 | 1.2268324 | 0.614346 | 0.7439746 | 0.4078715 |
| 1024 | 0.4760668 | | 0.3975632 | 0.5048306 | 0.4418519 | 1 | 1 | 1 |
| 1025 | 3.4627227 | | 2.2883081 | 1 | 1.3672561 | 6.2985683 | 2.1396117 | 3.7102671 |
| 1026 | 2.2431649 | | 1 | 1 | 0.5399253 | 2.2643735 | 1 | 2.499956 |
| 1027 | 1.9877867 | | 1 | 1 | 1.4362409 | 1.6183176 | 3.6064026 | 2.5578857 |
| 1028 | 2.5350894 | | 1.1883166 | 1.6486259 | 0.8589075 | 1.6410372 | 1.8182126 | 1 |
| 1029 | 2.3376609 | | 1.4285283 | 1.623611 | 1.2161187 | 3.8253957 | 1.4483849 | 1.779251 |

Table 4

| SEQ ID | Patient ID | | | | | | | | |
|--------|------------|-----|-----|-----------|-----------|-----------|-----------|-----------|-----------|
| | NO | 577 | 695 | 784 | 786 | 787 | 789 | 790 | 791 |
| 1030 | 0.4650012 | | | 0.4399068 | 0.3072377 | 1 | 0.3059601 | 0.780589 | 0.5436781 |
| 1031 | 2.0115667 | | | 0.8131757 | 3.0558538 | 1.4244585 | 2.2069304 | 3.3115115 | 3.0333171 |
| 1032 | 0.1880265 | | | 0.4142046 | 0.577794 | 0.3938241 | 0.255079 | 0.4519207 | 0.1360529 |
| 1033 | 1.8295632 | | | 1.1841643 | 1.4773676 | 1 | 1 | 1.316974 | 2.2394273 |
| 1034 | 2.2301461 | | | 1.3314905 | 1 | 1 | 1 | 1.4384761 | 2.6107789 |
| 1035 | 2.7977085 | | | 2.9098045 | 2.3444349 | 1.1988041 | 1.1291987 | 1 | 1 |
| 1036 | 0.7217756 | | | 0.6995425 | 1 | 0.4855702 | 1 | 0.6850444 | 0.0814178 |
| 1037 | 0.7585001 | | | 0.6467171 | 0.7085735 | 0.7161496 | 0.7355003 | 1.2120712 | 1 |
| 1038 | 1.6688889 | | | 1.6956606 | 2.0302632 | 2.0508542 | 2.9634027 | 1.2117606 | 1.6590283 |
| 1039 | 5.3225641 | | | 3.5178131 | 2.6756307 | 2.8783817 | 7.1229019 | 3.473312 | 1 |
| 1040 | 2.7105352 | | | 1 | 1.8289147 | 1.1348127 | 1.5344378 | 1.6530668 | 1 |
| 1041 | 2.7505274 | | | 1 | 2.4844279 | 1 | 1.2519937 | 2.4797132 | 1 |
| 1042 | 2.5633996 | | | 1 | 1.4533075 | 1 | 0.6172109 | 1.8387359 | 2.1494726 |
| 1043 | 3.0743862 | | | 1.2156764 | 1.9834473 | 1 | 1 | 3.7832356 | 2.2579165 |
| 1044 | 2.2838329 | | | 1 | 1 | 1 | 0.6868055 | 1.8009641 | 2.5851604 |
| 1045 | 2.8261672 | | | 1 | 2.6727294 | 1.6843573 | 3.4360744 | 5.6869147 | 8.0036566 |
| 1046 | 0.2712191 | | | 0.3301978 | 0.2508642 | 0.4477602 | 1 | 0.3971544 | 0.0885156 |
| 1047 | 0.3465322 | | | 0.062077 | 0.0417913 | 0.0441202 | 0.2425005 | 0.0112638 | 0.3338971 |
| 1048 | 0.117964 | | | 0.0616287 | 0.0431674 | 0.0915836 | 0.256601 | 0.0383929 | 0.1071698 |
| 1049 | 2.5102177 | | | 2.3322599 | 1.399062 | 1 | 5.2855906 | 2.3613587 | 3.4420394 |
| 1050 | 2.2441452 | | | 1 | 1 | 1 | 1 | 2.7293938 | 1 |
| 1051 | 0.1451379 | | | 0.1946725 | 0.2824907 | 0.1372515 | 1 | 0.4462606 | 0.0867422 |
| 1052 | 0.5653419 | | | 0.6801898 | 0.6362611 | 1.1578048 | 0.6247379 | 0.59787 | 0.4108055 |
| 1053 | 0.6677991 | | | 0.6586606 | 0.5840351 | 0.8671929 | 0.6248584 | 1.1882732 | 0.5411208 |
| 1054 | 0.5287362 | | | 0.5841656 | 0.4968959 | 0.8539825 | 0.3542738 | 1.3214767 | 0.4879073 |
| 1055 | 0.6256607 | | | 0.704547 | 0.5920165 | 0.678998 | 0.4940403 | 1.1415666 | 0.5275264 |
| 1056 | 0.6682744 | | | 0.4904705 | 1 | 0.7751561 | 0.588268 | 1.133267 | 0.4812496 |
| 1057 | 0.6332729 | | | 0.6120709 | 0.6320919 | 0.6824096 | 0.5063061 | 1 | 0.5397314 |
| 1058 | 1 | | | 0.4681868 | 1 | 0.7300611 | 0.5625312 | 1 | 0.438111 |
| 1059 | 2.6369377 | | | 1 | 1.7115913 | 1 | 2.3984923 | 2.1327236 | 2.5193201 |
| 1060 | 0.3781546 | | | 0.5297881 | 0.603773 | 0.3092861 | 0.2813331 | 0.4132597 | 0.1941871 |
| 1061 | 2.611056 | | | 1.9786722 | 0.8034832 | 1 | 1.6753888 | 1.2806984 | 2.066952 |
| 1062 | 2.7239551 | | | 0.6524168 | 2.2347113 | 0.5868415 | 3.8695658 | 1.826484 | 1 |
| 1063 | 2.8189634 | | | 1.0920993 | 1 | 1.2230873 | 4.1170925 | 1.6703295 | 2.6150981 |
| 1064 | 2.6297487 | | | 1.3874547 | 2.4192606 | 0.4856814 | 2.2724667 | 1.5522291 | 2.2145169 |
| 1065 | 3.6905408 | | | 1.3882975 | 3.2927711 | 3.5620824 | 3.079015 | 2.1446649 | 1 |
| 1066 | 0.5888322 | | | 0.8797918 | 0.696457 | 1.4204825 | 0.5903149 | 0.5872697 | 0.4750537 |
| 1067 | 3.5879128 | | | 1 | 5.0171598 | 2.0079482 | 5.8728277 | 6.6658198 | 9.9204354 |
| 1068 | 2.3524844 | | | 1 | 1 | 1.3978068 | 1 | 3.1750475 | 3.3097198 |
| 1069 | 0.4288337 | | | 0.5856703 | 0.6316617 | 1 | 0.4711701 | 0.6235594 | 0.2479315 |
| 1070 | 2.9703694 | | | 1.5575707 | 1.673718 | 1.1254329 | 4.5584854 | 1.162104 | 2.3836211 |
| 1071 | 0.5578782 | | | 0.6024354 | 0.527851 | 0.7532328 | 0.6769103 | 1 | 0.4561811 |
| 1072 | 2.6351256 | | | 1.6222959 | 2.0320524 | 1.1853971 | 6.5051479 | 1.6267847 | 1.9051273 |
| 1073 | 2.6650399 | | | 1.5809723 | 1.9032264 | 1.4277333 | 1 | 2.8711651 | 4.245373 |
| 1074 | 1.1177763 | | | 0.5528167 | 0.5088557 | 1 | 0.7660871 | 0.4997989 | 0.6389648 |
| 1075 | 0.0204454 | | | 0.0390871 | 0.0500336 | 1 | 0.0246322 | 0.2986739 | 1 |
| 1076 | 2.0498285 | | | 4.1696988 | 1.9233008 | 1 | 1 | 2.3242644 | 1 |
| 1077 | 2.0345297 | | | 1 | 2.6871983 | 1.7148737 | 2.9912868 | 2.8561044 | 4.0464934 |
| 1078 | 2.0788145 | | | 1.3410266 | 1.6033259 | 1.088307 | 1 | 1.6864065 | 2.5914328 |

Table 4

| SEQ ID | Patient ID | | | | | | | |
|--------|------------|-----|-----------|-----------|-----------|-----------|-----------|-----------|
| | 577 | 695 | 784 | 786 | 787 | 789 | 790 | 791 |
| 1079 | 2.6017653 | | 1 | 1 | 1 | 1 | 2.6891801 | 1 |
| 1080 | 2.3410548 | | 1 | 1 | 1 | 1 | 2.2793222 | 2.2886462 |
| 1081 | 0.3964092 | | 0.6108585 | 0.203622 | 0.1554895 | 0.3378668 | 0.3289365 | 0.2165539 |
| 1082 | 2.0505488 | | 1 | 1.7485195 | 0.6504481 | 1 | 1.2779742 | 1.7966427 |
| 1083 | 1.8234808 | | 0.6684415 | 1.2649891 | 0.8065447 | 1.2113537 | 2.1290537 | 1.4426333 |
| 1084 | 4.6158051 | | 2.3961531 | 2.477453 | 3.2675287 | 6.4815964 | 3.2769862 | 5.9345329 |
| 1085 | 0.3559194 | | 0.4229957 | 0.1400496 | 0.046882 | 0.3079935 | 0.1002167 | 0.1144693 |
| 1086 | 1.3857203 | | 2.0529625 | 2.3331856 | 1.2588452 | 2.6747989 | 1 | 1 |
| 1087 | 0.19197 | | 1 | 1.0589709 | 0.1323948 | 0.35478 | 0.138299 | 0.077747 |
| 1088 | 0.3505723 | | 0.6313921 | 0.4552746 | 1.7544879 | 0.6397363 | 1.2468647 | 0.2710894 |
| 1089 | 0.2192033 | | 0.193771 | 0.2837185 | 0.2916551 | 0.2674557 | 0.6828566 | 0.119411 |
| 1090 | 2.8220678 | | 1.2605339 | 1.8754126 | 1.7458006 | 2.9141502 | 1.806229 | 1 |
| 1091 | 1 | | 0.3166258 | 0.4912814 | 0.3917635 | 0.5582246 | 0.3529038 | 0.4554844 |
| 1092 | 3.1628592 | | 1 | 2.6884111 | 0.6933542 | 5.1204905 | 1.7308547 | 1 |
| 1093 | 2.4928321 | | 1.4836748 | 2.567141 | 1.6465216 | 1.6018186 | 1.6909939 | 2.5328839 |
| 1094 | 2.6882554 | | 1 | 1 | 1 | 1.7381409 | 1 | 1 |
| 1095 | 0.5997567 | | 0.7767831 | 0.5650551 | 1.3210581 | 0.6774698 | 0.6790455 | 0.4431194 |
| 1096 | 2.4730477 | | 1.5658897 | 2.8091757 | 0.3218637 | 1.2269083 | 1.7561912 | 1 |
| 1097 | 0.6187911 | | 0.7181084 | 0.5820852 | 1.5136223 | 0.7356912 | 0.6579577 | 0.4483148 |
| 1098 | 2.4661781 | | 1.6420825 | 2.5317705 | 1.8076886 | 1 | 3.2451144 | 2.7172314 |
| 1099 | 3.2634078 | | 1.217686 | 2.0459534 | 0.7620739 | 1.752243 | 2.2464907 | 2.1409716 |
| 1100 | 2.0347079 | | 1 | 1 | 1 | 1 | 1.8046481 | 1.907242 |
| 1101 | 3.3952521 | | 1.7543365 | 1.6537753 | 1.3347559 | 3.6809239 | 1.8925141 | 1 |
| 1102 | 2.2351145 | | 1.30265 | 1.7211528 | 1 | 1 | 2.9731179 | 1 |
| 1103 | 2.8170697 | | 1 | 1 | 1 | 1 | 2.8708687 | 4.25887 |
| 1104 | 2.1622151 | | 2.3899848 | 1.5320532 | 1 | 2.1772655 | 1.3954112 | 1.6833026 |
| 1105 | 1 | | 0.4101277 | 0.6064881 | 0.410754 | 0.5232457 | 0.4564799 | 0.4858439 |
| 1106 | 2.1493745 | | 0.9121803 | 1.6221004 | 0.51418 | 1 | 1.7101621 | 1.5020165 |
| 1107 | 2.3935163 | | 1.6402693 | 2.7699855 | 0.001 | 1 | 2.5056284 | 1 |
| 1108 | 3.0175208 | | 1 | 1.274712 | 1.9790563 | 2.455455 | 2.5002788 | 6.2130422 |
| 1109 | 0.5599947 | | 0.2773269 | 0.3871582 | 0.1847149 | 0.5360727 | 1.2484738 | 0.1887637 |
| 1110 | 2.9057952 | | 1.3765686 | 2.0063288 | 0.6748339 | 1 | 1.7912953 | 2.1771833 |
| 1111 | 1.8110561 | | 1 | 1.7074211 | 2.1129389 | 1 | 4.1943639 | 2.0959482 |
| 1112 | 1.8674388 | | 1 | 1 | 1.6495998 | 1.9128054 | 2.9200596 | 1 |
| 1113 | 3.4906393 | | 1.7528874 | 1 | 1 | 1 | 2.4725286 | 2.8990247 |
| 1114 | 1 | | 0.316483 | 0.5289604 | 0.4411422 | 0.7241021 | 0.4208677 | 0.5419445 |
| 1115 | 0.6771863 | | 1 | 0.5251095 | 1 | 0.262573 | 1.925148 | 1 |
| 1116 | 2.5918731 | | 1 | 1.7896266 | 1 | 1 | 2.5931133 | 2.2724586 |
| 1117 | 0.585765 | | 0.8185003 | 0.6215336 | 1.4323676 | 0.7178066 | 0.7246371 | 0.4630796 |
| 1118 | 0.4552204 | | 0.3907071 | 0.5345739 | 0.2494245 | 0.5228637 | 0.4484908 | 0.3993175 |
| 1119 | 0.1363671 | | 0.1429161 | 0.230405 | 0.4369097 | 1 | 0.4971735 | 0.0819498 |
| 1120 | 2.8195947 | | 1.3572825 | 1 | 1.1353942 | 1 | 1.3916848 | 2.977663 |
| 1121 | 2.3873002 | | 1.3141357 | 2.0320524 | 1 | 1 | 2.2179783 | 1 |
| 1122 | 2.665077 | | 1 | 1 | 0.5314604 | 1 | 0.6145399 | 2.7782659 |
| 1123 | 8.16556 | | 5.7653996 | 3.9704202 | 2.7181039 | 3.1573229 | 1.3929128 | 7.090348 |
| 1124 | 2.5236599 | | 1 | 1.5529564 | 1 | 1.719166 | 1.9047518 | 4.9406832 |
| 1125 | 3.0223555 | | 1 | 2.2627964 | 1.2859501 | 3.3106641 | 1.5567883 | 1.9369696 |
| 1126 | 2.0533412 | | 1.2917751 | 2.0583257 | 1.5657885 | 2.2413217 | 2.7484491 | 4.7003336 |
| 1127 | 2.2881924 | | 1.4337909 | 1.9877496 | 1.4885525 | 3.1897429 | 2.1002026 | 3.4979469 |

Table 4

| SEQ ID NO | Patient ID | | | | | | | |
|--------------|------------|-----|-----------|-----------|-----------|-----------|-----------|-----------|
| | 577 | 695 | 784 | 786 | 787 | 789 | 790 | 791 |
| 1128 | 2.984569 | | 1.6522498 | 2.8568935 | 2.5693863 | 5.4316037 | 2.2814677 | 3.4174821 |
| 1129 | 2.2617834 | | 1.2989669 | 1.9524043 | 0.6157847 | 2.0160272 | 1 | 1 |
| 1130 | 5.3023712 | | 5.0125028 | 3.4063799 | 4.6657288 | 6.1908123 | 5.5597524 | 1 |
| 1131 | 2.8257365 | | 1.5976072 | 1 | 1 | 1.4528742 | 1.5317341 | 1 |
| 1132 | 0.6700048 | | 0.6739101 | 0.6845447 | 1.3945747 | 0.6573218 | 0.4713853 | 0.4538028 |
| 1133 | 2.2075767 | | 1.3048814 | 1.3126338 | 1.2427533 | 1.8667738 | 2.4383703 | 2.7581961 |
| 1134 | 2.2705171 | | 1 | 1 | 1 | 1 | 2.2314723 | 1 |
| 1135 | 2.8913133 | | 1 | 1 | 0.8151037 | 1.3817576 | 1.8401615 | 2.6013267 |
| 1136 | 2.0597875 | | 0.9192932 | 1.6558057 | 1 | 1.6858511 | 1.9828502 | 2.6342735 |
| 1137 | 2.554146 | | 1 | 1.6036856 | 1 | 1.6658709 | 2.280649 | 1.8026665 |
| 1138 | 2.1614353 | | 1 | 2.6761316 | 1 | 1 | 3.3444136 | 3.0581996 |
| 1139 | 2.2633058 | | 1.2705791 | 1.5981638 | 1 | 1.4325901 | 1.6145752 | 2.0700377 |
| 1140 | 2.0276155 | | 1.6221482 | 1.5692875 | 1 | 2.4964528 | 2.6922713 | 2.9943591 |
| 1141 | 2.1123232 | | 1 | 1.5809846 | 0.6629574 | 1.2445272 | 2.9131573 | 1 |
| 1142 | 2.7793277 | | 1 | 1.7842213 | 1 | 0.7596203 | 2.0905196 | 2.1866402 |
| 1143 | 0.6105475 | | 0.645705 | 1 | 0.7350546 | 0.5598048 | 1 | 0.5525378 |
| 1144 | 0.7136435 | | 0.5741999 | 0.5953002 | 0.7908547 | 0.5627592 | 1 | 0.6306643 |
| 1145 | 2.2212194 | | 1 | 1 | 1 | 1 | 2.603629 | 2.1313874 |
| 1146 | 2.4698839 | | 1 | 1.3475252 | 1.5687298 | 2.3755443 | 2.2409152 | 2.1297793 |
| 1147 | 1.8541675 | | 1 | 1.5694942 | 0.5791632 | 1.2929195 | 1 | 1.7365993 |
| 1148 | 2.7142559 | | 1.6644377 | 1.7106901 | 1 | 1 | 1.1853091 | 2.3969948 |
| 1149 | 3.0402759 | | 1.64843 | 1 | 1.3853061 | 4.0908501 | 1.2375488 | 3.2086761 |
| 1150 | 0.2034663 | | 0.0573729 | 0.259177 | 0.1145757 | 0.2378235 | 0.2651366 | 0.0967313 |
| 1151 | 3.0070939 | | 1.4975856 | 2.2828141 | 0.7341312 | 1.4130405 | 1.5849054 | 2.4830697 |
| 1152 | 5.3760281 | | 1 | 3.3410991 | 3.0272446 | 10.092099 | 6.3356835 | 1 |
| 1153 | 2.7702599 | | 2.2290187 | 1.6681714 | 1.1702628 | 5.0894618 | 2.9008208 | 3.7580766 |
| 1154 | 1.9323918 | | 1 | 1.5511029 | 0.5959049 | 1.7198614 | 1.7536505 | 2.0906258 |
| 1155 | 1.8708253 | | 1.9757773 | 1 | 1.905762 | 1.908459 | 1.689159 | 3.8131958 |
| 1156 | 0.5746548 | | 0.8873069 | 0.6345327 | 1.508475 | 0.6976448 | 0.6459458 | 0.4288286 |
| 1157 | 3.7494411 | | 1.8637693 | 1.9621586 | 1.7026381 | 1 | 3.512947 | 1 |
| 1158 | 0.5868641 | | 0.6550493 | 0.5999419 | 1 | 0.5552314 | 1.0837797 | 0.5541999 |
| 1159 | 0.647985 | | 0.5546986 | 0.4849749 | 0.794899 | 0.5536093 | 1.1535079 | 0.527171 |
| 1160 | 1 | | 0.5218991 | 0.5390487 | 0.3192217 | 0.3046543 | 0.6644224 | 0.2435177 |
| 1161 | 0.6678883 | | 1 | 0.594083 | 0.6065331 | 0.5365885 | 1 | 0.5196428 |
| 1162 | 0.6459055 | | 1 | 0.4456576 | 1 | 0.5917526 | 1.6794761 | 0.6763837 |
| 1163 | 0.7179732 | | 0.7051267 | 1 | 0.7719839 | 0.7088687 | 1.1604525 | 0.5560598 |
| 1164 | 2.5588916 | | 1 | 1 | 1 | 1 | 1.3131206 | 1 |
| 1165 | 2.0241028 | | 1 | 1 | 1 | 1.8770234 | 1.8754914 | 1 |
| 1166 | 5.0212896 | | 1.4298805 | 2.1734872 | 1 | 2.8286074 | 1.483009 | 2.5345084 |
| 1167 | 1.9982211 | | 0.8580081 | 1 | 1.4310594 | 1.521194 | 2.9141595 | 3.5737072 |
| 1168 | 2.1367641 | | 1.1830954 | 1 | 1 | 2.3962113 | 1.4175859 | 3.1642289 |
| 1169 | 0.5630174 | | 0.0442745 | 0.0423871 | 0.1616544 | 0.5174117 | 0.0239532 | 0.0224628 |
| 1170 | 0.410646 | | 0.740703 | 0.4014618 | 1.2804009 | 0.5516252 | 1.3525157 | 0.2666239 |
| 1171 | 0.6064703 | | 0.7629261 | 0.5974846 | 1.4791213 | 1 | 0.6783257 | 0.5142132 |
| 1172 | 0.0757958 | | 0.2478685 | 0.2044958 | 1 | 1 | 0.1458929 | 0.1109576 |
| 1173 | 1.3940604 | | 0.6915956 | 1.9691315 | 0.6103039 | 1.8394667 | 1.5503518 | 1 |
| 1174 | 4.8692895 | | 2.8029219 | 2.5666801 | 2.9425356 | 5.0114797 | 2.5061506 | 6.7419696 |
| 1175 | 0.301334 | | 0.0497611 | 0.0913081 | 0.0622899 | 0.1848528 | 0.0307849 | 0.4168219 |
| 1176 | 0.606656 | | 0.4090022 | 0.5394433 | 0.7180307 | 0.4242938 | 1.262857 | 0.5203887 |

Table 4

| SEQ ID | Patient ID | | | | | | | | |
|--------|------------|-----------|-----|-----------|-----------|-----------|-----------|-----------|-----------|
| | NO | 577 | 695 | 784 | 786 | 787 | 789 | 790 | 791 |
| 1177 | | 0.5774324 | | 0.4192214 | 0.5676849 | 0.75148 | 0.5211014 | 1.1062508 | 0.500007 |
| 1178 | | 0.5576034 | | 1 | 0.4791106 | 1 | 0.4376437 | 1.6298617 | 0.3038051 |
| 1179 | | 2.0812132 | | 0.712016 | 1.2856714 | 0.7120539 | 1.4316253 | 1.1163713 | 1.8693498 |
| 1180 | | 2.1915278 | | 1 | 1.5261652 | 0.6255835 | 1.4324996 | 2.2893862 | 2.1954475 |
| 1181 | | 2.6735211 | | 1.4658374 | 2.0526513 | 1 | 2.0752497 | 1.7665657 | 2.3095792 |
| 1182 | | 1.9778945 | | 1 | 1.728896 | 1.2104327 | 1 | 1.9046248 | 2.8243321 |
| 1183 | | 2.045833 | | 1 | 1.1966497 | 1 | 1 | 1.8880114 | |
| 1184 | | 2.0819633 | | 1 | 1.4587946 | 1 | 1 | 2.4201054 | 1 |
| 1185 | | 2.0026325 | | 1.2726837 | 1.7546573 | 0.7680763 | 2.1688665 | 1.5656243 | 2.2375887 |
| 1186 | | 1.5553808 | | 1 | 1.7767263 | 1 | 1 | 3.7352304 | 2.8261499 |
| 1187 | | 1.9133648 | | 1.1993179 | 2.1009163 | 0.7971393 | 1.5798346 | 1.9132067 | 2.3623191 |
| 1188 | | 2.8792897 | | 1.2177692 | 1.6117494 | 1.5167347 | 2.6068451 | 1.504111 | 4.8266326 |
| 1189 | | 0.637818 | | 1 | 0.6410025 | 1.4822679 | 0.7716484 | 1 | 0.465518 |
| 1190 | | 0.288226 | | 0.3942256 | 0.6352319 | 0.6713026 | 1.0675355 | 0.2607327 | 0.486394 |
| 1191 | | 2.3056523 | | 1.6871865 | 0.8562775 | 0.8583261 | 2.0749965 | 1.166282 | 2.0120697 |
| 1192 | | 0.0769543 | | 0.1604845 | 0.1499065 | 0.3125438 | 0.1018609 | 0.4832702 | 0.0609222 |
| 1193 | | 0.6253339 | | 0.7972031 | 0.5370601 | 1.5376747 | 0.6216552 | 0.6622063 | 0.4172004 |
| 1194 | | 0.2726376 | | 0.6718021 | 0.438476 | 1 | 0.4006244 | 1 | 0.2409953 |
| 1195 | | 2.6101648 | | 1 | 1 | 0.7544299 | 1.5930042 | 1.6640201 | 2.6664454 |
| 1196 | | 0.5066569 | | 0.6002284 | 0.5847662 | 0.7241015 | 0.4545693 | 1 | 0.3300942 |
| 1197 | | 0.6732428 | | 0.6172337 | 1 | 0.5354363 | 1 | 0.8486375 | 0.0939274 |
| 1198 | | 0.5310459 | | 0.5202449 | 0.5477019 | 0.6305085 | 0.5017874 | 1 | 0.4018656 |
| 1199 | | 0.1293267 | | 0.0665658 | 0.0702165 | 0.0747991 | 0.2546007 | 0.0474688 | 0.0814249 |
| 1200 | | 0.5251269 | | 0.7148772 | 0.6031209 | 0.7976181 | 0.6004116 | 1 | 0.4637018 |
| 1201 | | 2.4935079 | | 1.1760237 | 1 | 1 | 1 | 1.3336862 | 2.7786566 |
| 1202 | | 2.6457828 | | 1.4108003 | 1.8790115 | 1.4058442 | 2.6739579 | 1 | 2.4689526 |
| 1203 | | 0.387475 | | 1 | 0.3111998 | 0.1406203 | 0.275061 | 1 | 0.2850901 |
| 1204 | | 2.5816541 | | 0.8672756 | 3.0926091 | 1.9964222 | 1.5660513 | 2.8247832 | 2.7335838 |
| 1205 | | 1.7779409 | | 1.3565801 | 1.8751174 | 1.2058069 | 2.3826995 | 1.2565335 | 2.8649766 |
| 1206 | | 2.0275932 | | 1 | 2.3803482 | 1.5299793 | 2.3012934 | 2.5457997 | 3.2546578 |
| 1207 | | 2.4472551 | | 1 | 1 | 0.796079 | 1.6189338 | 1.7920857 | 2.8072782 |
| 1208 | | 0.5318331 | | 1 | 1 | 0.2761703 | 0.4001837 | 0.2773602 | 4.7469135 |
| 1209 | | 2.4145113 | | 1.4163379 | 2.7798964 | 0.7490345 | 2.2676945 | 1.1640377 | 1.5866244 |
| 1210 | | 2.5680338 | | 1.3057799 | 2.5354524 | 1.6145003 | 1.5508078 | 2.1360971 | 2.5152312 |
| 1211 | | 2.2697447 | | 0.769254 | 1.4999995 | 0.6344417 | 1.3431557 | 2.4351379 | 1.786369 |
| 1212 | | 0.5415174 | | 0.738414 | 0.4994164 | 1.4444237 | 0.6656442 | 1 | 0.4336377 |
| 1213 | | 0.6887644 | | 0.3233433 | 1 | 1 | 0.839462 | 1 | 1 |
| 1214 | | 2.9316174 | | 1 | 1.7841768 | 1 | 2.4625656 | 2.492826 | 2.4916806 |
| 1215 | | 0.6483415 | | 0.8025583 | 0.6430671 | 1.4129068 | 1 | 0.616022 | 0.4645931 |
| 1216 | | 0.6361693 | | 0.433889 | 1 | 1 | 1 | 1 | 1.4575854 |
| 1217 | | 2.6678397 | | 1 | 1.4136716 | 1.6609804 | 2.954266 | 3.6669701 | 1 |
| 1218 | | 2.0900657 | | 6.1949894 | 1.8191865 | 2.6441256 | 1.5977931 | 1.6272222 | 2.4763013 |
| 1219 | | 0.3213189 | | 0.0370038 | 0.1161782 | 0.0892066 | 0.0560986 | 0.1799807 | 0.3181244 |
| 1220 | | 1.6984244 | | 0.8522487 | 1 | 1.5454043 | 2.8411291 | 1.125899 | 1 |
| 1221 | | 1 | | 1 | 1.8489259 | 0.7737367 | 2.0057443 | 1.9763432 | 1.9756064 |
| 1222 | | 0.3360013 | | 0.0392586 | 0.0318242 | 0.0348943 | 0.2144608 | 0.0174744 | 0.3118447 |
| 1223 | | 0.8138431 | | 1 | 2.1532557 | 2.4650882 | 8.9057254 | 3.497364 | 1.3925105 |
| 1224 | | 2.8696054 | | 0.8579916 | 1.415323 | 0.6640433 | 2.1820841 | 1 | 2.2144549 |
| 1225 | | 1.4459574 | | 1 | 1 | 1.5662074 | 1.957215 | 1.4583219 | 1.5400345 |

Table 4

| SEQ ID | Patient ID | | | | | | | | |
|--------|------------|-----------|-----|-----------|-----------|-----------|-----------|-----------|-----------|
| | NO | 577 | 695 | 784 | 786 | 787 | 789 | 790 | 791 |
| 1226 | | 0.0282805 | | 0.0396533 | 0.0843902 | 1 | 1 | 0.1876028 | 0.001 |
| 1227 | | 0.3985852 | | 0.3878372 | 0.3212633 | 0.2921596 | 0.3241277 | 0.7916975 | 0.1996784 |
| 1228 | | 3.8147506 | | 0.7640313 | 1 | 1 | 2.204356 | 1.3367915 | 2.0643067 |
| 1229 | | 2.0492195 | | 0.6172422 | 1 | 0.5573425 | 1 | 1.4889374 | 1 |
| 1230 | | 2.7489678 | | 1 | 3.1465191 | 2.3641504 | 4.7481042 | 2.7522037 | 1 |
| 1231 | | 2.0061155 | | 1.5590693 | 1 | 1.281521 | 4.0221613 | 1.4594511 | 2.4728923 |
| 1232 | | 0.2207926 | | 0.3104821 | 0.4512565 | 0.2406261 | 0.3527564 | 0.6121968 | 0.1799727 |
| 1233 | | 2.3294396 | | 0.810602 | 1 | 0.5252442 | 1.9864178 | 1 | 1.7032543 |
| 1234 | | 6.9069532 | | 6.8176633 | 9.6685344 | 2.7992389 | 5.4394208 | 2.4543767 | 1 |
| 1235 | | 2.4573404 | | 1 | 1 | 1 | 1.7227358 | 2.234507 | 4.287053 |
| 1236 | | 0.5185915 | | 0.2600192 | 0.4281003 | 0.3410509 | 0.6232784 | 0.5451081 | 0.5023428 |
| 1237 | | 2.1036416 | | 1.6110354 | 1 | 1 | 2.3888909 | 1.2326226 | 2.7979365 |
| 1238 | | 0.3793206 | | 0.5673213 | 0.5477438 | 1 | 0.4053967 | 1 | 0.2238539 |
| 1239 | | 2.4273964 | | 1.5688942 | 1.8622206 | 1 | 1 | 2.1759155 | 2.6573012 |
| 1240 | | 1.8502462 | | 1 | 1.3660935 | 1 | 1 | 2.107133 | 1.9328958 |
| 1241 | | 2.8423052 | | 1 | 1.6337045 | 1 | 1 | 2.1727114 | 2.3332382 |
| 1242 | | 1.5949423 | | 1 | 1.4285895 | 1 | 1 | 3.5983147 | 2.1707253 |
| 1243 | | 2.1058175 | | 1 | 1.7404727 | 1.1808739 | 1.5168864 | 2.207999 | 2.4725828 |
| 1244 | | 1.631897 | | 1 | 1.817013 | 1 | 1 | 2.3648734 | 2.4484544 |
| 1245 | | 1 | | 1 | 1.7199104 | 1 | 1 | 3.2913129 | 2.2808527 |
| 1246 | | 3.2729436 | | 1 | 1.7853354 | 1 | 1 | 2.5287347 | 2.0144287 |
| 1247 | | 1.9504607 | | 1 | 1 | 0.5174377 | 1.5765396 | 1.7803138 | 1.6969642 |
| 1248 | | 1.94016 | | 1 | 1 | 0.6756206 | 3.1188207 | 2.2546774 | 1 |
| 1249 | | 2.7688785 | | 1 | 1 | 0.4416039 | 1 | 1.9919121 | 2.4131689 |
| 1250 | | 0.6180855 | | 0.7168263 | 0.6366067 | 1.2940559 | 0.6712929 | 0.710028 | 0.4535085 |
| 1251 | | 0.5390814 | | 0.5405455 | 0.4953018 | 0.6693788 | 0.6506703 | 1 | 0.4969449 |
| 1252 | | 0.472309 | | 0.519287 | 0.5839779 | 0.4659213 | 0.3876268 | 0.4307058 | 0.2780416 |
| 1253 | | 1.6408609 | | 1.7922963 | 1 | 1.6250686 | 1 | 2.1599656 | 1 |
| 1254 | | 1.6200813 | | 1 | 1.288406 | 1 | 1 | 2.160883 | 2.1116276 |
| 1255 | | 2.2598376 | | 1 | 1.9023147 | 1 | 1.2296804 | 1.3903157 | 2.1471952 |
| 1256 | | 2.1315804 | | 1 | 1 | 0.5816856 | 1 | 2.113019 | 2.396704 |
| 1257 | | 0.7616416 | | 1 | 0.783517 | 1 | 1 | 1 | 1 |
| 1258 | | 1.7459843 | | 1 | 1 | 1.9009652 | 3.1984408 | 4.4103237 | 3.9778604 |
| 1259 | | 0.4836865 | | 0.6436672 | 0.5256771 | 0.852204 | 0.423657 | 0.8909544 | 0.4567056 |
| 1260 | | 0.5318851 | | 1 | 0.6295144 | 1 | 0.6514492 | 1 | 0.4434376 |
| 1261 | | 0.5768605 | | 0.7809212 | 0.5459366 | 1.5938082 | 0.6549361 | 0.5835856 | 0.420922 |
| 1262 | | 1.554304 | | 1.2096541 | 1.6542346 | 1 | 1.4908581 | 1.8278108 | 2.1017447 |
| 1263 | | 2.9844502 | | 2.3128325 | 1 | 1.1878339 | 4.7474415 | 2.411947 | 3.9080355 |
| 1264 | | 0.7115269 | | 0.7028746 | 0.4134797 | 1 | 0.5446127 | 1.6240464 | 0.6800268 |
| 1265 | | 0.4293907 | | 1 | 0.5730553 | 1 | 0.5041338 | 1.3906968 | 0.393812 |
| 1266 | | 0.6107109 | | 0.7324971 | 0.5217213 | 1 | 0.6537655 | 1.4712371 | 0.6650632 |
| 1267 | | 2.4746147 | | 3.4774605 | 1 | 1 | 1 | 1.4259702 | 1 |
| 1268 | | 3.2482279 | | 1.941264 | 1 | 1.1837468 | 5.3240598 | 3.2926821 | 2.7999188 |
| 1269 | | 2.5343913 | | 1 | 2.495966 | 2.1707569 | 1 | 3.308632 | 3.7582553 |
| 1270 | | 2.3796211 | | 0.8704604 | 2.2751122 | 1.1937423 | 1 | 1.9952574 | 2.2316498 |
| 1271 | | 8.5877617 | | 10.736937 | 5.7188155 | 5.3043688 | 17.551815 | 3.9248375 | 1 |
| 1272 | | 0.6148921 | | 0.5894897 | 0.6128949 | 0.8345559 | 0.6179173 | 1 | 0.5279386 |
| 1273 | | 1.8378587 | | 1 | 1.5092157 | 1.2831883 | 2.1879088 | 1.7285116 | 1 |
| 1274 | | 0.169965 | | 1 | 1 | 0.0832726 | 0.3719239 | 0.1310439 | 1 |

Table 4

| SEQ ID | Patient ID | | | | | | | | | | | |
|--------|------------|-----------|-----|-----|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|
| | NO | 577 | 695 | 784 | 786 | 787 | 789 | 790 | 791 | | | |
| 1275 | | 0.4009617 | | | 1 | | 1 | 0.6567669 | | 1 | | |
| 1276 | | 0.3420688 | | | 0.4796433 | | 1 | 0.6024587 | 1.3030566 | 0.4592052 | | |
| 1277 | | 2.7565504 | | | | 1 | 1 | 1.2747496 | 1.4495141 | 2.5515273 | | |
| 1278 | | 2.4510798 | | | | 1 | 1.7428492 | | 1 | 2.0748067 | 2.4708489 | 3.429196 |
| 1279 | | 2.9522411 | | | | 1 | 2.0426209 | | 1 | 3.0432978 | 2.5416809 | |
| 1280 | | | 1 | | 0.2309883 | 0.6367088 | | 1 | | 1.6005872 | 0.2240316 | |
| 1281 | | 1.1728148 | | | | 1 | | 1 | 2.1280917 | 1.1722527 | 2.3438941 | |
| 1282 | | 2.2549881 | | | 1.7139538 | 2.8205933 | 1.8946978 | 2.0707018 | 4.0113908 | 4.9586617 | | |
| 1283 | | 0.6492104 | | | 0.8236818 | 0.4155107 | 1.4565739 | 0.6454845 | 0.5627377 | 0.4541574 | | |
| 1284 | | 2.4556917 | | | | 1 | 0.7599278 | 1.5475622 | 2.0385058 | 2.9433975 | | |
| 1285 | | 1.714555 | | | | 1 | 1.4382767 | | 1 | 1.778305 | 1.5949412 | 1.6677451 |
| 1286 | | 1.4244723 | | | | 1 | 1.9077473 | 0.6572628 | 1.5302615 | 1.2866691 | | 1 |
| 1287 | | | 1 | | 1.7120443 | | 1 | 2.6516586 | 3.9952335 | 2.5109215 | 3.1797598 | |
| 1288 | | 1.7947028 | | | 0.6724407 | | 1 | 1.7172593 | 2.8837623 | 1.7093717 | 3.2971553 | |
| 1289 | | 4.4914765 | | | 2.6036256 | 1.8943993 | 1.4860301 | 3.4282824 | 2.3912684 | | 1 | |
| 1290 | | 3.0172832 | | | 1.9061811 | | 1 | | 1 | 3.5801204 | 2.9844092 | |
| 1291 | | 2.8795199 | | | 1.8328017 | 2.1388873 | | 1 | 2.1274262 | 2.126033 | 2.6007275 | |
| 1292 | | 0.3386377 | | | 0.043576 | 0.0974455 | 0.1111641 | 0.2744607 | 0.1498733 | 0.4512816 | | |
| 1293 | | 0.5986279 | | | 0.7873298 | 0.6070856 | 1.5131435 | 0.5984837 | 0.7231691 | 0.4408775 | | |
| 1294 | | 1.5229935 | | | | 1 | 1.1870512 | | 1 | 1.2566654 | 2.0200292 | 2.2859984 |
| 1295 | | 0.599066 | | | 0.7152099 | 0.6814838 | 1.4789332 | 0.5251805 | 0.6891378 | 0.5147155 | | |
| 1296 | | 0.2572794 | | | | 1 | 0.3901079 | | 1 | | 1 | 0.3956434 |
| 1297 | | 0.1886057 | | | 0.1745609 | | 1 | 0.1698168 | 0.6358379 | 0.3770405 | 0.123242 | |
| 1298 | | 1.4231652 | | | 2.2257345 | | 1 | | 1 | 2.0976454 | | 1.7675525 |
| 1299 | | 2.6171013 | | | | 1 | | 1 | | 1 | 3.3001348 | 4.7177287 |
| 1300 | | 0.5915132 | | | | 1 | 0.6325617 | 1.5500856 | 0.5038463 | 0.6739924 | 0.4088124 | |
| 1301 | | 2.163693 | | | 2.398539 | 1.7395832 | 2.1666398 | 3.9299195 | 1.6536173 | 2.4865069 | | |
| 1302 | | 0.6737256 | | | | 1 | | 1 | | 0.2893562 | | 1 |
| 1303 | | 0.2386164 | | | 0.5963568 | 0.3116679 | 0.3196971 | 0.2922111 | | 1 | 0.2997096 | |

Table 4

| SEQ ID | Patient ID | | | | | | |
|--------|------------|-----------|-----------|-----|-----|-----|-----|
| NO | 888 | 889 | 890 | 891 | 892 | 893 | 989 |
| 1 | 2.7545293 | 1 | 2.5044075 | | | | |
| 2 | 0.5461727 | 1 | 1.1739522 | | | | |
| 3 | 0.5476473 | 1 | 1 | | | | |
| 4 | 1 | 0.2650594 | 0.3620241 | | | | |
| 5 | 1 | 0.5119583 | 0.7874696 | | | | |
| 6 | 1 | 0.5949988 | 1 | | | | |
| 7 | 1.2866816 | 2.2515809 | 1.4073896 | | | | |
| 8 | 2.3662774 | 3.2537102 | 3.1788697 | | | | |
| 9 | 1 | 0.3589457 | 0.6256837 | | | | |
| 10 | 0.3834411 | 0.3620441 | 0.6984212 | | | | |
| 11 | 0.2154419 | 0.3647831 | 0.239354 | | | | |
| 12 | 2.4379808 | 3.2873349 | 1.9072563 | | | | |
| 13 | 1 | 1 | 0.4463772 | | | | |
| 14 | 1 | 3.5529666 | 1.4072825 | | | | |
| 15 | 0.604465 | 1 | 0.671821 | | | | |
| 16 | 2.5501204 | 3.2380293 | 2.8948333 | | | | |
| 17 | 1 | 1 | 2.5760741 | | | | |
| 18 | 3.2437827 | 2.2405637 | 1.3111795 | | | | |
| 19 | 0.6359832 | 0.5206266 | 0.5215846 | | | | |
| 20 | 0.7037088 | 1 | 1 | | | | |
| 21 | 1 | 1 | 1.7708313 | | | | |
| 22 | 1.4588616 | 3.6413274 | 1.7687995 | | | | |
| 23 | 1.3210761 | 1.9898344 | 1.6857127 | | | | |
| 24 | 1.1788999 | 2.539411 | 1.530618 | | | | |
| 25 | 1 | 0.5552093 | 0.7677945 | | | | |
| 26 | 1.653853 | 1 | 1 | | | | |
| 27 | 1 | 0.5932704 | 1 | | | | |
| 28 | 1 | 2.1887875 | 0.3345573 | | | | |
| 29 | 2.6490767 | 4.4547482 | 3.003886 | | | | |
| 30 | 2.6030196 | 5.9983918 | 3.9685578 | | | | |
| 31 | 9.2299382 | 5.9423645 | 2.2751731 | | | | |
| 32 | 4.4682224 | 2.1035442 | 0.6593283 | | | | |
| 33 | 2.1493872 | 3.2590202 | 1.5157567 | | | | |
| 34 | 4.1344083 | 4.1226474 | 2.0889151 | | | | |
| 35 | 3.8839179 | 4.6459045 | 2.3288034 | | | | |
| 36 | 2.6142523 | 2.9561547 | 1.5390222 | | | | |
| 37 | 3.005484 | 2.9851234 | 1.8079535 | | | | |
| 38 | 1 | 2.5970207 | 1.5197726 | | | | |
| 39 | 0.4133848 | 1 | 0.4567507 | | | | |
| 40 | 3.841673 | 2.5427343 | 2.9826969 | | | | |
| 41 | 0.7426844 | 0.8146166 | 1.613346 | | | | |
| 42 | 1.6556789 | 2.6012493 | 2.9448316 | | | | |
| 43 | 1 | 0.617056 | 1 | | | | |
| 44 | 0.4962052 | 1 | 1 | | | | |
| 45 | 1.814678 | 1.6157035 | 1.8058357 | | | | |
| 46 | 4.3095076 | 3.1071758 | 1.6976629 | | | | |
| 47 | 4.0298642 | 3.7256802 | 2.6884802 | | | | |
| 48 | 1 | 0.3158893 | 1 | | | | |
| 49 | 2.6156726 | 2.478136 | 2.158312 | | | | |

Table 4

| SEQ ID | Patient ID | | | | | | |
|--------|------------|-----------|-----------|-----|-----|-----|-----|
| NO | 888 | 889 | 890 | 891 | 892 | 893 | 989 |
| 50 | 1 | 0.5810995 | 0.5157391 | | | | |
| 51 | 2.0105479 | 2.207336 | 2.8986888 | | | | |
| 52 | 1 | 0.6408001 | 1 | | | | |
| 53 | 1 | 1 | 1 | | | | |
| 54 | 2.0600351 | 1.9375465 | 2.1373654 | | | | |
| 55 | 1.1257851 | 0.7457003 | 1 | | | | |
| 56 | 2.3023159 | 1.9023743 | 1.5590942 | | | | |
| 57 | 0.7868121 | 1.2311321 | 0.4463772 | | | | |
| 58 | 0.6738655 | 0.6514556 | 1 | | | | |
| 59 | 1.5259799 | 3.1003418 | 1.6758629 | | | | |
| 60 | 2.0723555 | 1 | 1.4845567 | | | | |
| 61 | 2.7998016 | 5.239467 | 2.2220206 | | | | |
| 62 | 2.221524 | 1 | 1 | | | | |
| 63 | 3.164231 | 2.3363902 | 1 | | | | |
| 64 | 2.9656331 | 2.5662428 | 1 | | | | |
| 65 | 1.1636339 | 2.748852 | 2.9469426 | | | | |
| 66 | 0.9069971 | 0.5554796 | 0.92843 | | | | |
| 67 | 2.8160915 | 3.2006912 | 2.0345815 | | | | |
| 68 | 2.3598678 | 2.3688005 | 2.4140452 | | | | |
| 69 | 2.8411056 | 2.8068062 | 2.2002179 | | | | |
| 70 | 0.3852237 | 1 | 1 | | | | |
| 71 | 1.7521149 | 2.1319907 | 2.6072063 | | | | |
| 72 | 0.3827256 | 0.4131698 | 0.3373639 | | | | |
| 73 | 1 | 1 | 2.2641045 | | | | |
| 74 | 3.7313557 | 3.3169109 | 1.4820591 | | | | |
| 75 | 1.7695015 | 2.5777448 | 1.8783533 | | | | |
| 76 | 2.2879203 | 2.5948647 | 1.4256927 | | | | |
| 77 | 1 | 0.6651868 | 1 | | | | |
| 78 | 1 | 0.5160078 | 1 | | | | |
| 79 | 1 | 0.5869589 | 1.4371561 | | | | |
| 80 | 3.1260608 | 3.2222099 | 3.7659794 | | | | |
| 81 | 1 | 5.408571 | 5.0035654 | | | | |
| 82 | 1.6240221 | 4.9823776 | 1.3441424 | | | | |
| 83 | 5.3934271 | 1 | 2.12454 | | | | |
| 84 | 1 | 2.4087223 | 2.8721366 | | | | |
| 85 | 0.6987314 | 0.2208448 | 0.1697523 | | | | |
| 86 | 2.0191126 | 2.7870024 | 2.8897461 | | | | |
| 87 | 2.0855372 | 4.4926088 | 2.6338398 | | | | |
| 88 | 1.5936642 | 2.4017214 | 2.2386921 | | | | |
| 89 | 3.1245659 | 2.2320767 | 1.4066137 | | | | |
| 90 | 1 | 2.2061167 | 2.3618055 | | | | |
| 91 | 1 | 2.4924843 | 2.0641504 | | | | |
| 92 | 1 | 4.5933631 | 2.2370002 | | | | |
| 93 | 1 | 0.5166382 | 1 | | | | |
| 94 | 1.9735484 | 2.8235626 | 1.8385442 | | | | |
| 95 | 2.1346911 | 4.8509262 | 8.3660518 | | | | |
| 96 | 2.5728566 | 2.7139841 | 2.0797563 | | | | |
| 97 | 1 | 1 | 1 | | | | |
| 98 | 2.7193198 | 2.2359644 | 3.8406461 | | | | |

Table 4

| SEQ ID | Patient ID | | | | | | |
|--------|------------|-----------|-----------|-----|-----|-----|-----|
| NO | 888 | 889 | 890 | 891 | 892 | 893 | 989 |
| 99 | 1.2283202 | 0.6240352 | 1 | | | | |
| 100 | 1 | 0.6153395 | 1 | | | | |
| 101 | 1.2371745 | 3.7971122 | 2.9804144 | | | | |
| 102 | 1 | 2.5906568 | 2.036037 | | | | |
| 103 | 0.4878614 | 0.5220519 | 0.5875074 | | | | |
| 104 | 1 | 0.4947949 | 1 | | | | |
| 105 | 2.8965207 | 1 | 1 | | | | |
| 106 | 3.2385003 | 1 | 0.7217671 | | | | |
| 107 | 5.3737835 | 2.7508505 | 1.130323 | | | | |
| 108 | 2.3856544 | 2.5666093 | 1 | | | | |
| 109 | 1.362962 | 2.5075245 | 2.1907727 | | | | |
| 110 | 2.7683669 | 2.7799971 | 2.5010217 | | | | |
| 111 | 2.58456 | 1 | 1 | | | | |
| 112 | 8.2800432 | 6.748402 | 1 | | | | |
| 113 | 1 | 1 | 1 | | | | |
| 114 | 1 | 0.5467682 | 1 | | | | |
| 115 | 1.3938005 | 3.1519961 | 2.8508911 | | | | |
| 116 | 1 | 0.5785322 | 0.8297756 | | | | |
| 117 | 1 | 0.662154 | 0.6950101 | | | | |
| 118 | 1 | 0.355833 | 0.3806683 | | | | |
| 119 | 1 | 0.4645694 | 0.6082288 | | | | |
| 120 | 1 | 0.4878181 | 0.5877594 | | | | |
| 121 | 1.8396026 | 2.1488141 | 1.6730969 | | | | |
| 122 | 0.3246765 | 0.3363954 | 0.5483425 | | | | |
| 123 | 4.0114856 | 2.7138817 | 3.9728191 | | | | |
| 124 | 1 | 3.8454521 | 5.8142318 | | | | |
| 125 | 1 | 2.6341318 | 3.1315162 | | | | |
| 126 | 6.6087211 | 3.3015259 | 1 | | | | |
| 127 | 1 | 0.5190666 | 1 | | | | |
| 128 | 1 | 0.5226516 | 1 | | | | |
| 129 | 1 | 1 | 1.7223995 | | | | |
| 130 | 1 | 1 | 1 | | | | |
| 131 | 1 | 3.308972 | 2.0268908 | | | | |
| 132 | 1.3527234 | 2.4505974 | 4.1915559 | | | | |
| 133 | 3.6320939 | 2.0491613 | 2.053952 | | | | |
| 134 | 1 | 0.6004705 | 0.5716494 | | | | |
| 135 | 1 | 0.5784345 | 1 | | | | |
| 136 | 0.2106747 | 1 | 0.7577852 | | | | |
| 137 | 1 | 1 | 2.4177523 | | | | |
| 138 | 1 | 0.6172679 | 0.4739586 | | | | |
| 139 | 1.4582337 | 4.3470024 | 5.1287586 | | | | |
| 140 | 1.9360406 | 1.9698788 | 3.1800992 | | | | |
| 141 | 2.528551 | 3.0220155 | 1.6928083 | | | | |
| 142 | 2.9953477 | 3.7247151 | 1.8384072 | | | | |
| 143 | 2.8119365 | 1 | 1.6772304 | | | | |
| 144 | 0.5659571 | 2.869202 | 3.141087 | | | | |
| 145 | 2.1987241 | 3.164901 | 2.4173574 | | | | |
| 146 | 2.1160749 | 2.8197971 | 2.2541041 | | | | |
| 147 | 1.3816121 | 2.0922796 | 1.6864042 | | | | |

Table 4

| SEQ ID | Patient ID | | | | | | |
|--------|------------|-----------|-----------|-----|-----|-----|-----|
| NO | 888 | 889 | 890 | 891 | 892 | 893 | 989 |
| 148 | 2.8976217 | 2.9282199 | 1.2899231 | | | | |
| 149 | 1 | 0.4792108 | 1 | | | | |
| 150 | 0.6573248 | 0.806438 | 0.7208811 | | | | |
| 151 | 1 | 2.6434301 | 4.4114539 | | | | |
| 152 | 3.3353235 | 2.4566268 | 1.5230257 | | | | |
| 153 | 2.2468418 | 2.4783069 | 2.3318857 | | | | |
| 154 | 5.1147843 | 3.867588 | 2.4904159 | | | | |
| 155 | 1 | 1.9115807 | 1.7936234 | | | | |
| 156 | 1.3092589 | 2.0807133 | 2.1467907 | | | | |
| 157 | 1.2650098 | 2.5872072 | 1.7898923 | | | | |
| 158 | 6.6495542 | 1 | 1.7811464 | | | | |
| 159 | 1 | 0.6739735 | 1 | | | | |
| 160 | 1 | 0.459398 | 1 | | | | |
| 161 | 1 | 0.4725301 | 1 | | | | |
| 162 | 0.6338196 | 1 | 0.5168378 | | | | |
| 163 | 1 | 1 | 1.7460119 | | | | |
| 164 | 2.1127516 | 2.7333838 | 4.4636101 | | | | |
| 165 | 0.6906391 | 0.560058 | 0.515405 | | | | |
| 166 | 1 | 4.0602466 | 3.641979 | | | | |
| 167 | 0.2569272 | 0.5302497 | 0.2423993 | | | | |
| 168 | 1.1246501 | 1 | 2.879065 | | | | |
| 169 | 2.4773308 | 2.5955205 | 1 | | | | |
| 170 | 0.8197313 | 2.7084627 | 2.3772079 | | | | |
| 171 | 1.67355 | 3.4716402 | 2.2540354 | | | | |
| 172 | 1.3558511 | 2.6806893 | 1.6380239 | | | | |
| 173 | 2.8408409 | 3.2460706 | 2.3976971 | | | | |
| 174 | 3.8283288 | 2.1964109 | 1 | | | | |
| 175 | 1.3578838 | 3.3968402 | 1.9734833 | | | | |
| 176 | 3.3251397 | 5.3177547 | 1.8364909 | | | | |
| 177 | 0.3658458 | 0.2467284 | 0.3070751 | | | | |
| 178 | 1 | 3.0234135 | 1.7363022 | | | | |
| 179 | 3.6810558 | 2.6409054 | 3.0965279 | | | | |
| 180 | 3.0505858 | 2.3101875 | 1 | | | | |
| 181 | 1.8352108 | 2.6368371 | 2.1748047 | | | | |
| 182 | 2.8330108 | 2.1362988 | 1 | | | | |
| 183 | 2.0749879 | 2.1584917 | 4.0781333 | | | | |
| 184 | 0.486608 | 1 | 2.3905708 | | | | |
| 185 | 1.7606805 | 3.254152 | 2.0102616 | | | | |
| 186 | 1 | 2.3123424 | 2.6883825 | | | | |
| 187 | 2.1332972 | 1.9035329 | 1 | | | | |
| 188 | 3.0143974 | 3.2405105 | 2.4248035 | | | | |
| 189 | 3.058337 | 2.5670675 | 1 | | | | |
| 190 | 0.3021257 | 1 | 0.8138057 | | | | |
| 191 | 1.9555756 | 1.9872492 | 1.9123825 | | | | |
| 192 | 1 | 0.4860864 | 0.8056718 | | | | |
| 193 | 4.2208239 | 2.1485573 | 1.4125748 | | | | |
| 194 | 1 | 0.404838 | 0.2867096 | | | | |
| 195 | 1 | 0.5789562 | 1 | | | | |
| 196 | 1.4311985 | 3.8707116 | 2.7153137 | | | | |

Table 4

| SEQ ID | Patient ID | | | | | | |
|--------|------------|-----------|-----------|-----------|-----|-----|-----|
| NO | 888 | 889 | 890 | 891 | 892 | 893 | 989 |
| 197 | | 1 | 0.694489 | 1.6159532 | | | |
| 198 | 0.7475824 | 2.3078144 | 2.4615857 | | | | |
| 199 | 1.1790671 | 1.6236218 | 2.141076 | | | | |
| 200 | | 1 | 2.6803973 | | | | |
| 201 | 2.8636067 | 3.7122135 | 3.0082823 | | | | |
| 202 | 1.1848397 | 2.6809892 | 2.2949302 | | | | |
| 203 | 2.3835409 | 2.0718386 | 2.7182062 | | | | |
| 204 | 2.1357377 | 1.6645225 | 2.4458825 | | | | |
| 205 | 1.6405947 | 2.6622251 | 1 | | | | |
| 206 | 2.7126269 | 3.0537221 | 1.6209088 | | | | |
| 207 | 3.7489413 | 2.2002426 | 1.4398126 | | | | |
| 208 | 3.8206539 | 3.0111299 | 7.1247572 | | | | |
| 209 | 0.7417329 | 1 | 0.237383 | | | | |
| 210 | | 1 | 0.5728116 | 1.3711408 | | | |
| 211 | 2.4541359 | 2.0651134 | 2.4087802 | | | | |
| 212 | 1.2409001 | 2.6342284 | 2.5012753 | | | | |
| 213 | | 1 | 0.4745106 | 1 | | | |
| 214 | 2.7363201 | 1 | 1.5275531 | | | | |
| 215 | 2.9535683 | 3.8526648 | 2.4796504 | | | | |
| 216 | | 1 | 0.577533 | 1 | | | |
| 217 | 1.4322741 | 2.0972236 | 2.2409294 | | | | |
| 218 | 2.3237798 | 1 | 1 | | | | |
| 219 | 2.5015154 | 1 | 1 | | | | |
| 220 | 1.4260447 | 2.2800015 | 1.8683464 | | | | |
| 221 | | 1 | 0.5085145 | 0.7873355 | | | |
| 222 | | 1 | 0.5327133 | 0.7785547 | | | |
| 223 | | 1 | 0.4544294 | 0.8266332 | | | |
| 224 | | 1 | 0.4602892 | 0.7002851 | | | |
| 225 | | 1 | 0.6078063 | 1 | | | |
| 226 | 2.0907805 | 1 | 2.5390382 | | | | |
| 227 | 2.3067281 | 2.0953287 | 1.5941945 | | | | |
| 228 | 2.2866621 | 2.4892911 | 1 | | | | |
| 229 | 0.772846 | 2.7195281 | 1.9327621 | | | | |
| 230 | 5.0309584 | 2.7250948 | 1.6346226 | | | | |
| 231 | | 1 | 0.4897122 | 1 | | | |
| 232 | | 1 | 2.2625646 | 3.467235 | | | |
| 233 | | 1 | 3.6768988 | 2.5710618 | | | |
| 234 | | 1 | 2.7202047 | | | | |
| 235 | 2.7126269 | 0.2981286 | 0.1705119 | | | | |
| 236 | 3.6773564 | 1.7768346 | 1 | | | | |
| 237 | 3.348509 | 1.6219734 | 1 | | | | |
| 238 | 0.060452 | 0.2965642 | 0.3986045 | | | | |
| 239 | | 1 | 0.3999284 | 1 | | | |
| 240 | 0.3305363 | 0.3861211 | 0.4342997 | | | | |
| 241 | 0.3757086 | 0.4804438 | 0.4694692 | | | | |
| 242 | 2.0616136 | 2.3246047 | 5.2622478 | | | | |
| 243 | 2.408391 | 1.7822969 | 1.5458382 | | | | |
| 244 | 1.094718 | 3.4908578 | 2.3521958 | | | | |
| 245 | 2.3004053 | 2.7763469 | 1.9246184 | | | | |

Table 4

| SEQ ID | Patient ID | | | | | | |
|--------|------------|-----------|-----------|-----|-----|-----|-----|
| NO | 888 | 889 | 890 | 891 | 892 | 893 | 989 |
| 246 | 2.9312329 | 1.7432704 | 1 | | | | |
| 247 | 5.7027565 | 3.0043347 | 2.156488 | | | | |
| 248 | 1.6132533 | 2.4831863 | 2.3084613 | | | | |
| 249 | 0.7808548 | 0.5228949 | 1 | | | | |
| 250 | 3.7070113 | 1.8772385 | 0.7105806 | | | | |
| 251 | 1.5070001 | 2.0777066 | 1 | | | | |
| 252 | 1 | 1 | 10.069088 | | | | |
| 253 | 1 | 1.7794294 | 2.0255592 | | | | |
| 254 | 1 | 0.3757519 | 1 | | | | |
| 255 | 0.6441925 | 0.4534176 | 0.7110039 | | | | |
| 256 | 1 | 1 | 1.9339239 | | | | |
| 257 | 1 | 0.4029749 | 1 | | | | |
| 258 | 1.5688204 | 2.0633352 | 2.4718643 | | | | |
| 259 | 1.4959594 | 2.3956388 | 2.59005 | | | | |
| 260 | 0.3731097 | 0.2893872 | 0.1686977 | | | | |
| 261 | 2.7348476 | 1.7462345 | 1 | | | | |
| 262 | 1 | 1 | 2.3885645 | | | | |
| 263 | 2.644329 | 6.067752 | 5.0263367 | | | | |
| 264 | 1.8000023 | 2.3246799 | 2.819713 | | | | |
| 265 | 0.9315091 | 0.4289653 | 1 | | | | |
| 266 | 0.0139634 | 0.0387452 | 0.0513245 | | | | |
| 267 | 3.3421474 | 1.5591812 | 0.7052373 | | | | |
| 268 | 2.0083408 | 3.4123185 | 2.576702 | | | | |
| 269 | 3.8227295 | 3.1125569 | 1.2928529 | | | | |
| 270 | 2.2989022 | 2.0845142 | 1.4964151 | | | | |
| 271 | 1 | 0.374014 | 1 | | | | |
| 272 | 1 | 0.4872098 | 1 | | | | |
| 273 | 4.583062 | 2.4216231 | 1.8308565 | | | | |
| 274 | 0.2141753 | 0.5192278 | 0.5332478 | | | | |
| 275 | 1 | 0.5969503 | 1 | | | | |
| 276 | 1 | 1 | 1 | | | | |
| 277 | 1 | 1 | 3.5094962 | | | | |
| 278 | 1.5155387 | 1 | 3.3574287 | | | | |
| 279 | 2.7236919 | 3.2981936 | 2.6916095 | | | | |
| 280 | 0.2853299 | 1 | 0.2028241 | | | | |
| 281 | 1 | 0.3841835 | 1 | | | | |
| 282 | 2.1926634 | 1.3864868 | 1.7181603 | | | | |
| 283 | 0.8706047 | 1.4031566 | 2.9657219 | | | | |
| 284 | 1 | 1.6844125 | 1.177539 | | | | |
| 285 | 0.3727782 | 1 | 0.3651918 | | | | |
| 286 | 1.6763101 | 1.9318194 | 0.8285956 | | | | |
| 287 | 1.7239492 | 1 | 2.2554782 | | | | |
| 288 | 2.0235343 | 2.68269 | 2.2778344 | | | | |
| 289 | 3.2733814 | 1.643179 | 1.289204 | | | | |
| 290 | 3.1137179 | 1.5854868 | 1.2192537 | | | | |
| 291 | 2.8820112 | 2.0692743 | 1.9314 | | | | |
| 292 | 1.3018617 | 1.9963546 | 3.2771359 | | | | |
| 293 | 1 | 0.4610774 | 1 | | | | |
| 294 | 1 | 1 | 1.9231178 | | | | |

Table 4

| SEQ ID | Patient ID | | | | | | |
|--------|------------|-----------|-----------|-----------|-----------|-----------|-----------|
| NO | 888 | 889 | 890 | 891 | 892 | 893 | 989 |
| 295 | 2.158007 | 1 | 3.0048619 | | | | |
| 296 | 0.9068263 | 0.4116816 | 0.8234505 | | | | |
| 297 | 0.803601 | 0.5114521 | 1 | 0.5584997 | 1 | 0.5523573 | 1 |
| 298 | 1.6720511 | 2.9073776 | 2.9825767 | 1.4213249 | 1 | 2.1417614 | 1 |
| 299 | 0.8178113 | 0.4902933 | 1 | 0.5891629 | 1 | 0.5764809 | 1 |
| 300 | 1.649737 | 1.9448849 | 2.7783183 | 1 | 1.402009 | 1.6662767 | 1.453829 |
| 301 | 1 | 1 | 2.7423833 | 1.6520824 | 1 | 0.5278236 | 1.9554773 |
| 302 | 1 | 1 | 3.7400924 | 1.6556462 | 1 | 1 | 1.2681309 |
| 303 | 0.4684353 | 1 | 0.5768994 | 0.3859588 | 0.515219 | 0.4235104 | 0.5235551 |
| 304 | 0.6182653 | 0.4726512 | 0.459308 | 15.001062 | 1 | 1.5662752 | 2.5379114 |
| 305 | 1 | 1 | 2.595774 | 1 | 1.1968086 | 2.4492101 | 1 |
| 306 | 0.1268552 | 0.1716953 | 0.7718227 | 0.600318 | 0.3284212 | 0.0368321 | 0.0398228 |
| 307 | 1.8753929 | 1 | 3.0709549 | 2.4346597 | 1 | 2.2318752 | 1.8509895 |
| 308 | 1 | 1 | 2.6149455 | 1 | 0.3515307 | 0.3180026 | 0.4418838 |
| 309 | 0.2252596 | 0.2380472 | 0.1877777 | 0.1855121 | 1 | 0.2600743 | 0.2989196 |
| 310 | 0.6170684 | 5.2147632 | 2.783125 | 0.4715223 | 1.441922 | 0.5316242 | 0.19744 |
| 311 | 0.6479524 | 1.5604334 | 0.6500894 | 0.4021552 | 0.5915888 | 0.4425841 | 0.3219423 |
| 312 | 5.9777767 | 2.940316 | 2.6600664 | 1.5411983 | 1.6949147 | 1.67415 | 1.1549701 |
| 313 | 1 | 1 | 3.2622549 | 2.3619334 | 1 | 1.8408842 | 1.7743521 |
| 314 | 1.7236244 | 1 | 1.6128889 | 0.8197787 | 1.6172424 | 0.1998911 | 1 |
| 315 | 0.0361824 | 0.2667886 | 0.3345937 | 0.133189 | 0.2944145 | 0.123253 | 0.3202927 |
| 316 | 1.2595233 | 1.9519611 | 1.5038966 | 1 | 0.6270527 | 1 | 1 |
| 317 | 1.5093871 | 1 | 1.9632732 | 1.6706495 | 1.2087374 | 1.3094397 | 2.1920366 |
| 318 | 1 | 0.1464966 | 3.7769359 | 1 | 1.4379371 | 0.3104181 | 1.332056 |
| 319 | 3.2464305 | 2.08391 | 1.935492 | 1.3706155 | 1.4458036 | 1.4679488 | 1 |
| 320 | 0.0879167 | 0.3341719 | 0.0326559 | 0.0230572 | 1 | 0.0735443 | 0.0756063 |
| 321 | 0.90522 | 0.5391494 | 0.6014608 | 0.455519 | 0.7888324 | 0.6186123 | 1 |
| 322 | 0.7868527 | 4.7184777 | 2.1758278 | 1.3756624 | 1 | 1.8481906 | 2.3705538 |
| 323 | 0.9087 | 0.5082844 | 1 | 0.6414018 | 1 | 0.5786967 | 1 |
| 324 | 1 | 1 | 1 | 0.6297941 | 1 | 0.5581599 | 0.4901248 |
| 325 | 0.2649621 | 1 | 0.4421867 | 0.5677916 | 0.5571437 | 0.4684252 | 0.3766729 |
| 326 | 0.9085646 | 0.5146153 | 1 | 0.6801129 | 1 | 0.6210698 | 1 |
| 327 | 1 | 1 | 5.0427783 | 1 | 1 | 1.5173177 | 1.743457 |
| 328 | 0.5407775 | 1 | 1 | 0.3169082 | 0.7171954 | 0.2692227 | 1.7448035 |
| 329 | 0.6900609 | 0.530743 | 0.3210383 | 0.4859567 | 0.659731 | 0.5812558 | 0.4607702 |
| 330 | 2.0552679 | 1 | 1.2338096 | 1 | 1.0869867 | 1.7205879 | 1 |
| 331 | 1 | 1 | 2.6011575 | 1 | 1.707153 | 1.5764636 | 1 |
| 332 | 1 | 1 | 2.2670178 | 1.6604741 | 0.6789073 | 0.7669683 | 0.8777875 |
| 333 | 1 | 1 | 3.8105839 | 1 | 2.5672612 | 1 | 1.7544589 |
| 334 | 0.7957992 | 0.4860569 | 0.7388468 | 0.6208127 | 0.7248813 | 0.5907792 | 1 |
| 335 | 0.5409821 | 0.5620898 | 0.5490831 | 0.4737273 | 0.5660806 | 0.4701005 | 0.6378682 |
| 336 | 3.3030481 | 1 | 13.432153 | 0.7687199 | 1 | 1 | 1 |
| 337 | 0.8038552 | 0.4937719 | 1 | 0.6523045 | 1 | 0.5854316 | 1 |
| 338 | 0.5575236 | 6.4895041 | 2.6687005 | 0.4490816 | 1.554078 | 0.5508219 | 0.2229737 |
| 339 | 1 | 3.2295924 | 2.6820489 | 1 | 1 | 1.6541008 | 1.1745358 |
| 340 | 1 | 1 | 6.3967608 | 2.009391 | 1 | 1.6707177 | 3.1429194 |
| 341 | 2.4991918 | 1 | 2.2174926 | 4.3489776 | 1 | 1.7795298 | 1.629241 |
| 342 | 1.2132189 | 2.9451342 | 2.0859708 | 1.4751598 | 1 | 1 | 1.7161888 |
| 343 | 1 | 1 | 2.6121762 | 1.4062376 | 0.8198471 | 1 | 1.2571289 |

Table 4

| SEQ ID | Patient ID | | | | | | |
|--------|------------|-----------|-----------|-----------|-----------|-----------|-----------|
| NO | 888 | 889 | 890 | 891 | 892 | 893 | 989 |
| 344 | 0.4545419 | 1 | 0.2408921 | 0.1588337 | 0.3917145 | 0.4852733 | 0.2867896 |
| 345 | 0.4103216 | 0.4568784 | 0.5145878 | 0.5548353 | 1 | 0.6839678 | 0.4072041 |
| 346 | 0.715012 | 0.4337613 | 0.5406266 | 0.5794735 | 0.6183737 | 1 | 0.7592046 |
| 347 | 0.7986269 | 0.4635689 | 0.7813498 | 0.634383 | 0.7793667 | 0.545599 | 1.1891282 |
| 348 | 3.6087387 | 2.2792063 | 2.404241 | 2.237184 | 1.546521 | 1 | 1.2633395 |
| 349 | 1.5521305 | 2.4608313 | 2.1447995 | 1.7260682 | 1 | 3.0005557 | 3.0022478 |
| 350 | 0.538175 | 0.7732763 | 0.5165599 | 0.4835043 | 0.5110665 | 1 | 0.4568886 |
| 351 | 1.3901574 | 3.3992494 | 2.5142784 | 1.2751932 | 1 | 2.0973193 | 1.2447685 |
| 352 | 1 | 1 | 2.3435543 | 1 | 1 | 1.1941654 | 1 |
| 353 | 0.6755775 | 1.5762054 | 3.8886819 | 1 | 1 | 1.8994544 | 0.5123955 |
| 354 | 1 | 1 | 0.2709388 | 0.4515428 | 1.3151677 | 1.67415 | 0.2213725 |
| 355 | 0.4542823 | 1 | 0.2050952 | 0.3718978 | 0.2445975 | 0.4515287 | 0.3807486 |
| 356 | 1 | 1 | 3.3759628 | 1.6423986 | 1.6737525 | 1 | 1 |
| 357 | 0.300579 | 0.5741475 | 0.3927922 | 0.4304044 | 0.7318581 | 0.5036314 | 0.4683878 |
| 358 | 3.241369 | 2.8606393 | 1 | 1 | 1.3889454 | 0.2543663 | 1.4604884 |
| 359 | 0.8746837 | 0.4718137 | 0.7109766 | 0.6855539 | 1 | 0.5414302 | 1 |
| 360 | 0.483427 | 0.7036659 | 0.3625225 | 0.2645917 | 1 | 1.856612 | 0.3250234 |
| 361 | 1 | 1 | 1.2057639 | 1 | 1 | 0.2732397 | 0.498822 |
| 362 | 1 | 1 | 8.9380032 | 3.5157339 | 1 | 1 | 1 |
| 363 | 2.9527103 | 1 | 1.4337033 | 2.2109845 | 1 | 2.5927885 | 2.1506854 |
| 364 | 1.4737388 | 3.8419584 | 2.7707241 | 1.4288316 | 0.6464353 | 1.5843558 | 1.76893 |
| 365 | 0.7518589 | 1 | 2.4972236 | 1 | 1 | 0.4896066 | 1 |
| 366 | 1.7094842 | 4.4697044 | 4.1050554 | 1.9474323 | 1.6491986 | 2.9455146 | 1 |
| 367 | 2.6682393 | 4.4289506 | 2.4213916 | 3.124198 | 2.2033375 | 1.5636831 | 0.2623234 |
| 368 | 3.1204092 | 1 | 2.5359057 | 2.4668111 | 1.2900722 | 1.3621051 | 2.9131408 |
| 369 | 3.0400424 | 1.7261507 | 1.215888 | 1.917083 | 0.6984704 | 1 | 1.2951686 |
| 370 | 0.7203553 | 0.4144943 | 0.4811734 | 0.7912105 | 2.0043917 | 0.5067948 | 1.71238 |
| 371 | 2.1769054 | 1 | 1.5297004 | 2.141514 | 1.5530464 | 1.863671 | 2.0105354 |
| 372 | 0.1626907 | 0.1386655 | 0.1757077 | 0.0503443 | 1.7426813 | 0.0828423 | 0.1180613 |
| 373 | 1 | 2.2541931 | 1 | 2.1307864 | 1.43176 | 2.2400039 | 1.5214174 |
| 374 | 1 | 1 | 4.2524986 | 1.450344 | 1.8821123 | 1.3480227 | 0.4652947 |
| 375 | 1.9532373 | 1.9894489 | 1 | 1 | 1.531897 | 1 | 1 |
| 376 | 2.0801782 | 1 | 1.5611994 | 1 | 1.6627909 | 1 | 1.2326263 |
| 377 | 0.2864898 | 1 | 0.7601595 | 0.745122 | 1 | 1.3163404 | 0.1790752 |
| 378 | 0.5013313 | 0.5839742 | 0.4823276 | 1 | 1 | 0.638478 | 0.5685938 |
| 379 | 0.8665061 | 0.5015504 | 1 | 0.6566906 | 1 | 0.6110342 | 1 |
| 380 | 0.3805111 | 1 | 0.5236998 | 0.5464874 | 1 | 1 | 1 |
| 381 | 0.7520629 | 0.4430479 | 0.7474745 | 0.6288126 | 1 | 0.5965637 | 1 |
| 382 | 2.4295633 | 1 | 1.2915667 | 1.6340368 | 1 | 3.1323247 | 1 |
| 383 | 0.5005686 | 1 | 0.5342218 | 0.372394 | 1 | 0.4940067 | 1.4912622 |
| 384 | 1.1666465 | 2.0549014 | 2.7694797 | 2.9509361 | 1.7659327 | 2.9391404 | 2.0178255 |
| 385 | 1 | 1 | 4.3713214 | 1 | 1 | 1.557333 | 1.2774346 |
| 386 | 0.7846726 | 0.4895354 | 0.6830644 | 0.6752479 | 1 | 0.5537366 | 1 |
| 387 | 0.7523288 | 0.4792971 | 1 | 0.5254854 | 1 | 0.4742418 | 1 |
| 388 | 0.7461616 | 0.5468972 | 0.3786154 | 0.527078 | 1 | 0.5325187 | 1 |
| 389 | 0.7425156 | 1 | 2.2065162 | 1 | 1.6059198 | 2.1098765 | 1 |
| 390 | 0.3560976 | 0.338365 | 0.3647814 | 0.5214919 | 0.5089645 | 0.4903763 | 0.4004841 |
| 391 | 0.3648099 | 0.5169317 | 0.2480083 | 0.1960763 | 0.6449265 | 0.5194295 | 0.3048148 |
| 392 | 3.3221208 | 3.1354992 | 1 | 1.7283497 | 1.7637146 | 1.8552911 | 1 |

Table 4

| SEQ ID | Patient ID | | | | | | | |
|--------|------------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|
| | NO | 888 | 889 | 890 | 891 | 892 | 893 | 989 |
| 393 | | 0.4090867 | 0.3814317 | 0.3493392 | 0.6342918 | 0.7672961 | 0.4859751 | 0.5366919 |
| 394 | | 0.7998279 | 0.4635211 | 0.6834113 | 0.598542 | 1 | 0.490786 | 1 |
| 395 | | 1 | 2.7074427 | 2.1662733 | 1.5283219 | 1.1475203 | 1.7661756 | 0.815318 |
| 396 | | 0.2026587 | 0.1600463 | 0.1553275 | 0.1674032 | 1.728715 | 0.2291045 | 0.2224763 |
| 397 | | 1.4672149 | 1 | 2.4395124 | 2.1949703 | 1.4912232 | 1.6969409 | 0.846577 |
| 398 | | 1.2942729 | 1 | 1.6206248 | 1 | 0.6982254 | 1 | 1 |
| 399 | | 3.1727912 | 1.3290209 | 0.4025313 | 0.4940284 | 0.1252326 | 0.6240841 | 0.4174782 |
| 400 | | 1 | 0.3499098 | 0.0949211 | 0.2061883 | 1 | 0.5714079 | 0.2853704 |
| 401 | | 0.148127 | 0.3803923 | 0.3865201 | 0.7107125 | 0.4860097 | 0.3449132 | 0.3017459 |
| 402 | | 0.1887723 | 1 | 1 | 0.1641433 | 1 | 1 | 1 |
| 403 | | 0.396721 | 0.3450628 | 0.2314382 | 1 | 1 | 0.2516952 | 2.4530378 |
| 404 | | 0.6159922 | 0.5644864 | 0.2887311 | 0.5192103 | 1 | 0.8216717 | 0.5352605 |
| 405 | | 0.2806381 | 0.5442062 | 0.1072526 | 0.3333947 | 0.3222311 | 0.3327892 | 0.2647615 |
| 406 | | 1.945428 | 6.0023984 | 4.0120217 | 1.7783654 | 1 | 1.86234 | 2.0891742 |
| 407 | | 1 | 0.1643495 | 0.1921026 | 1.3510256 | 1 | 1.4173948 | 1 |
| 408 | | 2.3218924 | 2.5217738 | 1.3964997 | 1.473313 | 1.3041029 | 1.5100427 | 1 |
| 409 | | 0.2527189 | 1 | 0.0850566 | 0.1546312 | 1 | 0.1398402 | 1 |
| 410 | | 5.0171621 | 6.2453936 | 4.2001208 | 3.7204278 | 1 | 2.7006244 | 1.3462117 |
| 411 | | 0.2127062 | 0.2130253 | 0.231702 | 0.3068599 | 0.5515727 | 0.3757266 | 0.2509333 |
| 412 | | 0.606521 | 0.5722918 | 0.7775729 | 0.6256036 | 1 | 0.4862107 | 0.8643232 |
| 413 | | 1 | 1 | 1 | 0.6939285 | 1 | 1.9846289 | 2.1110082 |
| 414 | | 0.0350955 | 0.0546861 | 0.0368619 | 0.0364996 | 1.5263646 | 0.0155338 | 0.0257156 |
| 415 | | 0.0092879 | 0.0173199 | 0.0148777 | 0.0246028 | 1.5085553 | 0.008612 | 0.0158054 |
| 416 | | 1.5177263 | 1 | 2.3204782 | 1.7264903 | 1 | 1.1762819 | 1.2450111 |
| 417 | | 1.5773686 | 4.3105124 | 2.3756053 | 2.3033011 | 1.1194071 | 2.5792481 | 1.8023239 |
| 418 | | 1 | 1 | 2.3914979 | 1 | 1 | 1 | 1.6805145 |
| 419 | | 1.2092416 | 1.9340021 | 1.6081918 | 1.1986487 | 0.7792249 | 1.8990671 | 0.6476692 |
| 420 | | 0.6469122 | 1 | 2.4864828 | 1.3921255 | 1.5118825 | 0.7537033 | 0.1052035 |
| 421 | | 0.5405218 | 1 | 0.3274337 | 0.7281483 | 1 | 0.4805056 | 1.436095 |
| 422 | | 1 | 0.5630936 | 0.3900612 | 0.2755222 | 0.8211109 | 0.6849235 | 0.6533097 |
| 423 | | 1.276074 | 2.4802735 | 1.4722107 | 0.8355719 | 1.5472819 | 1 | 1.0960668 |
| 424 | | 0.4486037 | 0.7843965 | 0.494743 | 0.7196144 | 1 | 0.8019519 | 0.451139 |
| 425 | | 1 | 3.0264682 | 1.9134209 | 1 | 2.2132029 | 1.7581735 | 1 |
| 426 | | 0.703449 | 0.5185312 | 0.1559584 | 1 | 0.8547178 | 0.8160968 | 1 |
| 427 | | 4.7859118 | 4.5633316 | 2.7642035 | 1 | 1.6492759 | 1.5784484 | 2.2343824 |
| 428 | | 1 | 0.5010959 | 0.6691238 | 0.6186967 | 0.7285309 | 0.5735293 | 1 |
| 429 | | 1.5773958 | 1.6770646 | 2.9494092 | 1.7743435 | 1.2632228 | 1.8733642 | 2.35658 |
| 430 | | 0.8181038 | 1 | 3.6275174 | 1.6089413 | 1 | 1 | 0.5212382 |
| 431 | | 0.2073868 | 0.3141501 | 0.4186813 | 1 | 0.6786752 | 0.1431814 | 0.1226222 |
| 432 | | 0.0984922 | 0.2388253 | 0.0495826 | 0.1267129 | 0.2872315 | 0.2520835 | 0.1576657 |
| 433 | | 2.2286683 | 2.9417598 | 2.6619803 | 0.874633 | 1.4261502 | 1.7648369 | 1.9924253 |
| 434 | | 1 | 0.5130215 | 0.6489037 | 0.6358111 | 1 | 0.5606801 | 1.2997902 |
| 435 | | 4.1824212 | 1 | 1 | 4.1763766 | 1 | 1000 | 2.5908224 |
| 436 | | 0.4587406 | 1 | 0.8185861 | 1 | 1 | 1 | 1 |
| 437 | | 1 | 0.504139 | 0.6349447 | 0.5348635 | 0.8265401 | 0.849399 | 0.4785164 |
| 438 | | 1 | 1 | 2.1264326 | 1 | 1.4753741 | 1.4692059 | 1 |
| 439 | | 3.3296177 | 2.4475938 | 1 | 1 | 0.735585 | 2.2276806 | 1 |
| 440 | | 2.5077558 | 2.3577687 | 1.4321494 | 1.3118439 | 1 | 2.2182815 | 1 |
| 441 | | 1 | 3.6133256 | 2.0079705 | 1 | 1.3521146 | 1.836166 | 2.2497026 |

Table 4

| SEQ ID | Patient ID | | | | | | |
|--------|------------|-----------|-----------|-----------|-----------|-----------|-----------|
| NO | 888 | 889 | 890 | 891 | 892 | 893 | 989 |
| 442 | 0.6131556 | 0.3399892 | 0.6878774 | 0.5815735 | 0.586611 | 1 | 1.2016706 |
| 443 | 0.7121065 | 0.4211673 | 0.5471869 | 0.735314 | 0.6971551 | 0.6172184 | 1 |
| 444 | 0.7639521 | 0.4945974 | 0.7564915 | 0.719629 | 1 | 0.5621013 | 1 |
| 445 | 1 | 1.643179 | 1 | 1.2549765 | 1 | 1.439681 | 1 |
| 446 | 0.5455961 | 0.5504439 | 0.4229336 | 0.3408378 | 0.5943614 | 0.5376128 | 0.4348362 |
| 447 | 1 | 1 | 1.3745283 | 2.3426562 | 1 | 1.3424986 | 1.4749716 |
| 448 | 1.549239 | 2.5466976 | 2.2119247 | 1.4077515 | 0.7221474 | 1.4477376 | 2.3821986 |
| 449 | 2.4111842 | 1.9579151 | 1 | 1.5120238 | 0.6999922 | 1 | 0.8823241 |
| 450 | 0.3622945 | 0.5430428 | 0.639571 | 0.581114 | 0.6000099 | 0.5004612 | 0.5610368 |
| 451 | 1.7432002 | 1 | 1.5565361 | 1 | 1.359749 | 1.4347067 | 1.3817647 |
| 452 | 2.6170944 | 1 | 1.5421012 | 1.4989598 | 1 | 2.6632246 | 2.958883 |
| 453 | 0.5637598 | 1 | 0.4127265 | 1 | 0.7169632 | 0.6479008 | 0.3613527 |
| 454 | 1 | 1 | 2.4076046 | 3.0610829 | 1.3618381 | 1.9808901 | 1.5957379 |
| 455 | 1 | 0.4846511 | 0.6748108 | 0.674577 | 1 | 0.6151393 | 1 |
| 456 | 0.4473729 | 1 | 0.4402295 | 0.432061 | 1 | 1 | 0.5888994 |
| 457 | 0.6381839 | 0.5993991 | 0.3730815 | 0.3794931 | 1 | 1 | 0.8525692 |
| 458 | 3.0896351 | 3.3729345 | 2.7223062 | 3.5826272 | 2.3204586 | 1.5559949 | 2.1647077 |
| 459 | 1.6159607 | 2.4134933 | 1.5574862 | 1.4673122 | 1 | 1 | 2.7074403 |
| 460 | 1 | 1 | 11.736357 | 4.3505853 | 1000 | 2.4890453 | 17.908077 |
| 461 | 0.6643469 | 0.4871504 | 0.7830696 | 0.6264472 | 1 | 0.6282822 | 1 |
| 462 | 1.6822597 | 1 | 1.9398047 | 2.8995565 | 2.8275273 | 1.5369925 | 5.1836463 |
| 463 | 3.1307682 | 2.0708837 | 1.9740624 | 2.1135656 | 2.0064809 | 2.4733695 | 0.7119461 |
| 464 | 3.8087233 | 2.3742768 | 1 | 1 | 1.7685377 | 2.018174 | 0.8663367 |
| 465 | 1.5319342 | 2.5842311 | 1.735325 | 1 | 1 | 2.074957 | 1 |
| 466 | 4.8459987 | 1 | 1.4219668 | 8.9572498 | 0.482128 | 0.6118887 | 1.8202399 |
| 467 | 2.451768 | 1.8511839 | 1.7660977 | 1.5579974 | 1.388997 | 1.7708772 | 2.1302949 |
| 468 | 2.7174618 | 3.9881685 | 2.8211105 | 1 | 1.402383 | 1.9131107 | 2.0599651 |
| 469 | 2.1760251 | 3.4282654 | 1 | 1.5719056 | 1 | 3.0799392 | 1 |
| 470 | 0.7979094 | 0.5012566 | 0.639107 | 0.5869542 | 1 | 1 | 1.2734681 |
| 471 | 0.2176144 | 0.3524919 | 0.1370986 | 0.267599 | 0.3707715 | 0.2426927 | 0.1638642 |
| 472 | 0.7332723 | 0.4725642 | 0.7865656 | 0.6356623 | 1 | 0.5315722 | 1.2507364 |
| 473 | 3.3723335 | 2.0964896 | 1.3825407 | 1 | 1.2174422 | 1.7092201 | 0.6772907 |
| 474 | 0.502764 | 1 | 1 | 0.805021 | 1 | 1 | 0.8232631 |
| 475 | 1 | 1.6779649 | 4.8914416 | 1.7820008 | 1 | 1 | 1.8514747 |
| 476 | 3.634114 | 2.4033272 | 1 | 2.241445 | 2.0850301 | 1.8182929 | 1 |
| 477 | 1.5796021 | 1.9771383 | 1.6481297 | 1.8237467 | 1.5267644 | 1.7784133 | 1.4785378 |
| 478 | 1.0495522 | 1 | 3.7686645 | 2.5756913 | 0.4142695 | 0.1730264 | 0.1794391 |
| 479 | 1.9880453 | 1 | 1 | 1.8108843 | 1.1958157 | 2.6803056 | 1.3364955 |
| 480 | 0.4518611 | 1 | 7.8246514 | 0.3952067 | 1 | 0.0475391 | 0.1651863 |
| 481 | 0.4270439 | 0.5823139 | 0.5463466 | 0.7006976 | 0.7456696 | 0.56153 | 0.3462145 |
| 482 | 0.7255545 | 1 | 1 | 1.465698 | 1.1736733 | 1 | 1 |
| 483 | 0.7202872 | 0.4667623 | 1 | 0.6544022 | 1.1518791 | 0.615029 | 1 |
| 484 | 0.5080244 | 0.4538757 | 0.3350982 | 0.6140481 | 0.647338 | 1 | 0.1866079 |
| 485 | 1 | 1 | 2.3957564 | 1.8519684 | 1 | 1.5832016 | 1.4186278 |
| 486 | 0.0428895 | 0.1152222 | 0.0972547 | 0.1683551 | 0.1043798 | 1 | 0.0201358 |
| 487 | 2.8848287 | 1.6257514 | 2.470049 | 3.0241124 | 1.6325886 | 3.1500326 | 1.5650247 |
| 488 | 0.7821834 | 0.4952141 | 0.8281505 | 0.6457247 | 1.2317696 | 0.6668345 | 1 |
| 489 | 1.7125244 | 2.7516928 | 2.080224 | 1 | 1.4531801 | 2.0275892 | 1 |
| 490 | 2.6341257 | 2.0727943 | 1 | 2.3733656 | 1.9653299 | 2.7311719 | 1.9402299 |

Table 4

| SEQ ID | Patient ID | | | | | | |
|--------|------------|-----------|-----------|-----------|-----------|-----------|-----------|
| NO | 888 | 889 | 890 | 891 | 892 | 893 | 989 |
| 491 | 0.7020077 | 0.4838715 | 0.4575953 | 0.5049775 | 0.7433097 | 1 | 1 |
| 492 | 3.2681189 | 2.0072238 | 2.0158475 | 1.769896 | 1.7633664 | 1.7824003 | 1 |
| 493 | 2.0135129 | 0.7012361 | 0.8138863 | 1.6661161 | 1 | 1 | 1.6202526 |
| 494 | 2.8232182 | 3.0783046 | 2.5798462 | 2.3464708 | 2.1657587 | 1.3625321 | 0.6729603 |
| 495 | 0.1930191 | 1 | 0.0979487 | 0.0442842 | 0.1608254 | 0.2379431 | 0.1777409 |
| 496 | 0.4945581 | 1 | 0.4459468 | 0.4792252 | 1 | 0.6007858 | 0.5259204 |
| 497 | 0.4193542 | 1 | 0.4754355 | 0.5631904 | 1 | 0.4507826 | 1 |
| 498 | 1 | 1 | 1.5046611 | 1.7953216 | 1 | 2.7229586 | 1.7166255 |
| 499 | 1.6811776 | 2.5125197 | 1.7794332 | 2.003689 | 0.9297335 | 1.5350382 | 1.2962239 |
| 500 | 1 | 1 | 4.5464321 | 0.1321649 | 3.6129938 | 0.3069744 | 1.9843588 |
| 501 | 1.4596531 | 1.369608 | 1.5460966 | 1.3731477 | 1.4648896 | 1.446517 | 1.5345542 |
| 502 | 0.2360172 | 0.5555869 | 0.3212795 | 0.5056936 | 0.5292498 | 1 | 1.4667475 |
| 503 | 1.1392161 | 1 | 2.4007309 | 1.6864506 | 1 | 1.9866852 | 2.0712339 |
| 504 | 1.1657544 | 2.3430913 | 1.9852371 | 1.6610209 | 1 | 1 | 1.4773612 |
| 505 | 0.5639857 | 1.3957196 | 0.4428536 | 0.6601472 | 1.0750193 | 1.3805949 | 0.4380992 |
| 506 | 3.7007127 | 1.699464 | 1 | 1 | 1.4711442 | 1.6131709 | 1 |
| 507 | 1 | 2.9523912 | 2.1388481 | 1.6141642 | 1 | 2.0455938 | 1 |
| 508 | 1 | 1 | 1.5238412 | 2.0839359 | 0.3877941 | 1.3767755 | 1.379278 |
| 509 | 1 | 1 | 3.2449451 | 1.781012 | 1 | 1 | 1.5514391 |
| 510 | 1 | 0.8342798 | 0.7759992 | 0.7024752 | 1 | 1 | 1 |
| 511 | 2.7294619 | 7.6847382 | 12.440775 | 6.7119772 | 4.135138 | 6.2964143 | 4.1948209 |
| 512 | 0.332653 | 1 | 0.4073172 | 0.5695044 | 1.6273528 | 0.4367753 | 1.9070665 |
| 513 | 0.8346982 | 0.4847524 | 0.5315661 | 0.5435552 | 1 | 0.4063216 | 1 |
| 514 | 2.4019408 | 7.9087707 | 4.5847415 | 1.8113953 | 2.0345296 | 1.8726108 | 1.421078 |
| 515 | 1 | 3.0814713 | 2.5026288 | 1.2435717 | 1 | 0.7155582 | 1.1329541 |
| 516 | 1 | 1 | 2.8612531 | 2.1442454 | 1 | 1.403541 | 1 |
| 517 | 0.2285822 | 0.2277921 | 0.1177224 | 0.3434155 | 1.2177001 | 0.3696234 | 0.5366433 |
| 518 | 1 | 1 | 2.8840022 | 3.451799 | 1 | 1 | 1.6417106 |
| 519 | 0.8154856 | 1 | 0.6046702 | 1 | 0.6104556 | 3.2794946 | 0.4296082 |
| 520 | 0.3796442 | 1 | 0.1834047 | 0.1115521 | 0.1991006 | 1 | 1 |
| 521 | 1.7482975 | 1.6982997 | 1.2117267 | 1.9200022 | 1.2299899 | 1.8025569 | 1.3926453 |
| 522 | 2.5685222 | 1.9402134 | 1.7146171 | 1.4884378 | 1 | 1 | 1.3577109 |
| 523 | 1.6171033 | 1 | 1.4974447 | 2.7885944 | 1 | 1 | 1.2130849 |
| 524 | 1 | 0.4917724 | 0.7677865 | 0.6521538 | 1 | 0.6409575 | 1 |
| 525 | 1.5230581 | 2.4917069 | 3.3986005 | 2.532549 | 1.2286487 | 2.7064544 | 1 |
| 526 | 1 | 1.7026437 | 1.5080956 | 1.6455372 | 1.5602294 | 1.7016803 | 0.8252888 |
| 527 | 1 | 2.0171926 | 1.4407938 | 2.4223816 | 1 | 1.3296839 | 1 |
| 528 | 0.6711463 | 1 | 1 | 1.5602351 | 1 | 1.772177 | 1 |
| 529 | 0.3734494 | 1 | 0.3140514 | 0.2052801 | 1 | 1 | 0.6380016 |
| 530 | 0.3329545 | 1 | 0.4623673 | 0.4281158 | 1 | 1 | 0.3655133 |
| 531 | 1 | 1 | 2.1618431 | 1.5370382 | 2.2230812 | 1.5186609 | 1 |
| 532 | 1 | 1 | 1 | 1 | 2.0624751 | 3.7614282 | 1 |
| 533 | 0.2166902 | 0.2630248 | 0.184057 | 0.2761742 | 0.4747902 | 0.4027172 | 0.1988714 |
| 534 | 2.2878059 | 2.0479355 | 1.9660377 | 1 | 1.7437775 | 1.6824887 | 1 |
| 535 | 0.2540806 | 1 | 1 | 1 | 1 | 1 | 1 |
| 536 | 0.7154146 | 0.4714641 | 0.7618892 | 0.6961726 | 1.3279089 | 0.5486062 | 1 |
| 537 | 2.6121621 | 2.675402 | 1 | 2.0626296 | 1 | 1 | 1 |
| 538 | 1 | 1 | 3.6520446 | 1.6501133 | 1 | 2.6506637 | 3.3572322 |
| 539 | 1 | 1 | 3.1612153 | 2.5062114 | 1.4273108 | 2.7196643 | 1 |

Table 4

| SEQ ID | Patient ID | | | | | | |
|--------|------------|-----------|-----------|-----------|-----------|-----------|-----------|
| NO | 888 | 889 | 890 | 891 | 892 | 893 | 989 |
| 540 | 0.63879 | 1 | 1 | 1 | 1 | 1.3637862 | 1.2917601 |
| 541 | 1 | 1 | 1 | 1 | 1 | 1.5336299 | 1.4777009 |
| 542 | 0.835911 | 2.0506811 | 1.5757273 | 1.3726405 | 1 | 1.2671151 | 1 |
| 543 | 0.7830807 | 0.4528749 | 0.7944273 | 0.712714 | 1 | 0.5563546 | 1 |
| 544 | 0.1991807 | 0.3431031 | 0.3796644 | 0.5158684 | 0.7092128 | 1 | 0.3648583 |
| 545 | 1 | 1 | 1 | 1.5806322 | 1.3156964 | 1 | 1 |
| 546 | 2.2962477 | 1 | 1.9389406 | 1.6689909 | 1 | 1 | 1.1126121 |
| 547 | 1.6220064 | 2.475576 | 1.7491072 | 1.6865714 | 1 | 2.2120343 | 1.759226 |
| 548 | 1 | 1 | 2.0264467 | 1 | 1 | 1.9143466 | 0.7346777 |
| 549 | 1.4627807 | 2.3652155 | 2.0097156 | 1.7166266 | 1 | 2.043606 | 1.3777982 |
| 550 | 1 | 1 | 2.1205826 | 1 | 1.3466983 | 1 | 1 |
| 551 | 0.0682166 | 0.1092209 | 0.0525621 | 0.0691959 | 0.0377593 | 0.0775838 | 0.0808465 |
| 552 | 0.4462098 | 1 | 1 | 1 | 1 | 1 | 1 |
| 553 | 0.3804858 | 1 | 0.3601914 | 0.3656484 | 0.4882923 | 1.4668588 | 0.6729603 |
| 554 | 0.6521606 | 0.4708095 | 0.684714 | 0.6402677 | 1.3887262 | 0.4400537 | 1 |
| 555 | 0.2083958 | 0.07867 | 0.0268529 | | 3.4279506 | 0.014628 | 0.0556888 |
| 556 | 2.1402539 | 1.2045938 | 1.207515 | | 1 | 1.1768128 | 1 |
| 557 | 0.6212814 | 1 | 0.4490317 | | 0.8813104 | 1.5503704 | 0.5036497 |
| 558 | 1 | 1 | 3.3084918 | | 0.7113359 | 1.2975812 | 1.8163705 |
| 559 | 1 | 1 | 1.1577884 | | 0.7133308 | 1.6213149 | 1 |
| 560 | 1 | 1 | 1 | | 1 | 1000 | 1 |
| 561 | 1.2728329 | 1.8537168 | 1 | | 1 | 1.4436981 | 1 |
| 562 | 1.1629222 | 2.2862976 | 1.3638877 | | 0.671035 | 8.1777564 | 1 |
| 563 | 0.7207088 | 0.4090223 | 0.5631186 | | 1 | 0.6660442 | 1.8193181 |
| 564 | 2.2551685 | 2.0691373 | 1.6954069 | | 1 | 1.3290063 | 1.6810361 |
| 565 | 0.7589191 | 0.4504457 | 0.7881406 | | 1 | 0.6313121 | 1 |
| 566 | 2.4713857 | 1.8668009 | 1.5496257 | | 1.2563152 | 1.8285951 | 1.3290962 |
| 567 | 7.6030041 | 4.1666786 | 4.8153659 | | 1.1395806 | 7.0372489 | 2.925659 |
| 568 | 0.7097406 | 0.497606 | 1 | | 1 | 0.6547133 | 1 |
| 569 | 1 | 0.2654781 | 0.4942969 | | 0.8063244 | 1 | 1 |
| 570 | 0.6867522 | 0.2193458 | 0.188231 | | 0.6836022 | 1 | 0.3798267 |
| 571 | 0.6331736 | 0.3936449 | 0.7474518 | | 1 | 1 | 3.5099247 |
| 572 | 2.3496195 | 0.5715888 | 0.8389765 | | 1 | 1 | 1 |
| 573 | 3.5520784 | 2.234486 | 1.6924211 | | 1 | 2.2847506 | 1 |
| 574 | 0.8854239 | 0.5891876 | 0.4186694 | | 1 | 1.3877953 | 0.2979613 |
| 575 | 1 | 0.3887922 | 0.8028658 | | 1 | 0.6659218 | 1.5761722 |
| 576 | 0.6734513 | 0.4865924 | 0.8139937 | | 0.5954716 | 0.5975972 | 0.8508952 |
| 577 | 1 | 0.4656578 | 0.7194793 | | 0.6578593 | 0.3452932 | 1 |
| 578 | 1.4632808 | 2.0731272 | 1.8405106 | | 1.2918299 | 1 | 2.6112858 |
| 579 | 0.74356 | 0.4303091 | 0.6351355 | | 1 | 0.4964973 | 0.4999258 |
| 580 | 0.8573036 | 0.3039827 | 0.7551251 | | 2.849367 | 0.5529148 | 2.0744362 |
| 581 | 3.5885689 | 1.3790007 | 2.3130796 | | 1 | 1.7884636 | 1 |
| 582 | 2.4414267 | 2.38711 | 1.9559043 | | 1.4523448 | 1.6499563 | 1 |
| 583 | 3.2098412 | 2.4132854 | 1.8414266 | | 1 | 1.6036473 | 1.4512453 |
| 584 | 1 | 3.3947017 | 1.8280974 | | 0.8536124 | 1.5057876 | 2.0075271 |
| 585 | 1.8530316 | 3.3986125 | 1.1231688 | | 1.0673158 | 2.667911 | 1.6382535 |
| 586 | 1.0922921 | 1.3866858 | 2.5492723 | | 1.3369775 | 1 | 1 |
| 587 | 0.7511801 | 0.280683 | 0.2190546 | | 0.8459356 | 0.8278801 | 1 |
| 588 | 0.5620861 | 0.4876923 | 1.8393668 | | 1.5763486 | 0.1201417 | 0.2013701 |

Table 4

| SEQ ID | Patient ID | | | | | | |
|--------|------------|-----------|-----------|-----|-----------|-----------|-----------|
| NO | 888 | 889 | 890 | 891 | 892 | 893 | 989 |
| 589 | 0.4223993 | 0.3376348 | 0.2208835 | | 2.1233144 | 0.2306283 | 0.1959965 |
| 590 | 0.8020784 | 0.4444644 | 0.7365523 | | 0.8896151 | 0.7506312 | 2.8576582 |
| 591 | 0.4712028 | 0.2390726 | 0.6019452 | | 0.6637031 | 1 | 0.6388992 |
| 592 | 0.6768817 | 0.4756434 | 0.8455434 | | 1 | 0.7344292 | 1 |
| 593 | 3.1693897 | 1.1600288 | 1 | | 2.2362014 | 0.7562826 | 23.594742 |
| 594 | 0.484467 | 0.4710424 | 0.7167128 | | 0.7612631 | 1 | 0.3650402 |
| 595 | 1 | 1.9323149 | 1 | | 0.7937777 | 1.5362319 | 1 |
| 596 | 1 | 0.4922861 | 0.7464716 | | 1 | 1 | 2.4070044 |
| 597 | 1 | 1 | 2.2405223 | | 1.4097324 | 1 | 5.1924648 |
| 598 | 1.4670679 | 2.3664486 | 1.6155651 | | 1 | 1.6004977 | 1.439734 |
| 599 | 1.4377035 | 0.6214809 | 1 | | 1 | 1 | 1 |
| 600 | 13.467123 | 4.5645147 | 11.885276 | | 0.3546965 | 1 | 1 |
| 601 | 0.6249588 | 0.3865708 | 0.5669759 | | 1.5468519 | 1 | 1000 |
| 602 | 1.3761206 | 4.1201869 | 1.7877734 | | 1 | 1 | 2.5081808 |
| 603 | 2.388031 | 1.7790007 | 1.2184707 | | 1 | 2.4355764 | 1 |
| 604 | 1 | 1.1947735 | 2.6763257 | | 2.0365992 | 0.8869082 | 5.9887023 |
| 605 | 0.6405284 | 0.4733214 | 1 | | 1 | 0.6465963 | 1 |
| 606 | 3.3571481 | 2.2815385 | 1.6918794 | | 1.6743421 | 1.4743227 | 1.3298604 |
| 607 | 1.4870925 | 2.7801294 | 3.4496167 | | 1.5086688 | 2.0703444 | 1 |
| 608 | 2.1582568 | 0.3939899 | 1 | | 1 | 1.8040533 | 1.6800293 |
| 609 | 1 | 1.6469159 | 2.6755515 | | 1 | 0.4664011 | 0.265089 |
| 610 | 0.721404 | 0.8233717 | 0.5073933 | | 0.5938018 | 0.7445702 | 1 |
| 611 | 0.4201672 | 0.5099065 | 0.4362122 | | 1 | 0.3265254 | 0.4914955 |
| 612 | 0.7035018 | 0.542624 | 1 | | 1.3129123 | 0.608951 | 1.2422818 |
| 613 | 0.6456145 | 0.4653271 | 0.7555414 | | 1.140407 | 1 | 1 |
| 614 | 1 | 0.4098347 | 0.5138018 | | 0.8257001 | 1 | 2.7977481 |
| 615 | 1 | 0.5625521 | 0.7515588 | | 1 | 0.6592751 | 1 |
| 616 | 3.0845073 | 2.2843566 | 1.2990034 | | 1.9998372 | 1.7182751 | 1 |
| 617 | 0.2014344 | 3.2781165 | 0.2918571 | | 1.2700615 | 0.2202491 | 0.6297775 |
| 618 | 0.2352995 | 3.1695902 | 0.3142381 | | 1.1587178 | 0.2775851 | 0.645692 |
| 619 | 0.6164148 | 0.5236449 | 0.6664541 | | 0.6044249 | 0.4846456 | 0.4338658 |
| 620 | 0.4412712 | 0.5469159 | 1.4035455 | | 1 | 0.5752398 | 0.1676002 |
| 621 | 0.2850269 | 0.4114306 | 0.2483679 | | 1 | 0.5223134 | 1 |
| 622 | 1 | 2.8023724 | 2.2044128 | | 0.5560085 | 1.8790879 | 1 |
| 623 | 1.0789546 | 1 | 3.2319064 | | 2.1916606 | 2.4548358 | 0.8067178 |
| 624 | 2.7694574 | 0.3656722 | 0.3886252 | | 1.6949621 | 1 | 1 |
| 625 | 1.5563595 | 1 | 2.1500967 | | 1 | 1 | 1 |
| 626 | 0.5895935 | 0.5205176 | 0.4552166 | | 0.6915905 | 0.733083 | 0.2287961 |
| 627 | 0.571243 | 0.3683178 | 0.4601706 | | 1.780938 | 0.4422058 | 1.5308545 |
| 628 | 1 | 1 | 0.5179846 | | 1.6196262 | 0.4649607 | 1 |
| 629 | 3.091606 | 1.9924371 | 1.5468076 | | 1.9828026 | 2.0628761 | 1 |
| 630 | 2.9293973 | 2.9077858 | 7.9456382 | | 2.9003126 | 1 | 1.5778098 |
| 631 | 0.216949 | 0.3595471 | 0.1729303 | | 0.5673263 | 0.8741713 | 1.3489652 |
| 632 | 0.3208588 | 0.4550539 | 0.2605444 | | 0.7698385 | 1 | 1 |
| 633 | 2.0500842 | 2.5335514 | 1.4640839 | | 1 | 2.1614307 | 1 |
| 634 | 1.5674558 | 2.3964845 | 1 | | 1.1658621 | 2.1454265 | 1.528283 |
| 635 | 0.6523473 | 0.4190295 | 0.4754385 | | 1.9491181 | 0.5051338 | 1.5928388 |
| 636 | 2.5542464 | 1 | 0.6060023 | | 0.7619153 | 1 | 1 |
| 637 | 1.9383622 | 2.0944716 | 1.8699989 | | 1.2655992 | 1.8709449 | 1.736737 |

Table 4

| SEQ ID | Patient ID | | | | | | | |
|--------|------------|-----------|-----------|-----------|-----|-----------|-----------|-----------|
| | NO | 888 | 889 | 890 | 891 | 892 | 893 | 989 |
| 638 | | 0.4325533 | 0.5068368 | 0.5396646 | | 0.5855328 | 1 | 1 |
| 639 | | 1.3304914 | 3.2764198 | 2.2090193 | | 1.3365341 | 1.553918 | 1.9955184 |
| 640 | | 1.1101669 | 3.2923293 | 3.5635795 | | 1.4263696 | 1.4592415 | 1 |
| 641 | | 0.2461762 | 0.4065996 | 0.5391102 | | 0.5234787 | 0.5824607 | 0.4108431 |
| 642 | | 0.7288137 | 0.4462545 | 0.7736221 | | 1 | 0.6359369 | 1.479302 |
| 643 | | 1 | 0.4769375 | 1 | | 1.190498 | 0.5641198 | 1 |
| 644 | | 1 | 2.1935658 | 4.2721395 | | 1 | 1 | 1 |
| 645 | | 1 | 2.7991517 | 2.0423871 | | 0.5260025 | 1.8661783 | 1 |
| 646 | | 1 | 0.5210784 | 0.6778459 | | 1 | 0.6351563 | 1 |
| 647 | | 1 | 0.5669303 | 1 | | 1 | 1 | 1 |
| 648 | | 1.906784 | 1 | 2.3645224 | | 1 | 1 | 3.2098891 |
| 649 | | 1 | 4.3294177 | 2.6868207 | | 0.6976025 | 1.5274138 | 0.8214557 |
| 650 | | 0.4536939 | 2.6772682 | 1.6756353 | | 0.7053597 | 1.6109386 | 0.6873101 |
| 651 | | 1.622928 | 1 | 1.8663202 | | 1 | 1.7784618 | 2.0360933 |
| 652 | | 1.7724395 | 1.4033573 | 2.2443277 | | 1.3971323 | 1 | 1 |
| 653 | | 1.7432764 | 1.2447448 | 0.4997415 | | 0.8799513 | 0.6460709 | 1 |
| 654 | | 0.290854 | 0.4900719 | 0.2070312 | | 0.3403712 | 0.1101365 | 0.4470026 |
| 655 | | 3.1321947 | 2.0090798 | 0.331879 | | 0.8337018 | 1.7633571 | 2.1882156 |
| 656 | | 0.2241758 | 0.3076348 | 0.7306541 | | 0.3327025 | 0.3079837 | 0.2437038 |
| 657 | | 0.3817922 | 0.3597915 | 1 | | 0.4633597 | 1 | 0.7653181 |
| 658 | | 1.674238 | 1.7001941 | 1.8452839 | | 1 | 1.5233094 | 1 |
| 659 | | 0.1780984 | 0.3612221 | 0.1656097 | | 0.6347994 | 0.2640775 | 0.2948439 |
| 660 | | 1 | 1 | 1.4867938 | | 1 | 1 | 3.3378485 |
| 661 | | 1 | 0.4634867 | 0.5282647 | | 1 | 0.8537483 | 1.2370902 |
| 662 | | 1 | 0.261064 | 1 | | 1 | 1 | 1 |
| 663 | | 0.2979527 | 0.3847017 | 0.4932656 | | 0.3745262 | 1 | 0.3129904 |
| 664 | | 2.7726682 | 2.2270669 | 2.2889671 | | 1.8737849 | 2.1536479 | 1.7843109 |
| 665 | | 1.9882725 | 1 | 4.006591 | | 1 | 1 | 1.4019975 |
| 666 | | 1.5570273 | 1.7969806 | 1.6486071 | | 1.5927021 | 1 | 1.5663348 |
| 667 | | 5.1884354 | 8.2847304 | 7.9661673 | | 1.392952 | 7.974688 | 6.1719138 |
| 668 | | 1.3013831 | 2.1216607 | 3.1126794 | | 1.1415477 | 2.8653777 | 0.7905121 |
| 669 | | 1 | 1.6491948 | 2.054123 | | 1 | 1 | 1.4805878 |
| 670 | | 1 | 1 | 2.9485866 | | 1.9310229 | 1 | 1 |
| 671 | | 0.3826979 | 0.4481021 | 1 | | 1 | 1 | 1.3111156 |
| 672 | | 1.9687969 | 2.2986269 | 3.5723534 | | 1.2940335 | 1.4070853 | 1.4149888 |
| 673 | | 1.0763932 | 1.2285478 | 1.5604422 | | 1.3676321 | 1.2404969 | 1 |
| 674 | | 1.6654927 | 0.7712868 | 1 | | 1 | 1.7621178 | 1.3396372 |
| 675 | | 1 | 0.5576779 | 2.3619563 | | 1.9293184 | 1000 | 1 |
| 676 | | 2.192497 | 1.4188785 | 1 | | 0.8790156 | 1 | 1 |
| 677 | | 1 | 1.9761035 | 1.8672621 | | 2.0597598 | 1 | 1 |
| 678 | | 1 | 0.5190798 | 0.7090418 | | 1 | 0.6576324 | 1 |
| 679 | | 1.4001336 | 0.7108339 | 1 | | 1 | 2.1232763 | 0.8663367 |
| 680 | | 1 | 2.1553127 | 6.0728542 | | 1 | 1 | 1 |
| 681 | | 1 | 0.6051546 | 2.5626031 | | 1 | 1 | 1 |
| 682 | | 0.147435 | 0.3133214 | 0.1932676 | | 3.9559342 | 0.0466735 | 0.1185708 |
| 683 | | 1.4284094 | 2.3956937 | 2.9543549 | | 1 | 1.7850846 | 1 |
| 684 | | 0.3050331 | 0.6021711 | 0.3807799 | | 0.5717861 | 0.3074492 | 0.3088177 |
| 685 | | 0.5180943 | 0.6561179 | 0.640956 | | 0.5186908 | 0.4565949 | 0.2459843 |
| 686 | | 1 | 0.4509346 | 0.2506163 | | 0.7303384 | 0.7858564 | 0.7252284 |

Table 4

| SEQ ID | Patient ID | | | | | | |
|--------|------------|-----------|-----------|-----------|-----------|-----------|-----------|
| NO | 888 | 889 | 890 | 891 | 892 | 893 | 989 |
| 687 | 1 | 0.6139037 | 0.1429212 | | 0.6625744 | 0.4870279 | 0.6801048 |
| 688 | 0.7084324 | 0.4741265 | 0.5165852 | | 0.813004 | 0.8045647 | 1.6978968 |
| 689 | 0.6992572 | 0.461977 | 0.5098334 | | 2.9721019 | 0.3822654 | 1.2174396 |
| 690 | 4.0679772 | 1 | 1 | | 1 | 1 | 1 |
| 691 | 1 | 1 | 1 | | 1 | 1 | 1 |
| 692 | 1 | 1.894982 | 2.1114458 | | 0.9059071 | 1 | 1.2971822 |
| 693 | 1 | 0.5636592 | 0.7884009 | | 1.1765519 | 0.6924752 | 1 |
| 694 | 1.7276245 | 1.3311143 | 1.2831679 | | 1.1053829 | 3.4191574 | 0.9070935 |
| 695 | 1 | 1.378138 | 1.1881078 | | 0.7254534 | 1.9160908 | 1.4942704 |
| 696 | 0.0422537 | 0.303271 | 0.023253 | | 0.7521434 | 0.1177467 | 0.4323496 |
| 697 | 5.4768927 | 3.2233357 | 2.8159574 | | 1.7534775 | 1 | 3.105935 |
| 698 | 1.116735 | 3.999583 | 2.410428 | | 1.1429439 | 2.1240372 | 1.2156322 |
| 699 | 1 | 0.5443206 | 0.8628466 | | 1.1707732 | 0.668791 | 1.2511731 |
| 700 | 1 | 1 | 1.9908453 | | 1 | 1 | 2.7084834 |
| 701 | 1 | 0.5174335 | 0.5778499 | | 1 | 0.6856222 | 1.6758808 |
| 702 | 1.4068663 | 1.3844357 | 1.8896736 | | 0.8904505 | 1.8683711 | 1 |
| 703 | 1 | 0.5682674 | 0.9247982 | | 1 | 1 | 0.5778368 |
| 704 | 3.096189 | 1.9093386 | 1.2936666 | | 1.7927974 | 1 | 1 |
| 705 | 1 | 0.5634723 | 0.4422501 | | 1.4608505 | 0.4841561 | 1.4166627 |
| 706 | 0.7234623 | 0.4895543 | 0.7940011 | | 1.1478473 | 1 | 1 |
| 707 | 0.5896118 | 0.4956722 | 0.5919297 | | 1 | 0.6116017 | 1.6399639 |
| 708 | 1 | 0.5458375 | 1 | | 1 | 1 | 0.1307493 |
| 709 | 3.2202514 | 3.030683 | 1.4513343 | | 1.4325332 | 2.2321809 | 1 |
| 710 | 1.7922354 | 5.3867721 | 2.595865 | | 1.4060742 | 1.7368609 | 2.0451544 |
| 711 | 2.4955633 | 1 | 1.8772097 | | 1 | 2.0659486 | 1.7394905 |
| 712 | 1 | 1 | 1 | | 1 | 1.6906918 | 2.7147789 |
| 713 | 1 | 1.4365277 | 1 | | 1 | 3.2445665 | 4.2499881 |
| 714 | 1 | 1 | 1 | | 1 | 1 | 2.4520674 |
| 715 | 0.6570676 | 0.4216247 | 0.7434044 | | 1 | 1 | 1 |
| 716 | 1 | 0.3446729 | 0.5566166 | | 0.6041786 | 1 | 1.5351364 |
| 717 | 0.6447919 | 0.513685 | 0.5491483 | 0.5601923 | 1 | 0.6128609 | 0.8047289 |
| 718 | 1 | 3.2485642 | 1 | 1.5483291 | 2.1704507 | 1 | 1 |
| 719 | 1 | 7.6593571 | 11.467182 | 5.4516677 | 4.9004218 | 1 | 5.4536463 |
| 720 | 1 | 7.3999718 | 10.671723 | 4.8629477 | 1 | 4.9667129 | 5.8975107 |
| 721 | 2.5674408 | 3.2393424 | 2.5840805 | 2.4443521 | 1 | 1 | 1 |
| 722 | 4.52033 | 2.7156245 | 1.6790953 | 1.4625709 | 1.3000343 | 2.2148901 | 0.8187537 |
| 723 | 1 | 1 | 1.7233221 | 2.2051154 | 1.2460216 | 1 | 1.127072 |
| 724 | 0.8397477 | 2.1760012 | 2.0324579 | 1.3762791 | 1 | 1.6983555 | 1 |
| 725 | 0.2868833 | 0.4298348 | 0.3412235 | 0.1349987 | 0.8802035 | 0.5294052 | 0.6932498 |
| 726 | 1.3654236 | 6.117839 | 1 | 1.9858256 | 2.6032965 | 0.4570975 | 2.8844553 |
| 727 | 2.5021312 | 1.79637 | 2.1469776 | 1 | 1.7351224 | 1.8182422 | 1 |
| 728 | 0.3639739 | 1 | 0.3977923 | 1 | 0.758126 | 1 | 1.2870436 |
| 729 | 0.4125142 | 0.5664121 | 0.3759837 | 1 | 1 | 1 | 1 |
| 730 | 0.5943868 | 0.8325407 | 0.3752496 | 0.6728222 | 0.84208 | 0.7595605 | 1 |
| 731 | 1 | 1.3533646 | 0.4517345 | 0.316353 | 1 | 1 | 1.792761 |
| 732 | 1.384351 | 2.2697078 | 1.9722735 | 1 | 1.9989692 | 1.4630403 | 1.7016919 |
| 733 | 3.9442037 | 5.2038166 | 1 | 0.3622809 | 5.9814239 | 3.8891054 | 0.1984059 |
| 734 | 1.9101674 | 4.3206158 | 1.4246771 | 1.5645218 | 1.8886033 | 2.6476495 | 1 |
| 735 | 1 | 1 | 0.2928075 | 0.6389756 | 1 | 1 | 0.63306 |

Table 4

| SEQ ID NO | Patient ID | | | | | | |
|--------------|------------|-----------|-----------|-----------|-----------|-----------|-----------|
| | 888 | 889 | 890 | 891 | 892 | 893 | 989 |
| 736 | 1 | 2.153255 | 1 | 1.8584024 | 1 | 1.5838554 | 1 |
| 737 | 0.4286467 | 1 | 8.0441057 | 0.3354984 | 1.6392671 | 0.328566 | 0.4109232 |
| 738 | 2.7088516 | 3.7388562 | 2.9237713 | 2.4329819 | 1.9724308 | 2.580984 | 1 |
| 739 | 1 | 1 | 0.3820934 | 0.4565823 | 0.4977017 | 0.3857373 | 0.3863574 |
| 740 | 1.7062956 | 1 | 1 | 2.1193385 | 1 | 1 | 1 |
| 741 | 1.4697845 | 2.6745062 | 2.2331521 | 2.1881004 | 1.5394473 | 1.9996035 | 2.8574794 |
| 742 | 2.592985 | 2.6560286 | 1 | 1 | 2.126711 | 1.8762757 | 1 |
| 743 | 0.1370275 | 0.1391389 | 0.001 | 0.1989552 | 0.1444923 | 0.3368089 | 1 |
| 744 | 0.7028761 | 2.7297511 | 2.2484876 | 1.4146899 | 0.890635 | 1.7891016 | 1.2068691 |
| 745 | 2.2043403 | 2.9030337 | 2.080224 | 1.1664712 | 1.3419024 | 1.7114187 | 1.686995 |
| 746 | 0.0824999 | 0.0420767 | 0.0185014 | 0.0492952 | 3.4731888 | 0.00855 | 0.0651657 |
| 747 | 1 | 4.3273777 | 2.1476007 | 2.0226296 | 2.1306463 | 1.7641205 | 1 |
| 748 | 0.5825283 | 1 | 0.2161041 | 0.394937 | 0.3506192 | 0.6642797 | 0.7636327 |
| 749 | 0.0696556 | 0.0596447 | 0.0093281 | 0.0264401 | 0.0835938 | 0.1127106 | 1 |
| 750 | 0.2561481 | 0.3669841 | 0.1842876 | 0.2074349 | 0.5358576 | 0.3379823 | 1 |
| 751 | 1.3150937 | 5.4450296 | 2.9384 | 1.9588859 | 1.5781426 | 1.2504186 | 1.4325869 |
| 752 | 0.7698541 | 1 | 11.873833 | 1 | 1.2240357 | 0.0787569 | 0.2820307 |
| 753 | 4.8388213 | 7.2339229 | 4.0864661 | 3.5201157 | 1 | 3.0983829 | 1.462362 |
| 754 | 0.7450677 | 0.6662533 | 0.7626273 | 0.6313653 | 1.0312305 | 0.6312448 | 1 |
| 755 | 0.1246178 | 0.0662982 | 0.0405532 | 0.0771275 | 3.9627416 | 0.0716169 | 0.1473958 |
| 756 | 1 | 1 | 14.159535 | 1 | 1 | 0.0605957 | 0.1485075 |
| 757 | 2.3982885 | 1.506038 | 2.4416052 | 0.5876234 | 2.4916821 | 1 | 1.2898492 |
| 758 | 1 | 3.0636123 | 1.6446132 | 1.4215252 | 1.1158852 | 1.6547725 | 1 |
| 759 | 1 | 1 | 1 | 1 | 0.5904901 | 1.445683 | 0.7427819 |
| 760 | 2.2120159 | 4.0171394 | 1.6866348 | 1.5310061 | 1.6904518 | 3.0361901 | 0.7372785 |
| 761 | 1 | 1 | 1.1764532 | 1.2649135 | 1.8725606 | 1.9425248 | 1 |
| 762 | 2.805985 | 5.2402308 | 2.2727273 | 5.4868288 | 0.732034 | 3.9040107 | 1.367824 |
| 763 | 0.5356195 | 1 | 0.3919496 | 0.3466968 | 0.5004055 | 0.3629055 | 0.3508539 |
| 764 | 2.5509026 | 1 | 3.6484434 | 2.1467879 | 0.7071699 | 1.3174576 | 1.4138188 |
| 765 | 1 | 1 | 3.1987952 | 2.2229568 | 1 | 2.2815523 | 1 |
| 766 | 1.9163298 | 2.2470065 | 1 | 1 | 1.4614465 | 1.698621 | 1 |
| 767 | 2.7282409 | 1 | 1 | 1.1470856 | 1.4454102 | 2.1243141 | 1.5216328 |
| 768 | 1.9951998 | 1.8872424 | 1.1885849 | 1.1639714 | 1.2630705 | 1.9076805 | 1 |
| 769 | 2.1663371 | 2.146889 | 1.687481 | 1.5768552 | 1 | 1.9559878 | 0.732656 |
| 770 | 0.5692926 | 1 | 0.2622043 | 0.6679658 | 1.5910515 | 0.5294611 | 1.1137432 |
| 771 | 1.5110077 | 1 | 2.1536636 | 1 | 1 | 1 | 1.3626611 |
| 772 | 1 | 2.294629 | 1 | 1.7521961 | 2.1565494 | 1 | 1 |
| 773 | 0.5740439 | 1 | 0.4357627 | 0.7136576 | 1.7173534 | 1 | 2.0098754 |
| 774 | 0.2420268 | 1 | 0.6045665 | 0.3508554 | 1.4238812 | 0.560574 | 0.6333939 |
| 775 | 1 | 5.7609365 | 3.4404746 | 0.4749892 | 1.3063158 | 1 | 1.6691206 |
| 776 | 3.072719 | 2.1418998 | 2.1104822 | 1.603024 | 1.8470016 | 2.0487437 | 1 |
| 777 | 0.8075666 | 0.5663006 | 0.726301 | 0.6926895 | 1 | 0.7113576 | 1 |
| 778 | 1 | 1 | 2.91387 | 1.2741577 | 3.2710082 | 1.3444366 | 1 |
| 779 | 1.4050397 | 2.3597035 | 1.6057838 | 1 | 2.1585347 | 1 | 1.7754164 |
| 780 | 0.1583806 | 0.2155747 | 0.066933 | 0.1405787 | 0.3607895 | 0.352557 | 0.1141549 |
| 781 | 4.0568503 | 4.7869707 | 2.8956262 | 1.5281896 | 1.7713974 | 2.5268633 | 1.9390626 |
| 782 | 0.104628 | 0.1174322 | 0.0315318 | 0.0656512 | 5.9066322 | 0.0267921 | 0.1249605 |
| 783 | 1.7319787 | 6.8337192 | 3.2972876 | 3.3898224 | 0.8631307 | 2.4123247 | 1.3542481 |
| 784 | 3.9482894 | 2.2818831 | 0.5351103 | 2.0746291 | 1.9099452 | 2.2153416 | 1 |

Table 4

| SEQ ID | Patient ID | | | | | | |
|--------|------------|-----------|-----------|-----------|-----------|-----------|-----------|
| | 888 | 889 | 890 | 891 | 892 | 893 | 989 |
| 785 | 0.1002438 | 0.3587594 | 0.0541177 | 0.1405289 | 0.2756558 | 0.3277154 | 0.1690058 |
| 786 | 1.5373148 | 2.1403694 | 2.4903321 | 1.382152 | 1.4124344 | 1.5393515 | 2.1437155 |
| 787 | | 1 | 1.9943329 | 1.4096907 | 0.7976218 | 1.6749242 | 0.7328818 |
| 788 | 3.313817 | 1.83643 | 1 | 2.5766311 | 1.6044329 | 2.015678 | 1.7544367 |
| 789 | 0.0562489 | 0.0554182 | 0.0350409 | 0.1114747 | 0.0918472 | 0.1464644 | 1 |
| 790 | 1.3123016 | 1 | 1.6026537 | 1.8642904 | 1 | 1.473956 | 1.8837744 |
| 791 | 1.1542227 | 2.6818894 | 2.1219812 | 1.8150738 | 1.3933735 | 1.7477099 | 1 |
| 792 | 0.345132 | 0.7190151 | 0.6179712 | 0.4146334 | 1.3139424 | 0.7013628 | 0.7667752 |
| 793 | 0.1206709 | 0.3883802 | 0.3466585 | 0.2244352 | 0.5207056 | 0.2370381 | 0.5591098 |
| 794 | 3.279131 | 3.2186034 | 1.2589572 | 1.633621 | 1 | 2.0518388 | 1.0716968 |
| 795 | 0.4114474 | 0.5907111 | 0.3302099 | 1 | 0.8509875 | 1 | 1 |
| 796 | 0.5050011 | 1 | 0.2926118 | 0.5877212 | 1 | 0.5991184 | 1.8950756 |
| 797 | 1.9582129 | 1.7199973 | 1.7886377 | 1.4848383 | 1.8705235 | 1.8841384 | 1.3079436 |
| 798 | 1.6860735 | 4.7477695 | 4.3723545 | 1.1863239 | 1.3360079 | 2.5444178 | 1.218875 |
| 799 | 0.8748844 | 2.8573421 | 1 | 2.2003054 | 1.3054959 | 2.237083 | 1.387348 |
| 800 | 2.7968911 | 3.0101213 | 1.609206 | 1 | 2.0307943 | 1.517989 | 0.5699384 |
| 801 | 0.6752533 | 0.5044184 | 0.4603509 | 0.7823736 | 2.1973743 | 0.535788 | 1.8872034 |
| 802 | 2.4117563 | 5.6571236 | 2.2987086 | 3.0228178 | 2.3347425 | 2.0409828 | 1.3262483 |
| 803 | 0.6191022 | 1 | 0.244254 | 0.5149692 | 1.2935922 | 0.4600684 | 1 |
| 804 | 0.4182727 | 0.607375 | 1.3862964 | 0.6773012 | 1 | 0.5897104 | 0.1664448 |
| 805 | 2.1697798 | 2.3472223 | 1 | 1.6006257 | 1 | 2.0219922 | 1 |
| 806 | 3.3561257 | 4.2471038 | 2.5291451 | 2.2099465 | 1.4269851 | 2.0031671 | 2.1103359 |
| 807 | 1.5915015 | 1.5924405 | 1 | 1 | 1 | 1.6471632 | 1 |
| 808 | 1.9770032 | 1 | 1.670717 | 1.6792713 | 1.3649397 | 2.1642291 | 1.1597667 |
| 809 | 1.5344782 | 3.2485642 | 1.5060698 | 2.2221173 | 0.7271182 | 7.7233828 | 1.4256667 |
| 810 | 1.8924638 | 1.8313309 | 1.6012319 | 1.5830064 | 2.323176 | 1.7056873 | 1.4845911 |
| 811 | 3.2768992 | 2.461674 | 1.9677107 | 1.834026 | 1.3823804 | 2.0227451 | 1 |
| 812 | 3.5050353 | 3.0772505 | 1.9850241 | 1.6452688 | 1.9526301 | 2.1263927 | 1 |
| 813 | 1.3422828 | 1 | 1.714776 | 0.6969078 | 1.2197751 | 1.2898282 | 1 |
| 814 | 1.7743753 | 2.5466074 | 1.9944404 | 1 | 1.1884792 | 1.7524078 | 0.5393005 |
| 815 | 2.0669706 | 1.841086 | 1 | 1.1966985 | 1 | 1.7930875 | 1 |
| 816 | 0.731326 | 0.6076317 | 0.7791039 | 0.640378 | 1.2564621 | 0.7037857 | 1.1094445 |
| 817 | 0.7346208 | 0.6120287 | 0.7668953 | 0.6803422 | 1.1114132 | 0.7108456 | 1.1401555 |
| 818 | 0.7487021 | 0.6715998 | 0.7680096 | 0.6705157 | 1.0593461 | 0.8080851 | 1.1545344 |
| 819 | 0.5869914 | 0.4360132 | 0.5351219 | 0.5545999 | 1.2378409 | 0.5948219 | 0.8354915 |
| 820 | 0.7471305 | 0.4913959 | 0.7567313 | 0.5911013 | 1 | 1 | 1 |
| 821 | 2.9365965 | 4.3514755 | 2.4870678 | 0.9303766 | 1.453032 | 1.315809 | 1.624851 |
| 822 | 1 | 2.4822431 | 1 | 1.7190924 | 1 | 1 | 1 |
| 823 | 3.2159577 | 1.8599003 | 1.2094689 | 1.2842852 | 0.8820216 | 1.6684088 | 0.6805545 |
| 824 | 0.5846168 | 1 | 0.1914659 | 0.6694414 | 0.6513435 | 1 | 0.3086687 |
| 825 | 0.4201844 | 0.3437462 | 0.23857 | 0.2611558 | 1 | 0.4629532 | 0.3106966 |
| 826 | 2.4750519 | 4.4240447 | 2.8518799 | 1.9706949 | 1 | 2.4853446 | 3.103016 |
| 827 | 0.7612819 | 0.5943642 | 1 | 0.6282811 | 1 | 0.6441176 | 1 |
| 828 | 0.3826855 | 0.2681119 | 0.116677 | 0.1723772 | 0.6970897 | 1 | 0.8193897 |
| 829 | 2.8583276 | 2.3718484 | 0.6222061 | 1.4460669 | 1 | 1.786699 | 1 |
| 830 | 0.0301962 | 0.0465149 | 0.6933625 | 0.0685519 | 0.1756487 | 0.0320615 | 0.0253342 |
| 831 | 0.1629121 | 0.1498654 | 0.0730297 | 0.1128078 | 0.5138238 | 0.4537854 | 0.4167984 |
| 832 | 1.4995642 | 4.3467396 | 4.789497 | 1.6517732 | 1.7512392 | 3.054112 | 1 |
| 833 | 0.0251378 | 0.0259313 | 0.7100147 | 0.0650657 | 0.1454786 | 0.0268786 | 0.0177807 |

Table 4

| SEQ ID | Patient ID | | | | | | |
|--------|------------|-----------|-----------|-----------|-----------|-----------|-----------|
| NO | 888 | 889 | 890 | 891 | 892 | 893 | 989 |
| 834 | 0.8055115 | 0.5669571 | 1 | 0.6731622 | 1 | 0.6361914 | 1 |
| 835 | 0.4606255 | 0.6760332 | 1 | 0.5001806 | 0.3907733 | 0.7939047 | 0.2067753 |
| 836 | 0.7434207 | 0.6106459 | 0.7605423 | 0.7326665 | 1 | 0.7347768 | 1.171709 |
| 837 | 0.7882901 | 0.5985208 | 0.775235 | 0.7147557 | 1 | 0.7243997 | 1.0336512 |
| 838 | 1.5628168 | 5.4314541 | 3.2516469 | 1.1374583 | 1.370641 | 1.5832016 | 1 |
| 839 | 3.9551177 | 5.5304813 | 3.8913404 | 3.0544621 | 1 | 2.0168628 | 1.8802703 |
| 840 | 1.4420505 | 2.7924151 | 1.8432614 | 1.3021909 | 1.1911027 | 1.5158712 | 0.7176198 |
| 841 | 1.9684947 | 5.7288012 | 3.5243727 | 2.0838129 | 1 | 1.6504994 | 2.0308053 |
| 842 | 1.5064541 | 2.5633148 | 1.8207206 | 2.3443673 | 1.2720534 | 1.8008639 | 1.3642856 |
| 843 | 0.6878349 | 0.512641 | 0.1747942 | 1 | 0.6310686 | 1.5584871 | 0.5365476 |
| 844 | 3.2134723 | 1 | 2.5353844 | 1.8286114 | 2.0915969 | 1.6099043 | 1 |
| 845 | 3.5809096 | 5.4732186 | 3.1609453 | 1.4650897 | 1.8430685 | 1.4626136 | 2.5943749 |
| 846 | 0.1188101 | 0.4025146 | 0.2044848 | 0.3089639 | 0.3239537 | 0.3716675 | 0.2591183 |
| 847 | 2.061753 | 2.8267822 | 2.5243997 | 1.4537781 | 3.3455133 | 1 | 2.1955546 |
| 848 | 1 | 1 | 0.5553967 | 0.6782119 | 1.1441404 | 1 | 1.2633574 |
| 849 | 0.7613769 | 0.5619097 | 0.7757226 | 0.6375793 | 1 | 0.6684549 | 1 |
| 850 | 2.6380758 | 2.8362617 | 1.5236216 | 1.3312845 | 2.1290986 | 2.1346084 | 1.2095166 |
| 851 | 0.1745652 | 0.2812142 | 0.1428467 | 0.4059703 | 0.2690922 | 0.456694 | 0.1735056 |
| 852 | 1 | 3.6750192 | 1 | 1 | 1.9206979 | 1 | 1 |
| 853 | 2.6370112 | 2.9885981 | 3.7598561 | 1.6098951 | 2.283439 | 1.9119886 | 1.1237829 |
| 854 | 1.686913 | 4.3905415 | 3.103541 | 1.5137743 | 1.2143765 | 1.8076048 | 1 |
| 855 | 0.6806899 | 1 | 0.7862229 | 0.3680882 | 1 | 0.5593571 | 1 |
| 856 | 1.4677093 | 2.8669136 | 2.1851444 | 1.3515686 | 1.4844259 | 1.4972801 | 1.1984863 |
| 857 | 0.3547058 | 0.5281772 | 0.2376696 | 0.8185812 | 0.6094725 | 1 | 1 |
| 858 | 0.157185 | 0.1683742 | 1.0604432 | 0.1806913 | 0.3344212 | 0.0678642 | 0.2277738 |
| 859 | 0.4366321 | 0.4873617 | 0.4313403 | 0.5744013 | 0.5681561 | 0.7469674 | 0.40376 |
| 860 | 0.351688 | 0.563098 | 0.1005601 | 0.3987148 | 0.3977212 | 0.7062253 | 0.157835 |
| 861 | 1.8433466 | 2.9008081 | 1 | 1.6854442 | 1.3247131 | 1.8273138 | 1 |
| 862 | 1.8433466 | 2.9008081 | 1 | 1.6854442 | 1.3247131 | 1.8273138 | 1 |
| 863 | 0.7676383 | 0.6048811 | 0.7673168 | 0.6186479 | 1 | 0.6582832 | 1 |
| 864 | 0.7021855 | 0.4711489 | 0.354051 | 0.4687178 | 0.4128342 | 1 | 0.1887767 |
| 865 | 0.4712903 | 0.6729514 | 1.3974228 | 0.3449826 | 0.6827987 | 0.1673802 | 0.2113137 |
| 866 | 3.016087 | 2.9126783 | 2.7077623 | 1 | 1.7069198 | 2.0697528 | 1 |
| 867 | 3.3327717 | 5.4470924 | 2.4610945 | 1.3772724 | 1.7832282 | 1.8706764 | 1 |
| 868 | 1 | 0.6075136 | 1 | 0.5855912 | 1 | 0.6807539 | 1 |
| 869 | 2.3175982 | 3.4993539 | 2.8401677 | 2.0368073 | 0.8018972 | 2.4055597 | 1 |
| 870 | 4.1202557 | 1.9682608 | 1.452873 | 0.825076 | 1.239876 | 1.6510009 | 0.6620529 |
| 871 | 2.2496598 | 4.5336902 | 2.0222379 | 2.6477426 | 2.4038978 | 1.5485291 | 1.553694 |
| 872 | 2.3949607 | 2.0982641 | 1.3181397 | 1 | 1.5453505 | 1.9687466 | 1 |
| 873 | 3.6812039 | 4.572038 | 2.3020697 | 1.3610517 | 1.8187389 | 1.7694353 | 1 |
| 874 | 2.6619502 | 2.7341114 | 1.6516244 | 1.2347428 | 1.5918175 | 1.7546717 | 1 |
| 875 | 1 | 2.1529326 | 1 | 1.2474163 | 1.1911467 | 1.8536031 | 1.440686 |
| 876 | 2.538233 | 4.0694399 | 2.2213535 | 1.3639437 | 3.2893636 | 1.2724076 | 3.2187019 |
| 877 | 0.1165699 | 0.1128856 | 0.042537 | 0.0923475 | 0.0693156 | 0.1237358 | 0.077302 |
| 878 | 0.231865 | 0.7189001 | 0.6391401 | 0.3850789 | 1.5232457 | 0.4954521 | 0.5861999 |
| 879 | 3.4087762 | 2.1931946 | 1.7473312 | 1.576468 | 1.7640071 | 1.5863992 | 1.2192793 |
| 880 | 1 | 0.5027992 | 0.6990084 | 0.6816427 | 1 | 0.6409197 | 0.8542554 |
| 881 | 0.1417805 | 0.1712565 | 0.0779406 | 0.1254314 | 0.4207021 | 0.3157921 | 0.4033237 |
| 882 | 0.3536677 | 0.4263956 | 0.4067597 | 0.3625953 | 0.3889465 | 0.3145412 | 0.4185284 |

Table 4

| SEQ ID | Patient ID | | | | | | |
|--------|------------|-----------|-----------|-----------|-----------|-----------|-----------|
| NO | 888 | 889 | 890 | 891 | 892 | 893 | 989 |
| 883 | 0.0911027 | 0.1167505 | 0.0595386 | 0.0650773 | 0.4799011 | 0.2585406 | 0.3021193 |
| 884 | 5.5721458 | 4.2333486 | 1.3852064 | 1.3353379 | 1.6693354 | 2.834235 | 1.8871741 |
| 885 | 2.3767289 | 1 | 1 | 1 | 1 | 1 | 1 |
| 886 | 5.5670592 | 2.9133865 | 2.2051354 | 1.6751281 | 1.7696715 | 1.8305976 | 1 |
| 887 | 2.9234578 | 2.2331167 | 0.582178 | 1.5863851 | 0.7280254 | 2.088986 | 0.6470783 |
| 888 | 3.0251634 | 2.187389 | 1.7897192 | 1.1206691 | 2.2861917 | 1.9428142 | 1.872665 |
| 889 | 0.2637985 | 0.5079755 | 0.2074538 | 0.3645441 | 1 | 0.7996109 | 0.6165936 |
| 890 | 3.1959584 | 3.2966812 | 1 | 1.7083616 | 2.225819 | 1.8237866 | 1 |
| 891 | 0.905238 | 0.6058394 | 1 | 0.5726126 | 1 | 0.602886 | 1 |
| 892 | 0.8098831 | 0.5768795 | 1 | 0.6667863 | 1 | 0.641216 | 0.8207481 |
| 893 | 4.7951941 | 1 | 1.5193046 | 1.3412735 | 2.4426461 | 2.0727799 | 1 |
| 894 | 3.830894 | 1 | 1.5032856 | 1.6432777 | 1.941401 | 2.111927 | 0.8254789 |
| 895 | 4.1895085 | 2.1759353 | 2.6832159 | 1 | 0.4525339 | 1.2953639 | 0.5778805 |
| 896 | 3.3584667 | 2.2428704 | 2.9026685 | 1.789135 | 1 | 1 | 1 |
| 897 | 2.9405612 | 2.0534927 | 0.6084289 | 1.9949709 | 1.8978308 | 1.6101031 | 1.1969489 |
| 898 | 2.1038596 | 2.3952398 | 2.062482 | 1.1585666 | 1.5886603 | 1.8329137 | 1.3444465 |
| 899 | 3.417691 | 2.8686296 | 1.826473 | 1.3934717 | 1.5135559 | 1.7431769 | 1 |
| 900 | 4.498324 | 2.3124168 | 0.5987259 | 2.0035184 | 2.081066 | 2.0310002 | 1 |
| 901 | 3.5908898 | 1.803807 | 1 | 1 | 1.6088364 | 1 | 1 |
| 902 | 5.1905309 | 2.6009669 | 0.5624894 | 2.0764593 | 1.712223 | 2.5476992 | 1 |
| 903 | 0.7314956 | 0.5507602 | 1 | 0.615445 | 1 | 0.6239467 | 1 |
| 904 | 2.4652469 | 2.0035317 | 1.4770595 | 0.7603756 | 1.5360001 | 1.2521478 | 0.6844561 |
| 905 | 0.6890992 | 0.3998305 | 1 | 0.7987918 | 1.9203261 | 0.4982275 | 1.5827244 |
| 906 | 2.8698954 | 1.7605174 | 1 | 1.092307 | 1 | 1.7740095 | 1 |
| 907 | 0.1234888 | 0.1051191 | 0.0368863 | 0.4927494 | 0.1570459 | 0.6082181 | 0.7007308 |
| 908 | 0.4908483 | 0.5460663 | 0.455623 | 1 | 0.4724501 | 0.4385647 | 0.3952286 |
| 909 | 0.4373439 | 0.519682 | 0.3462773 | 0.4147284 | 0.7159286 | 0.6132183 | 0.5139199 |
| 910 | 0.2080666 | 0.3345482 | 0.1590702 | 0.2185655 | 0.3886945 | 0.3380928 | 0.2214833 |
| 911 | 0.2059979 | 0.3602606 | 0.1557804 | 0.2323095 | 0.828501 | 0.4243429 | 0.3945011 |
| 912 | 0.7665383 | 0.5555698 | 0.6196479 | 0.7185013 | 2.2253965 | 0.5673699 | 1.9417009 |
| 913 | 1 | 0.53119 | 1 | 0.6123865 | 1 | 0.702224 | 1 |
| 914 | 1 | 0.5703395 | 0.7476179 | 0.6655607 | 1 | 0.6759191 | 1 |
| 915 | 0.1087122 | 0.1120072 | 0.0258657 | 0.0688957 | 4.1578379 | 0.0158325 | 0.0617398 |
| 916 | 0.578414 | 1 | 0.2533778 | 0.6428441 | 1 | 1 | 1.2978259 |
| 917 | 2.5410533 | 2.1580382 | 0.5931967 | 1.6104826 | 0.7693655 | 2.0944893 | 0.7604444 |
| 918 | 0.7695303 | 0.547226 | 0.7453137 | 0.6247788 | 1 | 0.6291371 | 1 |
| 919 | 2.9138663 | 2.8872937 | 1 | 1 | 1 | 2.058187 | 1 |
| 920 | 2.6704203 | 3.7254872 | 7.623916 | 1.2766688 | 1 | 1.9612248 | 1.9715242 |
| 921 | 0.5008153 | 0.4993487 | 0.3603914 | 0.5721671 | 0.5572771 | 0.5172945 | 0.4337642 |
| 922 | 1.5578399 | 2.211614 | 2.6619803 | 1.356476 | 1.316948 | 1.6326023 | 1.8542864 |
| 923 | 1.9868363 | 2.9593186 | 2.0759638 | 1.3590346 | 1.3110437 | 1.2067652 | 1.3207609 |
| 924 | 0.099252 | 0.0839553 | 0.0255 | 0.0641077 | 5.1308785 | 0.0075504 | 0.058699 |
| 925 | 2.2272574 | 2.3168883 | 2.1390954 | 1.5293149 | 1.6757781 | 2.6419628 | 1.2921713 |
| 926 | 1 | 0.5638798 | 1 | 0.6383806 | 1 | 0.6963361 | 1 |
| 927 | 1.3313625 | 1.9186209 | 1.8690071 | 1.0998956 | 0.8616428 | 2.0500322 | 0.6077215 |
| 928 | 0.7219585 | 0.7118458 | 0.4319673 | 0.6966465 | 1 | 1.3443534 | 1.4986595 |
| 929 | 0.5763296 | 0.5253288 | 1 | 0.3719761 | 0.5637894 | 0.1074255 | 0.2270753 |
| 930 | 0.2180086 | 1 | 0.1053968 | 0.1905957 | 0.1421478 | 0.2832585 | 0.2043384 |
| 931 | 4.0279123 | 2.0294356 | 1.444309 | 1 | 1.3853207 | 1.9834816 | 0.6477383 |

Table 4

| SEQ ID | Patient ID | | | | | | | |
|--------|------------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|
| | NO | 888 | 889 | 890 | 891 | 892 | 893 | 989 |
| 932 | | 10.738105 | 8.3525881 | 7.5608183 | 5.260374 | 2.4875007 | 1.3517401 | 2.8940901 |
| 933 | | 2.5544642 | 1.6770646 | 1.9978867 | 1 | 2.1009335 | 2.3565181 | 0.4948475 |
| 934 | | 1.3267283 | 1.947361 | 1.5800002 | 1.6958882 | 1 | 1.5910063 | 0.9204595 |
| 935 | | 2.0250574 | 2.2988113 | 1 | 2.2452938 | 1 | 2.0886513 | 2.3367817 |
| 936 | | 0.5425769 | 0.3652186 | 0.5518965 | 0.3046831 | 0.7913471 | 1 | 0.7899655 |
| 937 | | 0.3584951 | 0.58936 | 0.3072268 | 0.4481155 | 0.4311311 | 0.3198561 | 0.5504854 |
| 938 | | 1.9301989 | 2.2551831 | 1.6916086 | 1 | 1.1316704 | 1.6163706 | 0.6192725 |
| 939 | | 3.9863133 | 2.1537066 | 1.4324821 | 0.8106588 | 1 | 1 | 0.7958325 |
| 940 | | 1 | 0.552207 | 0.7117904 | 0.6064901 | 1 | 0.6171775 | 0.607019 |
| 941 | | 2.9762467 | 1 | 1 | 0.8219736 | 1 | 3.4502818 | 0.8323612 |
| 942 | | 0.0853774 | 0.1055799 | 0.0327586 | 0.0607411 | 0.3409877 | 0.173054 | 0.1543255 |
| 943 | | 0.1724762 | 0.1909641 | 0.0778934 | 0.1524692 | 1 | 0.4059496 | 1 |
| 944 | | 2.3878339 | 1 | 1.9763295 | 1 | 1.9066977 | 1.7640251 | 0.4323804 |
| 945 | | 3.4619254 | 3.529072 | 1.8620934 | 1.1884204 | 2.2896012 | 1.8251141 | 0.8467891 |
| 946 | | 0.0894629 | 0.103994 | 0.0343398 | 0.0676643 | 5.4381167 | 0.0145847 | 0.0559104 |
| 947 | | 2.7423082 | 2.395559 | 1.5378069 | 1.9154188 | 1.5141067 | 1.9801681 | 1 |
| 948 | | 4.3583743 | 1 | 3.1831087 | 1.8168952 | 1.530931 | 3.8346611 | 1.5605903 |
| 949 | | 1.8428267 | 4.074745 | 2.7170086 | 2.0914665 | 1.8596799 | 2.2731197 | 0.7429002 |
| 950 | | 1 | 2.9660338 | 3.218692 | 1.504902 | 0.7342555 | 1.7442496 | 1 |
| 951 | | 1 | 1 | 1 | 0.5764364 | 1.2285718 | 0.5724566 | 1 |
| 952 | | 1 | 3.5375812 | 3.9175038 | 2.4715601 | 1 | 1.2800776 | 2.0380732 |
| 953 | | 2.5100954 | 2.574975 | 2.6996617 | 1.5316371 | 1.4417259 | 1.5844329 | 1.4626794 |
| 954 | | 0.1942322 | 1 | 0.6715284 | 0.4192769 | 0.457592 | 1 | 0.3223603 |
| 955 | | 0.3195411 | 0.5487632 | 0.3170222 | 0.2193382 | 0.3782425 | 0.6546935 | 0.1525627 |
| 956 | | 3.7178589 | 1 | 1.5072355 | 1 | 0.7460387 | 2.3120571 | 1 |
| 957 | | 2.5979926 | 2.3716919 | 1 | 1.4746361 | 1.5551717 | 1 | 1 |
| 958 | | 1.8252872 | 2.1357276 | 2.479235 | 1.4001309 | 2.9220651 | 1.7020357 | 0.8357563 |
| 959 | | 2.8133201 | 2.0407269 | 1.4185865 | 1.1634728 | 1.9959681 | 1.7535862 | 1.1049472 |
| 960 | | 2.7548611 | 2.3683323 | 2.0467936 | 0.8396057 | 1.3085294 | 1.9321046 | 1.3068023 |
| 961 | | 3.3160994 | 2.6181116 | 1 | 1.0796471 | 2.216675 | 2.0411106 | 1.2470956 |
| 962 | | 3.2777211 | 2.0692743 | 1.7365875 | 1.6163443 | 1.3045583 | 2.1030024 | 0.7729265 |
| 963 | | 2.9541406 | 1.724329 | 2.0612181 | 1.2729633 | 1.9810056 | 1.5840864 | 0.907004 |
| 964 | | 1 | 1.4967256 | 2.9548268 | 1 | 1 | 1 | 1.6989747 |
| 965 | | 2.6856297 | 1.4537182 | 2.0417672 | 1 | 1 | 1 | 1 |
| 966 | | 2.5775688 | 2.4668265 | 1.6348031 | 1.5167658 | 1 | 2.0992779 | 1 |
| 967 | | 1 | 0.7168999 | 0.3494497 | 0.6816624 | 1 | 1 | 0.5651218 |
| 968 | | 4.4102747 | 2.3210023 | 1 | 1.4444694 | 2.4222295 | 1.6785899 | 1 |
| 969 | | 1 | 0.5314885 | 1 | 0.6156435 | 1 | 0.6526813 | 1 |
| 970 | | 4.9131488 | 2.2701379 | 1.3394466 | 1.1973073 | 0.7715796 | 1.9282757 | 0.4626504 |
| 971 | | 1.5723799 | 3.3540509 | 2.1083175 | 1.2121264 | 1 | 1 | 1.7489222 |
| 972 | | 0.3275479 | 0.3006269 | 0.1282627 | 0.3253497 | 0.3538236 | 0.5745098 | 0.2642097 |
| 973 | | 0.6889383 | 0.4311986 | 0.4615915 | 0.7450906 | 1.5624637 | 0.6289672 | 1.4258008 |
| 974 | | 0.7937829 | 0.5683196 | 1 | 0.6178846 | 1 | 0.6582632 | 1 |
| 975 | | 0.6424237 | 0.4589434 | 0.478612 | 0.7028738 | 1.4350199 | 0.5736353 | 1.3064785 |
| 976 | | 0.5839749 | 0.512652 | 0.5934012 | 0.3980046 | 1.1382629 | 0.8297134 | 0.6533413 |
| 977 | | 4.6601079 | 3.5053258 | 2.4189379 | 1 | 2.2894793 | 3.6502281 | 1 |
| 978 | | 2.8720579 | 3.6880278 | 1.4809616 | 1.7071225 | 2.0671887 | 2.2080635 | 1 |
| 979 | | 1.9414643 | 1 | 2.198453 | 1.6677295 | 0.8800594 | 1.8202729 | 1 |
| 980 | | 2.7480749 | 2.3104845 | 2.3463038 | 0.8352457 | 2.9802066 | 1.7319698 | 0.7136428 |

Table 4

| SEQ ID | Patient ID | | | | | | |
|--------|------------|-----------|-----------|-----------|-----------|-----------|-----------|
| | 888 | 889 | 890 | 891 | 892 | 893 | 989 |
| 981 | 0.3758877 | 1 | 1 | 0.6226302 | 0.6021052 | 0.3799174 | 1.2128787 |
| 982 | 1.3533037 | 2.1449674 | 2.3628613 | 1.4525519 | 1.6004505 | 1.5131621 | 1.3598197 |
| 983 | 1 | 1 | 1 | 1 | 1 | 1 | 1 |
| 984 | 3.0262643 | 2.7136768 | 3.0435458 | 2.2929047 | 1 | 2.0448239 | 1.0485823 |
| 985 | 0.1418729 | 0.1766353 | 0.02701 | 0.0946345 | 5.7555789 | 0.0228109 | 0.1019596 |
| 986 | 2.0742822 | 1.9496319 | 1 | 1.4297574 | 0.8769295 | 1.9385392 | 1 |
| 987 | 0.1882339 | 0.4361428 | 0.2602292 | 0.3183542 | 0.6105892 | 0.3573692 | 0.2199667 |
| 988 | 1 | 0.5256361 | 1 | 0.6048328 | 1 | 0.6851467 | 1 |
| 989 | 0.5720623 | 0.7688272 | 0.1888444 | 0.5502178 | 1.1948439 | 0.4496942 | 1 |
| 990 | 2.0886323 | 2.8397348 | 2.6548175 | 1.7572545 | 1.197807 | 1.5768449 | 1.2403497 |
| 991 | 0.4703912 | 0.6049473 | 1 | 0.5679515 | 1 | 0.6875166 | 0.2870231 |
| 992 | 1 | 0.5730491 | 1 | 0.824835 | 1 | 0.5941713 | 1 |
| 993 | 0.6501074 | 1 | 0.4143187 | 0.5800828 | 1 | 1 | 1 |
| 994 | 2.7305211 | 1 | 1 | 1 | 3.5013847 | 1 | 2.5015983 |
| 995 | 0.6829106 | 0.5429239 | 1 | 0.6069593 | 1 | 0.6136396 | 1 |
| 996 | 2.2593835 | 1.4905193 | 1 | 1.1577687 | 1 | 1.5761968 | 1 |
| 997 | 1 | 4.1639575 | 2.7322574 | 1 | 1.4058749 | 1 | 0.1945563 |
| 998 | 1.7118194 | 2.8018835 | 1.9749581 | 1.5889196 | 0.5430262 | 1.599516 | 1.4684874 |
| 999 | 0.4749608 | 0.4632582 | 0.3432065 | 1 | 0.5600555 | 1 | 0.771339 |
| 1000 | 1 | 1 | 0.2439721 | 1 | 1 | 0.5429498 | 1 |
| 1001 | 0.0978471 | 0.319361 | 0.0447358 | 0.1316847 | 1 | 0.2322476 | 0.3772447 |
| 1002 | 0.4230095 | 0.4380509 | 0.3339052 | 0.3854636 | 0.8368288 | 0.5521374 | 0.4916564 |
| 1003 | 3.0535389 | 1.5921231 | 1 | 1.6920275 | 1.822543 | 1 | 1 |
| 1004 | 2.6787091 | 2.1095935 | 2.2476681 | 1.0357169 | 1.5493608 | 1.7254148 | 1 |
| 1005 | 1 | 0.532114 | 0.802213 | 0.6288406 | 1 | 0.7045767 | 1 |
| 1006 | 2.3376755 | 0.4291574 | 1 | 1 | 1.3292053 | 1 | 4.4824655 |
| 1007 | 0.1810548 | 0.1393925 | 0.1616938 | 0.2253592 | 0.2258908 | 0.2590893 | 0.0793701 |
| 1008 | 1 | 0.5684724 | 1 | 0.6123599 | 1 | 0.6357571 | 1 |
| 1009 | 1 | 0.5364779 | 0.8408164 | 0.6500944 | 1 | 0.6301527 | 0.8040887 |
| 1010 | 3.182062 | 2.8387256 | 2.3053688 | 1.6740161 | 1.1830604 | 1.879142 | 1.2535136 |
| 1011 | 0.8141357 | 0.5521137 | 0.8401291 | 0.6838145 | 1 | 0.6980659 | 1 |
| 1012 | 2.3570101 | 3.1998365 | 2.6647603 | 1.7040738 | 1.736992 | 1.3312588 | 1.2423951 |
| 1013 | 2.6543806 | 1.4923448 | 2.2246258 | 1.9751601 | 1.6741464 | 1.9989291 | 1.2433247 |
| 1014 | 0.7869813 | 0.4639488 | 0.705439 | 0.5570193 | 0.8330502 | 0.6769649 | 1 |
| 1015 | 3.351085 | 4.4153498 | 2.6058291 | 1 | 1.113092 | 1.7706848 | 1 |
| 1016 | 1 | 0.5894084 | 0.7719757 | 0.6421776 | 0.8086046 | 0.7244963 | 1 |
| 1017 | 2.2773262 | 1.5174503 | 1.8940752 | 1.8436031 | 1.7415898 | 1.3958777 | 1 |
| 1018 | 0.2968347 | 0.6444767 | 0.6806141 | 0.3787359 | 1.5385841 | 0.5322362 | 0.6354478 |
| 1019 | 2.4921789 | 3.8207231 | 2.4929329 | 1.2564504 | 2.7398551 | 1.7410355 | 1 |
| 1020 | 2.9584398 | 3.364883 | 5.7278217 | 2.5574067 | 1.9317749 | 1 | 1.7797667 |
| 1021 | 3.7919879 | 2.4675039 | 1.7542073 | 1.273767 | 1.5696333 | 1.7663192 | 0.8861453 |
| 1022 | 2.592838 | 1 | 2.7055842 | 3.3507332 | 1.4322468 | 2.1572824 | 1.3942689 |
| 1023 | 0.8168984 | 0.5247345 | 0.8126707 | 0.6746092 | 1 | 0.6642865 | 1 |
| 1024 | 0.6986034 | 1 | 0.3530241 | 0.5012494 | 0.5851608 | 0.4370739 | 0.8043553 |
| 1025 | 1 | 4.9102333 | 4.3751983 | 2.5417567 | 0.651867 | 1.3490269 | 1 |
| 1026 | 2.5488414 | 2.4948198 | 1 | 1.2858287 | 1 | 1.7255518 | 1 |
| 1027 | 3.6425069 | 4.1574558 | 3.2989046 | 1.3671126 | 1.2733471 | 2.0073613 | 1.5628825 |
| 1028 | 4.8002265 | 1 | 1.5109286 | 1.4261189 | 1.9093796 | 2.2690848 | 1 |
| 1029 | 1.6568185 | 3.955038 | 2.2118586 | 1.1615015 | 1 | 1.6283613 | 1 |

Table 4

| SEQ ID NO | Patient ID | | | | | | |
|--------------|------------|-----------|-----------|-----------|-----------|-----------|-----------|
| | 888 | 889 | 890 | 891 | 892 | 893 | 989 |
| 1030 | 0.4713631 | 0.284189 | 0.5801468 | 0.6680417 | 0.5743377 | 1 | 1 |
| 1031 | 3.8714257 | 5.5215611 | 2.8751497 | 1.3302061 | 1.6214998 | 2.0442468 | 1.7969572 |
| 1032 | 0.2553523 | 0.3213726 | 0.3440187 | 0.4386423 | 0.5367766 | 1 | 0.305825 |
| 1033 | 3.9530667 | 2.9238135 | 2.0524708 | 0.770658 | 1 | 2.0735051 | 1 |
| 1034 | 2.96208 | 2.6321065 | 1.5921022 | 0.7502603 | 1 | 2.1640136 | 0.4296832 |
| 1035 | 2.7378761 | 2.2424507 | 1.6041825 | 1.8649305 | 1.2545431 | 1.7442496 | 1 |
| 1036 | 0.3897155 | 1 | 0.3148397 | 1 | 0.4246517 | 1 | 0.3779758 |
| 1037 | 1 | 0.4231579 | 0.4832315 | 0.8600068 | 1.8966585 | 0.5342162 | 1.8976846 |
| 1038 | 1.6554093 | 2.9836367 | 2.4107421 | 1.1709008 | 1 | 1.2936417 | 1.145853 |
| 1039 | 2.6376194 | 4.9576392 | 4.0631303 | 1.795276 | 1.11979 | 2.1247295 | 1.4730527 |
| 1040 | 2.5268747 | 1 | 1.8427565 | 1.1945323 | 1 | 1.9624646 | 1 |
| 1041 | 1 | 1000 | 2.2697297 | 1.434288 | 1 | 1 | 1.7168901 |
| 1042 | 3.2764297 | 4.3007135 | 2.8438789 | 1 | 1.5310037 | 1.4817618 | 1.4842278 |
| 1043 | 3.5116283 | 2.1954719 | 1 | 1.8777258 | 1.953843 | 1.8173805 | 1 |
| 1044 | 2.1068152 | 2.0315001 | 1.1278078 | 1 | 1.1260675 | 0.8927623 | 1 |
| 1045 | 1 | 3.3878759 | 6.1505883 | 1.9866637 | 6.6525406 | 2.9056057 | 2.1335725 |
| 1046 | 0.2640444 | 0.2528168 | 0.1985242 | 0.3596019 | 0.3067003 | 0.4933375 | 0.1845611 |
| 1047 | 0.1116063 | 0.0942957 | 0.0306811 | 0.0990502 | 4.3618975 | 0.0160932 | 0.06705 |
| 1048 | 0.1119244 | 0.1467994 | 0.0964542 | 0.1356101 | 1.3259254 | 0.0671307 | 0.0675913 |
| 1049 | 1 | 3.9771369 | 4.2652446 | 1.6079887 | 0.8604815 | 0.6639482 | 2.5920465 |
| 1050 | 1 | 1 | 1 | 1 | 2.517511 | 1 | 1 |
| 1051 | 0.1097952 | 0.2513214 | 0.074933 | 0.2557638 | 0.3236147 | 0.2115532 | 0.163296 |
| 1052 | 1 | 0.5310645 | 0.7805174 | 0.590938 | 1 | 0.6503504 | 0.7610885 |
| 1053 | 0.747332 | 0.5910122 | 0.6396871 | 1 | 1.5896786 | 0.8140587 | 1.3377742 |
| 1054 | 0.4658565 | 0.459398 | 0.4649384 | 0.5340503 | 1 | 0.5935006 | 0.8602593 |
| 1055 | 1 | 0.5223895 | 0.573106 | 0.7080826 | 1.2317872 | 0.6688596 | 1 |
| 1056 | 0.6670063 | 0.4549441 | 0.4933281 | 0.7126564 | 1.660437 | 0.6634685 | 1.3460578 |
| 1057 | 1 | 0.5637206 | 0.6774364 | 0.6902721 | 1.187527 | 0.6421381 | 1 |
| 1058 | 1 | 1 | 0.4757748 | 0.709798 | 1 | 0.5960564 | 1.5762459 |
| 1059 | 3.922051 | 1.9620831 | 2.3198234 | 1.8992415 | 2.3148358 | 2.270191 | 0.6282695 |
| 1060 | 0.3692795 | 0.3563993 | 0.2791135 | 0.3638134 | 0.5022981 | 0.6923648 | 0.4585197 |
| 1061 | 1.2880767 | 1.7250738 | 1.8350791 | 1.1315705 | 0.7910073 | 1.9479808 | 0.7577745 |
| 1062 | 1 | 1.1177562 | 2.2921577 | 1.6218389 | 2.7872288 | 1.384318 | 1 |
| 1063 | 1.274616 | 2.3327512 | 2.3352709 | 1.5073435 | 0.6301651 | 1.6735053 | 1 |
| 1064 | 4.6219643 | 2.4548652 | 2.3852538 | 1.5644525 | 1.8285903 | 2.0532605 | 0.8643911 |
| 1065 | 3.3393414 | 4.3422763 | 2.6053703 | 1.7677691 | 1.8280978 | 1.7068484 | 2.3287961 |
| 1066 | 1 | 0.5546653 | 1 | 0.6653851 | 1 | 0.6656022 | 1 |
| 1067 | 1 | 3.9013798 | 7.2397738 | 4.3857143 | 6.6649181 | 4.4147812 | 4.3741661 |
| 1068 | 5.0007061 | 3.3803887 | 2.5302694 | 1.7604967 | 2.008496 | 1.9744707 | 1 |
| 1069 | 0.8093027 | 0.6942945 | 0.6059328 | 0.5498022 | 1 | 0.6119232 | 0.5075675 |
| 1070 | 1.6709821 | 2.870233 | 2.0400785 | 1.556109 | 0.8094624 | 1.8788171 | 0.6599816 |
| 1071 | 0.7358736 | 0.4743321 | 0.4531564 | 0.8018852 | 1.5509074 | 0.5101698 | 1.4320457 |
| 1072 | 1 | 2.4139796 | 4.123355 | 1.9623155 | 1.1930311 | 1.7052857 | 1 |
| 1073 | 6.8175523 | 2.1530616 | 2.501529 | 1.9765424 | 1.8729685 | 1.5488234 | 1 |
| 1074 | 0.3234721 | 0.5212419 | 0.862374 | 0.613099 | 0.8175913 | 1 | 0.4469303 |
| 1075 | 0.0427225 | 0.0681994 | 0.0273349 | 0.0204776 | 0.2650957 | 0.0879952 | 0.2601291 |
| 1076 | 1 | 1 | 1.5986374 | 1.7811018 | 1 | 1 | 1.4858277 |
| 1077 | 5.6321831 | 3.947654 | 2.9153624 | 1.5599593 | 1 | 1.7981816 | 1 |
| 1078 | 3.7155937 | 2.4397029 | 1.6959897 | 1.3238217 | 1.6807797 | 1.874172 | 1.1402412 |

Table 4

| SEQ ID | Patient ID | | | | | | |
|--------|------------|-----------|-----------|-----------|-----------|-----------|-----------|
| NO | 888 | 889 | 890 | 891 | 892 | 893 | 989 |
| 1079 | 1 | 1 | 1 | 1 | 2.3124697 | 1 | 1 |
| 1080 | 3.505304 | 3.4676214 | 1 | 1 | 2.8487375 | 1.7478036 | 1 |
| 1081 | 0.4155858 | 0.2362767 | 0.1788015 | 0.1708502 | 0.1242529 | 0.4659044 | 0.2651436 |
| 1082 | 2.5866794 | 2.3688785 | 1.5811143 | 1.4292365 | 1.6310361 | 2.2745473 | 1 |
| 1083 | 2.1515104 | 1.6422031 | 1.9379758 | 1.4623589 | 1.8719897 | 1.9633511 | 1 |
| 1084 | 1.8979609 | 2.7254047 | 3.6538479 | 1.9634068 | 1.6303762 | 1 | 1 |
| 1085 | 0.2077957 | 0.1195964 | 0.0620321 | 0.0977846 | 0.0809739 | 0.1506257 | 0.0740294 |
| 1086 | 2.7386138 | 2.9727795 | 2.5184715 | 1.1531552 | 1.2371521 | 2.2222891 | 2.7063811 |
| 1087 | 0.3395932 | 3.1668528 | 0.3097928 | 0.2653314 | 1.229462 | 0.2923548 | 0.721191 |
| 1088 | 0.4506812 | 0.4767258 | 0.2961236 | 0.9058603 | 0.6482234 | 1 | 1 |
| 1089 | 0.3761304 | 0.3473301 | 0.231845 | 0.2535414 | 0.6680074 | 0.5318627 | 0.3966528 |
| 1090 | 1.3388645 | 2.571567 | 3.1260922 | 1.8985776 | 1.4201962 | 1.34391 | 1.4210237 |
| 1091 | 0.3498293 | 1 | 0.6475692 | 0.4505171 | 1 | 0.5897637 | 0.3495919 |
| 1092 | 1.5065533 | 1.4874969 | 2.2244921 | 1.7835312 | 2.0166622 | 1.7303149 | 1.4274787 |
| 1093 | 1 | 2.1427936 | 1.2168878 | 2.0121395 | 1 | 2.2088116 | 1.5067387 |
| 1094 | 3.5807695 | 2.7867863 | 1.7848842 | 1 | 1.6808892 | 1.7096235 | 0.4887798 |
| 1095 | 1 | 0.5319092 | 0.85915 | 0.6676942 | 1 | 0.6971105 | 1 |
| 1096 | 3.0435826 | 1.9038858 | 1.6778769 | 1.1732549 | 1.2115358 | 2.1121323 | 1 |
| 1097 | 1 | 0.5002451 | 0.8387007 | 0.5992125 | 1.1165905 | 0.6373544 | 1 |
| 1098 | 2.6615629 | 2.4550328 | 2.0724172 | 1.6402239 | 1 | 1.4508306 | 1.5340255 |
| 1099 | 2.9579615 | 2.2358253 | 2.8415855 | 2.4188962 | 2.540223 | 2.3759275 | 0.7743575 |
| 1100 | 3.6613135 | 2.1474662 | 1 | 1.5210788 | 1.9747263 | 1.6156095 | 1 |
| 1101 | 1.9516538 | 2.2422408 | 3.3264881 | 1 | 1.2028458 | 2.3018528 | 1.2400454 |
| 1102 | 2.186636 | 1 | 2.2249603 | 1 | 1.3503471 | 1 | 2.6414355 |
| 1103 | 1.624224 | 2.2922877 | 1 | 2.4179851 | 1 | 4.8173409 | 1.7257569 |
| 1104 | 2.09533 | 3.4925537 | 2.2396407 | 1.2437469 | 1.1131304 | 1.3434115 | 1.4260019 |
| 1105 | 0.4404372 | 1 | 0.7386772 | 0.4545718 | 1 | 0.575047 | 0.4148484 |
| 1106 | 2.7034878 | 1.3958009 | 2.0792303 | 1.245546 | 1 | 1.6166511 | 1 |
| 1107 | 2.8683656 | 1 | 1 | 1 | 1 | 2.1174145 | 1 |
| 1108 | 1.423803 | 2.5587531 | 3.5104952 | 1.3600293 | 1 | 1.456861 | 1 |
| 1109 | 0.3723003 | 0.4031308 | 0.4289151 | 0.6637526 | 0.4468049 | 0.468294 | 0.3567018 |
| 1110 | 5.4023456 | 2.1226114 | 1.862234 | 1.6774761 | 1.4297696 | 1.8886689 | 0.8876692 |
| 1111 | 3.9835358 | 3.4514728 | 2.2656296 | 1.3266322 | 3.597297 | 1.7747822 | 2.2334745 |
| 1112 | 2.3177743 | 2.0331088 | 1 | 1.3906724 | 1 | 1 | 1 |
| 1113 | 3.2615937 | 2.455536 | 2.702225 | 2.8657819 | 1 | 2.2692427 | 1 |
| 1114 | 0.4604724 | 1 | 0.7832602 | 0.5457693 | 0.8845141 | 0.6562489 | 0.3577686 |
| 1115 | 1 | 0.4242843 | 1 | 1 | 1 | 1 | 3.7523975 |
| 1116 | 3.436823 | 3.3761025 | 1.8967454 | 1.728392 | 2.6949657 | 2.1769484 | 1 |
| 1117 | 1 | 0.537316 | 0.8432597 | 0.6540567 | 1.1398022 | 0.6810525 | 1 |
| 1118 | 0.3679457 | 0.6297366 | 0.2505798 | 0.4119796 | 0.4347282 | 0.6378284 | 0.1319164 |
| 1119 | 0.3053763 | 0.4726171 | 0.2042167 | 0.2521723 | 0.4747878 | 0.4171129 | 0.2228718 |
| 1120 | 5.4135352 | 2.0534341 | 1.4600684 | 0.9157998 | 1 | 1 | 0.6840046 |
| 1121 | 2.030902 | 1.7156053 | 1.6210153 | 1.5552178 | 1 | 1.8460971 | 1.7994096 |
| 1122 | 2.8814665 | 1 | 1 | 1 | 1 | 1 | 0.5533254 |
| 1123 | 3.997986 | 5.3963914 | 1.7643291 | 3.9983012 | 1.2333541 | 2.1425356 | 1 |
| 1124 | 5.9205176 | 2.3894282 | 2.6075738 | 1.9305537 | 1.4065343 | 1.4927547 | 1 |
| 1125 | 1 | 2.2539104 | 3.3308304 | 1.5096316 | 1.1460622 | 1.6909549 | 1 |
| 1126 | 4.3504978 | 4.5977696 | 2.7977515 | 1.0890387 | 1.7591943 | 1.6759145 | 1 |
| 1127 | 3.3932237 | 4.2761555 | 2.7372097 | 1.3026474 | 1.3038197 | 1.5559578 | 1 |

Table 4

| SEQ ID | Patient ID | | | | | | |
|--------|------------|-----------|-----------|-----------|-----------|-----------|-----------|
| NO | 888 | 889 | 890 | 891 | 892 | 893 | 989 |
| 1128 | 2.3135538 | 3.8199111 | 2.5527902 | 2.042877 | 0.7302102 | 1.9708297 | 1 |
| 1129 | 2.1130932 | 1 | 1.4801618 | 1 | 1 | 2.1757133 | 0.6256125 |
| 1130 | 9.1541997 | 4.7147643 | 1 | 3.3601409 | 3.4803125 | 1 | 4.0722463 |
| 1131 | 1.9211592 | 1.9649791 | 2.2573359 | 1.1960904 | 1.7084349 | 1.6030164 | 1.5092508 |
| 1132 | 1 | 0.5226972 | 1 | 0.5628582 | 1 | 0.5972578 | 1 |
| 1133 | 2.8222601 | 1.8205715 | 1 | 1.3070843 | 1.5011175 | 2.0480358 | 1 |
| 1134 | 1 | 3.1330396 | 1 | 1 | 2.2589203 | 1 | |
| 1135 | 2.5468544 | 2.2332554 | 2.2529374 | 1.4564769 | 2.2071902 | 1.7658407 | 0.7165389 |
| 1136 | 3.5530924 | 2.3659161 | 2.2475998 | 1 | 2.0753726 | 1.8678358 | 1 |
| 1137 | 2.0598031 | 1 | 2.8227247 | 1.8037603 | 2.6912538 | 1.705598 | 0.7736463 |
| 1138 | 2.7302766 | 3.2729673 | 2.2222875 | 1.4662763 | 1 | 2.1399335 | 1.8840962 |
| 1139 | 2.3044618 | 2.0404952 | 1.7208774 | 1.425054 | 1.5608184 | 1.712048 | 1 |
| 1140 | 2.0574867 | 1.7979424 | 4.2468852 | 2.2348473 | 1.9920525 | 1 | 1 |
| 1141 | 4.0676739 | 2.6210707 | 1 | 1.8408155 | 1.9363288 | 1.7751205 | 1 |
| 1142 | 3.59781 | 1.8252863 | 1 | 1 | 1 | 1.4068727 | 0.6484134 |
| 1143 | 0.7738332 | 0.5581968 | 0.5632944 | 0.8484026 | 1.3076935 | 0.551325 | 1.6529263 |
| 1144 | 1 | 0.5221733 | 0.5161132 | 1 | 1.6986907 | 0.6671143 | 1.7897719 |
| 1145 | 2.9790575 | 1.6965763 | 1 | 1 | 2.6407187 | 1 | 1 |
| 1146 | 2.020049 | 1.9077761 | 3.1469647 | 1 | 1 | 1.5351467 | 1.8102586 |
| 1147 | 2.6007994 | 2.4376348 | 1.6806588 | 1.4281669 | 1.8841608 | 2.1051075 | 0.8136134 |
| 1148 | 2.8114179 | 2.2103901 | 1 | 1 | 0.7638876 | 1.6136101 | 1 |
| 1149 | 1.6008315 | 2.1150552 | 1.9141634 | 1.3382991 | 1 | 1.3682227 | 1 |
| 1150 | 0.2726728 | 0.2769502 | 0.1747434 | 0.2597618 | 0.4269249 | 0.4794172 | 0.1780671 |
| 1151 | 5.2567473 | 2.1172353 | 1.3547983 | 1 | 0.7841676 | 1.9055616 | 0.3825014 |
| 1152 | 1 | 3.647424 | 1 | 4.9700852 | 4.8709915 | 3.7596929 | 5.3908715 |
| 1153 | 1 | 2.9422414 | 4.1684164 | 1.9515229 | 0.7982637 | 1 | 2.4158053 |
| 1154 | 2.3514965 | 1.6020218 | 1.4648374 | 1.2359964 | 1.4535561 | 1.7267401 | 1.320804 |
| 1155 | 3.5378395 | 1.8026762 | 2.4105065 | 1 | 3.9117754 | 1.8302379 | 1.2871119 |
| 1156 | 1 | 0.5271045 | 0.8190935 | 0.7371795 | 1 | 0.6839893 | 1 |
| 1157 | 2.7967201 | 1.6602556 | 2.046737 | 1.492307 | 1.8870833 | 2.0187989 | 2.0884986 |
| 1158 | 0.7239411 | 0.5465271 | 0.6415061 | 0.6297885 | 1.2102737 | 0.6379594 | 1 |
| 1159 | 0.5866526 | 0.5257207 | 0.5568722 | 0.5552847 | 1.2276829 | 0.6331207 | 1 |
| 1160 | 0.4851807 | 1 | 0.3028957 | 0.5769875 | 0.7128852 | 1 | 0.8056589 |
| 1161 | 0.7975268 | 0.5000051 | 0.398858 | 0.7359195 | 1.589855 | 0.4899709 | 1 |
| 1162 | 0.4591205 | 0.647635 | 0.6658424 | 0.4739308 | 1.3154569 | 0.6134722 | 0.7114286 |
| 1163 | 0.6640479 | 0.5729166 | 0.596549 | 0.5569974 | 1.2950732 | 0.7213538 | 1 |
| 1164 | 4.6686699 | 2.7402602 | 2.0068269 | 1.2828619 | 1.6038342 | 2.2052253 | 1 |
| 1165 | 2.3746928 | 2.1966123 | 1.8460204 | 1.4918971 | 2.2998912 | 1.4141358 | 1.7771071 |
| 1166 | 2.7432128 | 1.6428786 | 2.9076871 | 2.066977 | 1.9518912 | 1.8326561 | 1 |
| 1167 | 4.4428323 | 3.4189721 | 1.8849563 | 1.6566173 | 2.979518 | 2.1312588 | 1 |
| 1168 | 3.9659203 | 2.0250909 | 1.2993455 | 1.2071943 | 1 | 2.2778056 | 1 |
| 1169 | 0.032016 | 0.0152808 | 0.8786868 | 0.4070116 | 0.271805 | 0.0139598 | 0.0157203 |
| 1170 | 0.4092038 | 0.5289817 | 0.4007112 | 1 | 0.8312942 | 1.1254739 | 1 |
| 1171 | 1 | 0.5369708 | 0.8144686 | 0.6233337 | 1 | 0.6414116 | 1 |
| 1172 | 0.1597552 | 0.1821572 | 0.1029691 | 0.2740125 | 0.1477614 | 0.0975551 | 1 |
| 1173 | 2.1651578 | 2.0358724 | 1.4488904 | 1 | 1.8177135 | 1 | 1 |
| 1174 | 2.2404035 | 3.8239748 | 3.1357627 | 2.6597107 | 1.3806192 | 2.7178503 | 1 |
| 1175 | 0.1360997 | 0.0731395 | 0.0450175 | 0.0841455 | 3.5984011 | 0.0466654 | 0.1279888 |
| 1176 | 0.6499827 | 0.4309763 | 0.4631023 | 0.8021949 | 2.1696839 | 0.5072759 | 1.9530495 |

Table 4

| SEQ ID NO | Patient ID | | | | | | |
|--------------|------------|-----------|-----------|-----------|-----------|-----------|-----------|
| | 888 | 889 | 890 | 891 | 892 | 893 | 989 |
| 1177 | 0.6897383 | 0.4481714 | 0.4672665 | 0.8196931 | 2.1895024 | 0.517393 | 1.8855606 |
| 1178 | 1 | 0.2774397 | 1 | 1 | 1.3788036 | 0.6465643 | 3.127659 |
| 1179 | 3.7463313 | 2.3518296 | 1.1705908 | 1.7043205 | 1.7672221 | 2.2645133 | 0.6815334 |
| 1180 | 2.6942514 | 2.1897209 | 2.027335 | 1.5403242 | 2.1692459 | 1.8069535 | 1.2292881 |
| 1181 | 2.5642742 | 2.9554255 | 2.2905968 | 1.7416077 | 2.2862322 | 2.2517641 | 1.2726357 |
| 1182 | 4.3735856 | 2.9275044 | 2.3614287 | 0.8244209 | 1.3886173 | 2.3635237 | 1.6906395 |
| 1183 | 3.0945475 | 2.3168136 | 1 | 1 | 2.1939723 | 1.8576701 | 1 |
| 1184 | 3.142923 | 3.2814828 | 1 | 1 | 2.9478479 | 1.7156072 | 1 |
| 1185 | 2.4574323 | 1.7957418 | 2.3114178 | 1.4575292 | 1.6194635 | 1.6148891 | 1 |
| 1186 | 5.2798059 | 2.4322741 | 1 | 1.7194691 | 1.8616127 | 1.5150258 | 1 |
| 1187 | 3.8765115 | 2.7837648 | 2.082097 | 1.2652308 | 2.0137965 | 1.741175 | 1.2679398 |
| 1188 | 1.3746362 | 2.4786487 | 2.7514586 | 1.5301103 | 1 | 1.3989029 | 1.1469473 |
| 1189 | 1 | 0.4818801 | 1 | 1 | 1 | 0.7618238 | 1.0471249 |
| 1190 | 0.4456034 | 0.7032047 | 1 | 0.5916907 | 1 | 0.7630276 | 0.2816385 |
| 1191 | 1.2758604 | 1.5922289 | 1.8970372 | 1 | 0.8395746 | 1.9479808 | 0.6524136 |
| 1192 | 0.1801782 | 0.1858069 | 0.0919611 | 0.0974172 | 0.520149 | 0.3562229 | 0.3980155 |
| 1193 | 1 | 0.5074377 | 0.7924451 | 0.627717 | 1 | 0.6696909 | 1 |
| 1194 | 0.508643 | 0.5367984 | 0.3668648 | 0.4049621 | 0.675945 | 0.5113423 | 1 |
| 1195 | 3.8715895 | 2.5374392 | 1.6461499 | 1.6922303 | 2.1510458 | 1.8981824 | 1 |
| 1196 | 0.7546313 | 0.368387 | 0.4304195 | 0.5331914 | 1.0676251 | 0.596329 | 0.8008292 |
| 1197 | 0.5161857 | 0.6402238 | 0.3458856 | 1 | 0.4983769 | 1 | 0.4469056 |
| 1198 | 0.6401937 | 0.3822734 | 0.5294856 | 0.5914528 | 0.8598446 | 0.6188295 | 0.7251489 |
| 1199 | 0.1292881 | 0.1668265 | 0.0599936 | 0.0638021 | 1.4513804 | 0.0371152 | 0.0674027 |
| 1200 | 1 | 0.4534091 | 0.6230181 | 0.6216873 | 1.2461661 | 0.635534 | 1 |
| 1201 | 3.9319973 | 2.4552844 | 1.5499503 | 1.3320882 | 1.2634789 | 2.2270718 | 1 |
| 1202 | 1.5555088 | 2.8812763 | 1.7222793 | 1.4760232 | 1.0338678 | 1.4650787 | 1 |
| 1203 | 0.3980381 | 0.22925 | 0.1731735 | 0.1652148 | 0.14384 | 0.4129699 | 0.3963185 |
| 1204 | 2.8176528 | 3.9374918 | 2.7299391 | 1.7574732 | 1 | 2.562218 | 2.9337074 |
| 1205 | 2.285234 | 1 | 1.3138335 | 1 | 1 | 1.534713 | 1 |
| 1206 | 2.8854656 | 3.5419385 | 2.5705259 | 1.8924714 | 1.4595443 | 2.3983031 | 1.9624974 |
| 1207 | 4.1539332 | 2.6726171 | 1.6682687 | 1.7811917 | 2.1577402 | 1.9182332 | 1 |
| 1208 | 5.7605741 | 4.5157491 | 1 | 0.3981842 | 4.9497006 | 4.9975526 | 0.1744167 |
| 1209 | 1.7324379 | 1 | 1.1591668 | 1.4924648 | 1 | 1.7754105 | 1 |
| 1210 | 1.0986227 | 1.9900547 | 1.1807143 | 2.0982408 | 1.3405771 | 2.0890529 | 1.6394107 |
| 1211 | 5.3681073 | 3.4179968 | 1.8959678 | 2.0899808 | 1.7591943 | 1.8935512 | 1 |
| 1212 | 1 | 0.466932 | 0.7634298 | 0.6873826 | 1.2932549 | 0.654904 | 1 |
| 1213 | 4.9047192 | 2.0616193 | 0.5510786 | 1.9789244 | 1.7003481 | 2.4861976 | 1 |
| 1214 | 3.2582247 | 2.0740501 | 1 | 2.0264026 | 2.3888024 | 2.1943142 | 0.5796367 |
| 1215 | 1 | 0.523962 | 0.8555244 | 0.6292441 | 1 | 0.6510453 | 1 |
| 1216 | 5.4496555 | 2.2868189 | 0.5689945 | 2.013287 | 1.6130221 | 2.5598034 | 1 |
| 1217 | 2.5570347 | 1 | 1 | 1 | 2.4141581 | 1.9252008 | 1 |
| 1218 | 1.6250318 | 2.5842311 | 2.248351 | 0.6494068 | 3.0556227 | 1 | 3.0010639 |
| 1219 | 0.1732976 | 0.1067804 | 0.0829383 | 0.1721045 | 0.5543593 | 0.2345547 | 0.0391149 |
| 1220 | 2.5194282 | 1 | 3.0544757 | 1.2588248 | 1.6084351 | 2.8305433 | 0.6635341 |
| 1221 | 2.588436 | 2.2048988 | 2.8243408 | 1.6641527 | 2.0339332 | 2.22464 | 1.2300111 |
| 1222 | 0.1176218 | 0.0825109 | 0.0300034 | 0.0719069 | 4.6084944 | 0.0144217 | 0.0882524 |
| 1223 | 1 | 1.9357206 | 5.2708689 | 7.0370739 | 3.3372884 | 1.506971 | 3.3867545 |
| 1224 | 2.1194578 | 2.1130037 | 1.6620859 | 1 | 1.3152691 | 1.7255062 | 0.5945874 |
| 1225 | 4.4793809 | 2.5383351 | 1 | 1.436418 | 2.7687378 | 3.2129059 | 1 |

Table 4

| SEQ ID | Patient ID | | | | | | |
|--------|------------|-----------|-----------|-----------|-----------|-----------|-----------|
| | 888 | 889 | 890 | 891 | 892 | 893 | 989 |
| 1226 | 0.0584969 | 0.0963024 | 0.0463612 | 1 | 0.2238834 | 0.0560895 | 0.0439884 |
| 1227 | 0.632247 | 0.2364337 | 0.1883431 | 0.2574255 | 0.7055604 | 0.4057526 | 0.8260579 |
| 1228 | 2.7353383 | 1 | 0.6301218 | 1.1315161 | 2.3674457 | 1.8303921 | 1 |
| 1229 | 2.5003531 | 1.7606898 | 1 | 1 | 1.2348894 | 1.9541117 | 1 |
| 1230 | 4.3084927 | 1 | 2.3866386 | 1.8389936 | 1.765166 | 2.5893901 | 1 |
| 1231 | 1.8416395 | 2.2642035 | 1.7723582 | 1.2403822 | 1.2671039 | 1.5334135 | 1 |
| 1232 | 0.6622356 | 0.4134693 | 0.2783795 | 0.2204131 | 0.7511971 | 0.4248074 | 0.2869926 |
| 1233 | 2.7964636 | 2.2797123 | 1.5810805 | 1.4717776 | 1 | 2.1841689 | 1 |
| 1234 | 8.1662129 | 8.833955 | 4.3210352 | 9.8164882 | 1.4808633 | 6.3702437 | 2.3257598 |
| 1235 | 1.5730288 | 2.4028452 | 1.4013394 | 2.2712213 | 0.7431967 | 7.9922857 | 1 |
| 1236 | 0.4351429 | 0.5571629 | 0.256703 | 0.4690354 | 0.657095 | 0.3103087 | 0.2479974 |
| 1237 | 1.7999315 | 3.2735634 | 1.5418763 | 1.1401398 | 1 | 2.0161144 | 1 |
| 1238 | 0.5998749 | 0.3983969 | 0.4269477 | 0.715335 | 0.7624604 | 1.3751492 | 0.652361 |
| 1239 | 3.6355583 | 2.0405531 | 1 | 1.5957062 | 1.7004378 | 1 | 1.4886541 |
| 1240 | 3.2767818 | 2.7685418 | 1 | 1 | 1.829109 | 2.1704979 | 1.8332678 |
| 1241 | 5.5353938 | 2.0474105 | 1 | 1.4790532 | 1 | 1.9300454 | 1 |
| 1242 | 3.7517089 | 1.9429926 | 1 | 1 | 1 | 1 | 1 |
| 1243 | 3.5992256 | 2.0065515 | 1.9345811 | 1 | 1.5724084 | 1.7083691 | 1 |
| 1244 | 4.4671314 | 1.9612267 | 1.7383417 | 1 | 1.4456695 | 1.702658 | 1 |
| 1245 | 2.7752538 | 1.8031735 | 1 | 1 | 1 | 1.8592595 | 1 |
| 1246 | 4.0432229 | 3.1734231 | 1 | 1 | 1 | 2.2128602 | 2.6327213 |
| 1247 | 2.5100265 | 1.6235851 | 1 | 1 | 1.4285975 | 1.9184026 | 1 |
| 1248 | 1.8600634 | 1.8992583 | 2.3660345 | 1.5227846 | 3.3501195 | 1.918459 | 1 |
| 1249 | 2.7442003 | 2.0458956 | 1 | 1 | 1 | 1 | 1 |
| 1250 | 1 | 0.5212003 | 0.7595041 | 0.6374815 | 1 | 0.6474247 | 1 |
| 1251 | 0.8467433 | 0.4201802 | 0.4067664 | 0.77419 | 1.9529258 | 0.5025366 | 1.6526786 |
| 1252 | 0.7552793 | 0.4281198 | 0.5942065 | 0.4566886 | 0.7169435 | 0.4756778 | 0.5854332 |
| 1253 | 2.095426 | 2.3189809 | 1 | 1.6920681 | 1.8655716 | 1 | 1.7918341 |
| 1254 | 2.8304687 | 1.8271419 | 1 | 1 | 1.8996479 | 1.7729963 | 1.7130833 |
| 1255 | 2.9641916 | 1.9774102 | 1 | 1 | 1.9734873 | 1.1675605 | 1 |
| 1256 | 2.9959362 | 1.6935788 | 1 | 1 | 1.8181491 | 1.2339695 | 1 |
| 1257 | 0.5145337 | 0.5011867 | 0.5185509 | 0.5894482 | 0.8193471 | 1 | 0.6026431 |
| 1258 | 1.6575089 | 3.4121565 | 1 | 2.0948171 | 1.455722 | 1.883322 | 1.7499315 |
| 1259 | 0.7293494 | 0.4605339 | 0.4361608 | 0.3912887 | 0.5788206 | 0.5264809 | 1.2087573 |
| 1260 | 1 | 0.4252581 | 0.6388918 | 1 | 1 | 0.6829861 | 1.6082414 |
| 1261 | 1 | 0.4894754 | 0.7527438 | 0.6180793 | 1 | 0.6566388 | 1 |
| 1262 | 3.4516061 | 2.6795902 | 1 | 1 | 2.5745044 | 1 | 1.6053255 |
| 1263 | 1.2118688 | 3.4366235 | 4.1339513 | 2.4961997 | 0.8235803 | 1.1173721 | 2.5823895 |
| 1264 | 0.4321621 | 0.6195073 | 0.6117739 | 0.4462886 | 1.4941432 | 0.5710726 | 0.7782576 |
| 1265 | 0.7253417 | 0.7141865 | 0.4880441 | 0.4214365 | 1 | 0.7174955 | 1 |
| 1266 | 0.5580542 | 0.5938732 | 0.608539 | 0.4952863 | 1.4149295 | 0.5962745 | 0.8633083 |
| 1267 | 1 | 2.1733041 | 1 | 1 | 1.6047323 | 3.1965224 | 1 |
| 1268 | 1 | 3.442383 | 4.5506259 | 3.2718595 | 0.8284212 | 1.3113097 | 2.5430836 |
| 1269 | 8.2479413 | 2.3283692 | 1.7088755 | 2.7154559 | 3.2802437 | 6.71955 | 2.7602685 |
| 1270 | 3.7989168 | 1.6503461 | 2.4283844 | 1.2884566 | 1.6933152 | 2.1042921 | 1.5236779 |
| 1271 | 18.428267 | 11.173566 | 8.2137561 | 6.647524 | 2.4278385 | 1.7164203 | 4.1287995 |
| 1272 | 0.8586412 | 0.4624179 | 0.4783181 | 0.7487249 | 1.6360851 | 0.5821486 | 2.1361651 |
| 1273 | 1.7738592 | 3.5825348 | 3.0410442 | 1.9441615 | 1.8405432 | 2.0224313 | 1.756698 |
| 1274 | 0.1531062 | 4.3404411 | 0.2911325 | 0.2482038 | 1 | 0.2036285 | 0.6864199 |

Table 4

| SEQ ID NO | Patient ID | | | | | | |
|--------------|------------|-----------|-----------|-----------|-----------|-----------|-----------|
| | 888 | 889 | 890 | 891 | 892 | 893 | 989 |
| 1275 | 1.7898242 | 1 | 0.5807433 | 0.4684722 | 1.3015694 | 1 | 1.1446204 |
| 1276 | 0.5738675 | 0.4625578 | 0.366378 | 1 | 1 | 1 | 1.8273852 |
| 1277 | 3.8082477 | 2.6387728 | 1.7657184 | 1.3212207 | 2.0686146 | 1.6778123 | 0.7159721 |
| 1278 | 3.9313214 | 1.7183939 | 1 | 1.2304609 | 1.3984807 | 2.3457496 | 1.1866214 |
| 1279 | 7.6174467 | 3.2783404 | 1 | 1 | 2.1327253 | 2.4079587 | 2.7735858 |
| 1280 | 2.0815983 | 1.3254923 | 1 | 1.2160929 | 0.806007 | 0.4266535 | 1 |
| 1281 | 2.5993952 | 2.6888105 | 1.450026 | 1.0589541 | 2.7766067 | 1.7566575 | 1.5135257 |
| 1282 | 4.3198865 | 3.9392179 | 2.7525845 | 1 | 2.2588411 | 1.739224 | 2.6371285 |
| 1283 | 1 | 0.4975481 | 0.7596367 | 0.57878 | 1 | 0.6259477 | 1 |
| 1284 | 4.1115519 | 2.2764638 | 1 | 1.6825124 | 2.3835043 | 1.8869197 | 1.3561558 |
| 1285 | 3.1822834 | 1.9746944 | 1.9208215 | 1 | 2.1373204 | 2.8201356 | 1 |
| 1286 | 1.6764022 | 1.6562394 | 1 | 1.4999788 | 1 | 1.9830593 | 1 |
| 1287 | 1.5999636 | 1.9209792 | 3.2423858 | 1.9900231 | 1.6179803 | 1.6193014 | 1.7436178 |
| 1288 | 1.8659062 | 2.2971953 | 1.6182856 | 2.2031201 | 1 | 1.3974037 | 1 |
| 1289 | 3.7044593 | 1 | 1 | 2.3015744 | 2.2559565 | 1.9264524 | 1.7397415 |
| 1290 | 1 | 2.2396563 | 1 | 2.5255741 | 1 | 2.03119 | 1.9497846 |
| 1291 | 3.9911831 | 1.9433077 | 1 | 2.147702 | 2.4486291 | 2.3816562 | 1 |
| 1292 | 0.1408241 | 0.1284479 | 0.0878548 | 0.056648 | 3.6349146 | 0.0346367 | 0.3653658 |
| 1293 | 0.6903473 | 0.6340073 | 0.7171017 | 0.6364415 | 1.1709965 | 0.6234276 | 1 |
| 1294 | 2.1495892 | 3.1989822 | 1.5186186 | 1.2762535 | 1.6801008 | 1.5799785 | 1.3003023 |
| 1295 | 0.7048637 | 0.6177665 | 0.7497845 | 0.6054915 | 1.2462263 | 0.5854999 | 1 |
| 1296 | 1 | 1 | 0.2692804 | 0.3511363 | 0.7372906 | 0.3685432 | 0.2734408 |
| 1297 | 0.2572459 | 1 | 0.3194128 | 0.7560038 | 1 | 0.4519106 | 0.5561362 |
| 1298 | 1 | 1 | 1.5179644 | 1 | 1 | 1 | 1 |
| 1299 | 1 | 1 | 1 | 2.1690781 | 1 | 0.6252273 | 1.3990499 |
| 1300 | 0.7556162 | 0.4985626 | 0.729883 | 0.6705921 | 1 | 0.5892786 | 1 |
| 1301 | 0.8852216 | 2.106441 | 1 | 1.5130606 | 1 | 1.3318299 | 1 |
| 1302 | 0.4889279 | 1 | 0.6818433 | 0.2377617 | 1 | 0.5416417 | 0.4307848 |
| 1303 | 0.2267066 | 1 | 0.4667478 | 0.6182308 | 0.5572727 | 1 | 0.2768187 |